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is derived by analysis of the total score distribution.
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ALIGNMENTS

R;Kokubo, T.; Gong, D.W.; Roeder, R.G.; Horikoshi, M.; Nakatani, Y. Proc. Natl. Acad. Sci. U.S.A. 90, 5896-5900, 1993
A;Title: The Drosophila 110-kDa transcription factor TFIID subunit directly interacts A;Reference number: A48184; MUID:93317591; PMID:8327460
A;Accession: A48184 RESULT 1 A48184 A;Cross-references: GB:S63550; NID:g398432; PID:g398433 A;Experimental source: embryo nuclear extract A;Note: sequence extracted from NCBI backbone (NCBIN:13 transcription initiation factor IID 110K chain - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999 Ş 밁 δÃ 밁 δÃ Ър Q 밁 ş 밁 Q A; Cross-references: FlyBase: FBgn0010280 C; Keywords: transcription initiation A; Gene: FlyBase: Taf110 C; Genetics: A; Molecule type: mRNA; J A; Residues: 1-921 <KOK> A; Status: preliminary C; Accession: A48184 Matches Query Match 346 133 330 LNPLAGPYGAKAGYYTLHSYGPTAA 277 247 288 188 244 128 185 77 25 Local TMLENVK-KCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELK ASPQPCLIGFLKKSLPLLRQALYTKELVIEGIKPPPQHVLGLAGLSQQLPKIQAQIRPIG SSPQPHLVPFLKKSVVALRQL-----TQQGNTKEKCRKFLANLIEL--STREPKPVEKNVRTLIQELVNANVEPEEFCDRLERLLN 345 APQLPQITQIQTIPAQQSQQQQVNNVSSAGGTATAVSSTTA----KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSP 187 NTTSTTNHPTTTQ-IRLQTVPAAASMTNTTATSNIIVNSVASSGYANSSQPPHLTQLNAQ NITSRPAVPANPQTVKICTVPNSSSQ------LIKKVAVTPVKKLAQIGTTVVTTVP PQSPSITLSTLNTGQTPA------LLVKTDNGFQLLRVGTTTGPPTVTQTITNTSNNS PQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLML-----VSPQQTVTRAETTS 76 PSQTTTIGQTQVRMI--TPNALGTPRPTIGHTTISKQPPN---IRLPTAPRLVNTGGIRT 1 Similarity 24.9 96; Conservative -QCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVS----VQT protein 12.28; 58; Score 216; DB 2; Pred. No. 4.7e-06; 8; Mismatches 141 (NCBIN:134863, Length 921; ---LPNSQSFIQ-------ATT NCBIP: 134864) 90; Gaps 243 405 276 246 287 14;

В

461

QIP-SLQVPGQANIVQIR--GPQHA

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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1275 <GET>
A;Residues: 1-1275 <GET>
A;Cross-references: EMBL:AF077538; PIDN:AAC64622.1; GSPDB:GN00028; CESP:H02F09.3
                                                                                                                               C;ACCession. Fig. 1998
R;Gelsel, C.; Harmon, G.
Submitted to the EMBL Data Library, July 1998
Submitted to the EMBL Data Library, July 1998
Submitted to the EMBL Data Library, July 1998
                                                                                                                                                                                            C; Species: Caenorhal
C; Date: 29-Oct-1999
C; Accession: T33369
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A; Accession: A45183
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: nucleic acid
A; Residues: 1-921 <HOE>
A; Note: sequence extracted from NCBI backbone (NCBIP:123832)
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                                                                                       A; Status: preliminary; translated
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                                                                                                                                                                                                                 hypothetical protein H02F09.3 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #te
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A;Reference number: A56088; MUID:95181425; PMID:7876203 A;Accession: A56088
                                                                                                                                         R;Kristie, T.M.; Pomerantz, J.L.; To
J. Biol. Chem. 270, 4387-4394, 1995
A;Title: The cellular Cl factor of 1
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                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; not compared with conceptual A;Molecule type: mRNA; protein A;Residues: 1-2035 <WILD A;Cross-references: PIDN:AAB27583.1; PID:9399752 A;Experimental source: HeLa cell
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A;Introns: 42/1; 78/3; 106/3; 135/2; 161/2; 224/1
C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosida
                                                                                                                                                                                  A;Cross-references: EMBL:U52112; NID:g1302657; PIDN:AAC51751.1; PID:g1302663 R;KT1stle, T.M.; Pomerantz, J.L.; Twomey, T.C.; Parent, S.A.; Sharp, P.A.
                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-2035 < PLA>
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A; Title: The VP16 accessory protein HCF is a family of A; Reference number: A40718; MUID:93327419; PMID:8392914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change
C;Accession: A40718; G02511; A56088; I37453
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                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: sequence extracted from NCBI backbone (NCBIP:135349)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Homo sapiens (man)
Residues: 1-664,'T',666-1637,'E',1639-1684,'A',1686-1734,'Q',1736-2035 Frattini, A.; Faranda, S.; Redolfi, E.; Zucchi, I.; Villa, A.; Patrosso
                                                Molecule type: mRNA
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                                                                   Status: preliminary; not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TLVTKVAPVSAPPKVSSGP----RLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSN- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVTVPTTVPTTVTNPSTVVTAPSTV--VTVPTTVMTSRSTVITTPTTGGSSPSTAGTSLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLAQIGTTVV----TTVPKPSSVQSVAVPTSVVT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVTAPSTVVTVPSTVVTKPNTV--VTSSPTVATTPTTV--VTTPST------VVTVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVTVPTTTTVTGPTTVVTVPTTVVTIPSTVVTSPITTPSTVVTVPSTVVTVPSTAVTKPST 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSTYIPVSSASSIYSTLSGSTGSTA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSTATAGTSPQASTVTTVTDISTVSGSTVTSQTAESSLSTESPTSAGSSI-STVSTVSSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PATQQSTKPTIGTSMSSGPTTVAPGASTESTVLQSSTPSGTTV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEMGQNVKKLVEQLLDA--KIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVTTETSIGSSSTP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTLKPSSLGASSTPSNEPNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LaMarco, K.; Peterson, M.G.; Herr, W.
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Pred. No. 0.0011;
2; Mismatches 19
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Patrosso,

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Genomics 23, 23-35, A;Title: Genomic organic organic A;Reference number: A;Accession: I37453
                                                                         A; Nedecule type: mRNA
A; Nelecule type: mRNA
A; Residues: 1-528 <TUR>
A; Residues: 1-528 <TUR>
A; Cross-references: EMBL:U10281; NID:g915205; PIDN:AAC48526.1; PIT
R; Turner, B.S.; Bhaskar, K.R.; Hadzopoulou-Cladaras, M.; Specian,
R; Turner, B.S.; Bhaskar, K.R.; Hadzopoulou-Cladaras, M.; Specian,
Biochem. J. 308, 89-96, 1995
                                                                                                                                                                                                                                                     147141

gastric mucin (clone PGM-2A) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Peb-1997 #sequence_revision 21-Feb-1997 #text_change 03-Nov-2000
C;Accession: 147141; S55315
R;Turner, B.S.; Bhaskar, K.R.; Hadzopoulou-Cladaras, M.; Specian, R.D.; LaMont, Gastroenterology 106, 200, 1994
A;Title: Pig gastric mucin: isolation and characterization of a cDNA clone with A;Reference number: 147141; MUID:94102478; PMID:7506218
A;Accession: 147141
A; Status:
A; Molecule
                                            Biochem. J. 308, 89-96, 1995
A;Title: Isolation and characterization of
A;Reference number: S55315; MUID:95275264;
A;Accession: S55315
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A;Map position: Xq28-Xq28
A;Introns: 65/1; 114/3; 1
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A;Residues: 100-563,'R',565-603,'VS',604-1163,'P',1165-1872,'A',1874-2035 -
A;Cross-references: EMBL:X79198; NID:g558348; PIDN:CAA55790.1; PID:g558349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene:
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                        preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLVSPQQTV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDMVIATCTTTVTTSPVVTTTVSSSQS-----EKSIIVSGATAPRTVSVQTLNP 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKIEAEEFTRKL-YVELKSSP-QP----HLVPFLKKSVVALRQLLPNSQSFIQQCVQQTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIIKTIPMSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAP-----AKIITAV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKIATGHGQQGVTQVVLKGAPGQPGTILRTVP----MGGVRLVTPVTVSAVKPAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TQIIQTKGPLPAGTILKLVTSADGKPTTIITTTQASGAGTKPTILGISSVSPSTTKPGTT 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRAETTSNITSRPAVPANPQT------VKICTVPNSSSQ---LIKKVAVTPVKKL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGSSPQMSGMAALAAAAAATQKIPPSSA---PTVLSVPAGTTIVKT-----MAVTPGTTT 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -TTLVVKGTTGVTTLGTVTGTVSTSLAGAGGHSTSASLATPITTLGTIA--TLSSQVINP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQVVTTVVGGVTKTITLVKSPISVPGGSALISNLGKVMSVVQTKPVQTSAVTGQASTGPV 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.9%; Score 176; DB 2; llarity 24.2%; Pred. No. 0.0045; Conservative 57; Mismatches 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDB:388714; OMIM:600196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168/2; 238/1; 266/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --VVTVTPGKPLNTVTT-----LKPSSLGASST-----PSNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359
                                                                    cDNA clones encoding pig gastric mucin. PMID:7755593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VP16 accessory protein (HCF), a housekeeping PMID:7829076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302/1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2035;
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                                                                                                                                    PID:g915208
an, R.D.; La
                                                                                                                                                                                                                                                                                                      cDNA clone with a
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                                                                                                                                       LaMont,
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A; Residues: 626-1895 < GU2>
A; Cross-references: GB:M94131; NID:g186395; PIDN:AAA59163.1;
A; Note: sequence extracted from NCBI backbone (NCBIP:116706)
A; Accession: B45106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 10-Mar-1993 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C;Accession: A49963; A45106; B45106; A43932; B35532; A61257; PQ0328; PQ0329
R;Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Siddiki, B.; Kim, Y.S.
J. Biol. Chem. 269, 2440-2446, 1994
A;Title: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identifice A;Reference number: A49963; MUID:94132002; PMID:8300571
A;Accession: A49963
A;Cross-references: GB:M94132; NID:g186397; PIDN:AAA59164.1; A;Experimental source: colon A;Note: sequence extracted from NCBI backbone (NCBIP:116698) R;Toribara, N.W.; Gum Jr., J.R.; Culhane, P.J.; Lagace, R.E. J. Ciln. Invest. 88, 1005-1013, 1991 A;Title: MUC-2 human small intestinal mucin gene structure. A;Reference number: A43932; MUID:91358717; PMID:1885763
                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:L21998
R;Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.;
J. Biol. Chem. 267, 21375-21383, 1992
A;Title: The human MUC2 intestinal mucin has
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A;Cross-references: GB:U10281; NID:g915205; PIDN:AAC48526.1; PID:g915208
C;Superfamily: pig submaxillary mucin
                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A45106; MUID:93016075; A; Accession: A45106
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                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 2037-3020 <GU3>
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23.3%;
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A;Molecule type: DNA
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1343-1350,'L',1352-1411,'S',1413-1448,'P',1450-1503,'T',1505-1915
A;Cross-references: GB:M74027; NID:9188863; PIDN:AAA59975.1; PID:9188864
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:55749, NCBIP:55750)
R;Gum, J.R.; Byrd, CC; Hicks, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.
J. Biol. Chem. 264, 6480, 6487, 1989
A;Title: Molecular cloning of human intestinal mucin cDNAs. Sequence analysis
A;Reference number: A33532; MUID:89197956; PMID:2703501
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C;Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology;
C;Keywords: glycoprotein; intestine; tandem repeat
F;2766-2834/Domain: von Willebrand factor type C repeat homology <VWC>
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A; Residues: 3328-2342,'K',2344-2354 <XUG1>
C; GenetLcs:
A; Gene: GDB: MUC2
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A;Title: Human intestinal mucin-like protein (MLP) is homologous with rat MLP A;Reference number: PQ0328; MUID:92198477; PMID:1550588
A;Accession: PQ0328
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A; Molecule type: mRNA
A; Residues: 1916-2193 <GU4>
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A; Cross-references: GB: M86523
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A; Residues: 2328-2468 < XUG>
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IIVSGATAPRTVS-VQTLNPLAGPVGAK---
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                                                                                              VVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTV-----SSSQSEKS
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11p15.5-11p15.5
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22.0%; Pred. No. 0.021;
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R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Accession: C87719
                                                                           A; Map position:
A; Introns: 48/1;
C; Superfamily: E
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
T29634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein R119.6 [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 10-May-2001 #sequence_revision 10-May-2001
                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-825 < NHA>
                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, March A; Description: The sequence of C. elegans A; Reference number: Z20656
                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein C12D12.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te
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A; Residues: 1-549
                                                                                                                                    A; Gene: CESP:C12D12.1
                                                                                                                                                                       A; Experimental source:
                                                                                                                                                                                                                                            A; Status: preliminary; translated
                                                                                                                                                                                                                                                                  A; Accession: T29634
                                                                                                                                                                                                                                                                                                                                       R; Nhan, M.; Hawkins,
                                                                                                                                                                                                                                                                                                                                                            C; Accession:
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Best Local :
     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158 PSSLGASSTPSNEPNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEM-
                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --GQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSF 274
                                                                         48/1; 86/3; 137/1; 172/3; 224/3; 253/1; 287/3;
11y: Epstein-Barr virus membrane antigen gp350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63; Conserv
                       Similarity
                                                                                                                                                                                                                                                                                                                                                            T29634
     Conservative
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                                                                                                                                                                     EMBL:U51998; PIDN:AAA96080.1; GSPDB:GN00028; CESP:C12D12.1
se: strain Bristol N2; clone C12D12
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                   9.4%;
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                     Score
Pred.
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     Mismatches
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                   166.5;
No. 0.(
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                                      Length
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137;
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                                                                                          487/3;
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 16;
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VTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPAN-LQLPPGTVLIKSNSGPLML 62

	Qy 222 KLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ 281 : : : : : : : : : : : : :	,o
	QY 163 ASSTESNE-ENIKAENSAAVQINISPTMLENVKKCKNELAMLIKLACSGSQSPEMGQNVK 221 : : : : : : : : ::::::::::::::::::	<u> </u>
	110 TPVKKLAQI 1676 PSCKKAAAT	<u> </u>
* * * *	Qy 61 MLVSPQQTVTRAETTSNITSR-PAVPANPQTVKICTVPNSSSQLIKKVAV 109 : - - - - - - - - - - - - -	<u> </u>
	QY 2 TLVTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTT-IQFPANLQLPPGTVLIKSNSGPL 60	B 8
	Query Match 9.3%; Score 165.5; DB 2; Length 2187; Best Local Similarity 22.7%; Pred. No. 0.023; Matches 90; Conservative 64; Mismatches 134; Indels 109; Gaps 20;	
	A;Gene: Naca .;Map position: 10 A;Introns: 24/1; 1996/1; 2024/3; 2050/3; 2099/3; 2142/3; 2183/3 A;Note: differential splicing converts alphaNAC into a tissue-specific DNA-binding activa;Note: differential splicing; DNA binding; transcription factor	02222
	x.MOLECULE TYPE: DNA %;Residues: 1-2187 <yot> %;CenetLos: ;GenetLos:</yot>	0 > > >
	Accession: T308 Status: prelimi	> >
icle	7; St-Arnaud, R. 0, 1763-1772, 1996 ferential splicing-in of a proline-rich exon converts alphaNAC into a mus number: 220889; MUID:96312450; PMID:8698236	*
	s: Mus musculus (hous 22-Oct-1999 #sequence 1on: T30826	രര
	RESULT 9 T30826 nascent polypeptide-associated complex alpha chain, muscle splice form gp220 - mouse N;Alternate names: alpha-NAC protein	× 2 1 2
		<u> </u>
	307 SSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTT 359	οy
	696 PTAPANLTTPTTAPVNPTSSTTAPTAPVNPTSPTTAPTVPP	<u> </u>
	O// O// DEPARTMENT OF THE PROPERTY OF THE PROP	2 5
	206 LACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALR 2	2 0
	VVPSSATVPTTPPTTVTVAATTTSKAPVVTTS	므
	QY 154TTLKPSSLGASSTPSNEPNLKA-ENSAAVQINLSPTMLENVKKCKNFLAMLIK 205	,O
	QY 119 GTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTV- 153	<u> </u>
	ISPHLSTITGSIVTSTPTMAPQTSA	₽
		,O
	Db 472 VTTVSTMS-PPTTVTVPTTPTPVPTTTNTP-PANPTTATPTTVGTSKQTNT 520	<u> </u>

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glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae)
N;Alternate names: extracellular glucoamylase; mucin-like protein MUCl; protein YIRO1
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Nov-1999
C;Accession: S48478; A26877; B26877; S27281; JC6123
R;Rowley, K.
submitted to the EMBL Data Library, October 1994
A;Reference number: S48478
A;Accession: S48478

A;Molecule type: DNA
A;Residues: 1-1367 <ROW>
A;Residues: 1-1367 <ROW>
A;Cross-references: GB:Z47047; EMBL:Z38061; NID:g603997; PID:g763364; GSPDB:GN00009;
R;Yammashita, I.; Nakamura, M.; Fukul, S.
J. Bacteriol. 169, 2142-2149, 1987
J. Bacteriol. 169, 2142-2149, 1987
A;Title: Gene fusion is a possible mechanism underlying the evolution of STA1.

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A:Gene: CBFA2/MITOB
A:Note: AML1 is a synonym for GDB:CBFA2
C:Keywords: fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Miyoshi, H.; Kozu, T.; Shimizu, K.; Enomoto, K.; Maseki, N.; Kaneko, Y.; Kamada, N. EMBO J. 12, 2715-2721, 1993
A;Title: The t(8;21) translocation in acute myeloid leukemia results in production of A;Reference number: A57784; MUID:93327761; PMID:8334990
A;Accession: A57784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-752 <MIY>
A;Residues: 1-752 <MIY>
A;Cross-references: GB:D13979; NID:g407726; PIDN:BAA03089.1; PID:g407727
A;Cross-references: GB:D13979; NID:g407726; PIDN:BAA03089.1; PID:g407727
C;Comment: This sequence is the chimeric product of a translocation mutation.
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C;Species: Homo sapiens (man)
C;Date: 15-Feb-1996 #sequence_revision 15-Feb-1996 #text_change 08-Dec-2000
C;Accession: A57784
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     372
                                                                                                                                                                                                                                                                                                                                                       121 TVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSL-GASSTP---SNEPNLKAE 176
                                                                                                                                                                                                                                                                                                                                                                                                                     152 VFTNPPQVATYHRAIKITVDGPREPRN-RTEKHSTMPDSPVDVKTQSRLTP------
                                                        292
                                                                                                                                                                                                        255 SSLANQ-QLPPACGARQLSKLKRFLTTLQQF--GNDISPEIGERVRTLVLGLVNSTLTIE 311
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                                                                                                                                                                                                                                                                                                              202 ---PTMPPPPTTQG-APRTSSFTPT---TLTNGTSHSPTALNGAPSPPNGFSNGPSSSSS 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 MLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 9.3%; Score 164.5; DB Local Similarity 28.8%; Pred. No. 0.0067;
TSPVDSSELL 381
                                                   TTTVTTSPVV 301
                                                                                                      EFHSKLQEATNFPLRPFVIPFLKANLPLLQRELLHCARLAKQNPAQYLAQHEQLLLDAST 371
                                                                                                                                                                                                                                                           NSAAVQINLSPTM-LENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAE 235
                                                                                                                                                    EFTRKLYVELKSSPQPHLVPFLKKSVVAL-RQLLPNSQSFIQ---QCVQQTSSDMVIATC 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TLNPLAGPYGAKA----GVVTLHSVGPTAAT 355
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T34369
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A;Cross references: GB:U30626; NID:g1304386;
C;Genetics:
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                  hypothetical protein T19D12.1 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
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A;Title: Mucl, a mucin-like protein that is regulated by Mss10, A;Reference number: JC6123; MUID:96323237; PMID:8710886
A;Accession: JC6123
A;Status: nucleic acid sequence not shown
A;Residues: 1-1367 <LAM>
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A:Accession: A26877
A:Molecule type: DNA
A:Residues: 1-242 <YAM>
A:Residues: 1-242 <YAM>
A:Coss references: EMBL:M16164; NID:g172522; PIDN:AAA35014.1;
A:Accession: B26877
A:Molecule type: DNA
A:Residues: 762-1331 <YA2>
A:Cross-references: EMBL:M16165; NID:g172523; PIDN:AAA35015.1;
R:Pardo, J.M.; Ianez, E.; Zalacain, M.; Claros, M.G.; Jimenez, EBS Lett. 239, 179-184, 1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: SGD:MUC1; STA2; MAL5; DEX2; SGD:S0001458
A;Cross-references: MIPS:YIR019c; SGD:S0001458
A;Map position: 9R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Similar short elements in the 5' regions of the A;Reference number: $27281; MUID:89031230; PMID:3141213 A;Accession: $27281 A;Accession: $27281 A;Residues: 1-31 <PAR>
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Best Local S
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  29-Oct-1999
                                                                                                                                                                                                                                       PFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSP----VVTTTVSSSQSE
                                                                                                                                                                                                                                                                                         --APVSSSTTESSVAPVPTPSSSSNITSSAPSSIPFSSTTESFSTGTTVTPSSSK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNSGPLMLVSPQQT---VTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAV--
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                                                                                                                                  SAGETTSGCSPKTYTTTYPTTTTTSYTTSSTTTITTTYCSTGTNSAGETT
                                                                                                                                                                       KSIIVSGATAPRTV--SVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -TPVKKLAQIGTTVVTT------VPKPSSVQS-----VAVPTSVVTVTPGKPLNT-
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  #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                          -VTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSPTMLENVKKCKNFLA
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21.2%;
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                                                                                                                                                                                                               ETSVSSTTETTIVPTKTTTSVTTPSTTTITTTVCSTGTN
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#text_change
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tion; transmembrane protein
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  29-oct-1999
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                                                                                                                                             A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-798 <WIL>
                                                                                                                                                                                                                    submitted to the EMBL Data Library, June J
                                                                                                                                                                                                                                                                  hypothetical protein F31D5.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #t.C;Accession: T34248
                                                                                                                                                                                                                                                                                                                                RESULT
T34248
                                                                                                      A; Experimental C; Genetics:
                                                                                                                                                                                                         A; Reference number:
                                                                                                                                                                                                                                                       R; Wilcox,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-1777 <FAV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, Novemb
A;Description: The sequence of C. elegans
A;Reference number: 221513
A;Recession: T34369
                                                                                                                                                                                           A; Accession: T34248
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 Best Loc
Matches
                                                                                                               Cross-references: EMBL:U28941; PIDN:AAC71100.1; GSPDB:GN00020; Experimental source: strain Bristol N2; clone F31D5
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:Favello, A
                             Query Match
                                                                                      Gene: CESP:F31D5.4
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                                                         position: :
rons: 63/1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLIKKVAVTPVKKLAQIGTTVVTTVPKPSSVQ-SVAVP---TSVVTVTPGKPLNTVTTLK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSTQGVPTSTSNQPTPSTSNPTTPKSTVTASP--STTGATSTASPSTITSSAPTSQSHSP
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             Similarity
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                                                            95/2;
 Conservative
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                                                         122/3; 189/2;
          8.98;
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 6;
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            Score 158;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 158.5; DE Pred. No. 0.049;
                                                                                                                                                                             from GB/EMBL/DDB:
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Mismatches
                                                         309/2;
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cosmid T19D12.
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                                                      350/3; 364/3; 411/2;
                           DB 2; Length 798;
             .019;
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82;
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                                                                                                                                  CESP: F31D5
                                                         414/1;
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A; Introns: 62/3; 124/3; 169/1; 216/1; 262/3; 371/1; 581/3; 608/1
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A;Residues: 1-796 <WIL>
A;Coss-references: EMBL:Z48582; PIDN:CAA88469.1; GSPDB:GN00020; CESP:ZK945.10
A;Experimental source: clone F27E5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, A; Reference number: Z19425
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ATHTTDDKKVYYTYANVYIQEYSSTTIESESSTSAVASSTSSTPSTPSSTLSTSTVTEPS
                                                                                                                                                                                                                                                                                                                          LVSPQQTVTRAETTSNITSRPAVPA--NPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIG
                                                                                                                                                                             A-AVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDA-----
                                                                                                                                                                                                                                   TTVVTTVPKPSSVQSVAV-PTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENS 178
                                                                                                                                                                                                                                                                                        VTSTSSTVTTTEPTTTLTTSTASTSTTEPSTSTVTTSPSTS------PVTSTVTSS
                                                                                                                                                                                                                                                                                                                                                              TLSTSIPTTTPEITSTLSSLPDNAICSYLDETTTSTTFTTTMLTSTTTEEPSTSTTTTE
                                                                                                                                                                                                                                                                                                                                                                                                  TLVTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRENISTLMKPLHGNL----KVTWWDIGRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I--RLLKSRRRRWSTGFGIPQAETYT------PPPR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATVLAPTLKNLSDNSMAILHNLD-NMLYGIKLSRNYGRQYSRPTDRVLEWAKFGVQLQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT-----TLKPSSLGASSTPSNEPNL 173
                                                                   NSGLGIIGYQTSIECTSPTSSNYVSTTKDGACFTKSVSMPRLGGTYPASTFVGPGNYTFR
                                                                                                                                           ASSTQSSTSTQQSSTTTKSET-----TTSSDGTNPDF-YFVEKATTTFYDSTSVNLTL
                                                                                                                                                                                                                  SSSSTTVTTPTSTESTSTSPSSTVTTSTTAP--STSTTGPSS--SSSTPSSTASSSVSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QTLN----PLAGPVGAKAGVVTLHSVGPTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFYEAEPYQMNATSQTVPLSPCARQTSLPPTPVMSATVMNNGVAVSV---SATSEATMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFIQQCVQQ---TSSDMVIATCT--TTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSV 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVEQLLDAK------IEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQ 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KA-----ENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKK 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVVTTVPTTTATSTSTASTTTTTPSTSTHTTTVTYSTNATSSTTSPTTSPTPEPEPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPSSTEASSTVTSTTTARTTTMIPTTPTTTTIA----STSTVTSIVTSTTVTSTTVPTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPQQTVTRAETTSNITSRPA---VPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T21460
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                     -KIEAEEFTRKLYVE-----LKSSPQPHL------VPFLKKSVVALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.9%; Score 157; DB 2; Length 796; 20.5%; Pred. No. 0.021;
                                QSFIQQCVQQTSSDMVIATCTTTVTTSP---VVTTTVSSSQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                       64; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               March
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C; Keywords: DNA binding: transportation from the first from the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 313-1292,'ISNREQLLAPP',1304,'QSPLLL' <ADA>
A;Cross-references: GB:U08191; GB:S79520; NID:947623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-1324 <NIE>
A; Cross-references: EMBL: X80878; NID: g695578; PID: g695579
R; Adams, B.S.; Leung, K.Y.; Hanley, E.W.; Nabel, G.J.
New Biol. 3, 1063-1073, 1991
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C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 01-Dec-2000
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A;Title: Cloning of R kappa B, a novel DNA-binding protein A;Reference number: A45580; MUID:92135142; PMID:1777480
A;Accession: A45580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Nieters, A.; Bouwmeester, T.; Scheidereit, C. submitted to the EMBL Data Library, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            뭐
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A; Accession: S52863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Local Similarity 22.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 VTKVAPVSAP--PKVSSGPRLPAPQIVA---VKAPNTTTIQFPANLQLPPGTVL-----
                                                                                                                                                          AAVSKTVAVASGAASTPISISTGAPTVRQVPVSTTVVSTSQAGK--LPTRITVPLSVISQ 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KQVAITGQLGVK--PQTGNSIPLTATNFRIQGKDVLRLPPSSITTDAKGQTVLRITPDMM 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IKSNSGPLMLVSPQQ----TVTRAETTSNITSRPAV----PANPQTVKICTVPNSSSQ-LI 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRVVAQPSLPAVPQQSGGPAQTLPQMPAGPQIRVPATAT-----QTKVVPQTVMATVPVK 884
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                                                                                                                                                                                                                                                                                                                             PPKAGQTITVATHAKQGASVASGSGT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTVVKVTPDLKPTEASSSAFRLMPALGVSVADQKGKSTVASSEAKPAATIRIVQGLGVM 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATLAKSQVTTVKLTQDLFGTGGNTTGKGISATLHVTSNPVHAADSPAKASSASAPSSTPT 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQTTAATVQRPGPGQTGLTVTSLPATASPVSKPATSSPGTSAPSASTAAVIQNVTGQNII
PMKGKSVVTAPIIKGNLGA
                                                                                                                                                                                                                                     SFIQQCVQ----QTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTV---
                                                                                                                                                                                                                                                                                                                                                                                               SPEMGQNVKKLVEQLLDAKTEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---PLNTVTTLK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKVAVT---PVKKLAQIGTTVVTTVPK-----PSSVQSVAVPTSVVTVTPGK- 148
                                                                           ----SVOTLNPLAGPVGA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----EPNIKAENSAAVQINISPTMLENV--KKCKNFL-----AMLIKLACS-GSQ 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 156; DB 2
Pred. No. 0.048;
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                                                                                                                                                                                                                                                                                                                        -VHTSAVS----LPSMN 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -PSSLGASSTPSN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             that recognizes the interl
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Search completed: Job time : 21.146

February 16, 2003, 22:00:49

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OM protein - protein search, using sw model

Run on: February 16, 2003, 20:54:50; Search time 6.91863 Seconds (without alignments) 2152.161 Million cell updates/sec

BLOSUM62 Gapop 10.0 , Gapext 0.5

Title: Perfect score: Sequence: US-09-763-909-2_COPY_1_359 1773 1 GTLVTKVAPVSAPPKVSSGP......KAGVVTLHSVGPTAATGGTT 359

Scoring table:

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

140 7.9 9.5 7.9 7.5 7.8 7.7 7.7 5.5 7.6 5.5 7.6	112.2 127.7 12.2 10.0 10.0 9.4 8.8 8.8 8.8 8.3 8.3 8.3 8.3 8.3	Query Score Match
1216 1260 1002 1802 1 860 1 745 1 1858 1 1907 1	1	Length DB
YPX5_CABEL ALS1_CAML YEMA_DROME YJH8_YEAST CHI2_COCIM OCT1_PIG P3K2_DICDI VGP3_EBSV FLO5_YEAST MUC1_XEMLA	T2DT_HUMAN T2D3_HUMAN T2D3_DROME HFC1_HUMAN MT2D3_DROME HFC1_HUMAN MUC2_HUMAN MUC2_HUMAN MUC2_HUMAN MTGB_HUMAN MTGB_HUMAN MTGB_HUMAN MTGB_HUMAN MTGB_HUMAN MTGB_MOUSE CPN_DROME MTGB_MOUSE PODX_HUMAN VGLX_HUMAN	ID
·	99.750 009.268 94.7825 95.1610 95.1610 95.1610 90.817 90.02817 90.02817 90.0284 00.0284 00.0284 00.0455 93.6170 00.08799	Description
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Query Match 100.0%; Score 1773; DB 1; Length 801; Best Local Similarity 100.0%; Pred. No. 2.2e-100; Matches 359; Conservative 0; Mismatches 0; Indels 0

Indels 0;

Gaps

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1 GTLYTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPL 60

4444 30 30 30 30 30 30 30 30 30 30 30 30 30	34
128.5 127.5 127.5 127 127 127 126.5 125.5 125.5 125.5	131
77.77.22	7.4
743 3866 1574 634 1306 2700 784 1794 1794 11048 1322 1147	1036
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OCTI_HUMAN HRX_MOUSE SYJI_RAT HWPI_CANAL MSB2_YEAST ZAN_HUMAN YAVI_SCHPO P100_HCMYA YAG3_YEAST SREI_HUMAN	P200_MYCPN
P14859 homo sapien P55200 mus musculu Q62910 rattus norv P46593 candida alb P32334 saccharomyc Q9y493 homo sapien Q02446 homo sapien Q10172 schizosacch P08318 human cytom P39712 saccharomyc P36956 homo sapien	

ALIGNMENTS

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EMBL; Y09321; CAA70499.1; Genew; HGNC:11538; TAF4B. MIM; 601689; InterPro; IPR003894; TAF_hom. SMART; SM00549; TAFH; 1. Transcription regulation; Nuclear protein. NON_TER 1 1 SEQUENCE 801 AA; 85658 MW; D12B4932FE4A9CD2 CRC64;	HUMAN TADT HUMAN THOMAN TADT HUMAN TADT HUMAN TADT HUMAN 15-JUL-1998 (Rel. 36, Crea 15-JUL-1998 (Rel. 36, Last 15-JUL-1998 (Rel. 36, Last 15-JUL-1998 (Rel. 37, Last Transcription initlation f (TAFIIO5) (Fragment). TAF48 OR TAF2C2 OR TAFIIIO Homo sapiens (Human). Eukaryota; Metazoa; Chorda Mammalia; Eutheria; Primat SEQUENCE FROM N.A., AND PA MEDLINE-97011146; PubMed-8 Dikstein R., Zhou S., Tja "Human TAFII 105 is a cell THOMETION: CELL TYPE-SP OCACTION: CELL TYPE-SP NUMBER OF TBP-ASSOCIAN PROMOTER RESPONSES TO 1- SUBCELLUAR LOCATION: CELLS: TISUS SPECIFICITY: FO CELLS: TISUS SPECIFICITY: FO CELLS: TISUS SPECIFICITY: FO CELLS: TISUS SPECIFICITY: FO This SWISS-PROT entry is company to the Swiss Institu The European Bioinformatic use by non-profit institute This SWISS-PROT entry is company to the Swiss Institute This SWISS-PROT entry is company to the Swiss Institute This SWISS-PROT entry is company to the Swiss Institute The European Bioinformatic This SWISS-PROT entry is company to the Swiss Institute The European Bioinformatic This SWISS-PROT entry is company to the Swiss Institute The European Bioinformatic This SWISS-PROT entry is company to the Swiss Institute The European Bioinformatic This SWISS-PROT entry is company to the Swiss Institute The European Bioinformatic This SWISS-PROT entry is company to the Swiss Institute The European Bioinformatic This SWISS-PROT entry is company to the Swiss Institute The European Bioinformatic This SWISS-PROT entry is company to the Swiss Institute The European Bioinformatic This SWISS-PROT entry is company to the Swiss Institute The European Bioinformatic This SWISS-PROT entry is company to the Swiss Institute The European Bioinformatic This SWISS-PROT entry is company to the Swiss Institute The European Bioinformatic This SWISS-PROT entry is company to the Swiss Institute The European Bioinformatic This SWISS-PROT entry is compan	

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RA Dones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman R.M., Clark S.Y., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
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RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Hammond S., Harley J.L., Heath P.D., Ho.S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., Ho.S., Holden J.L., Howden P.J.,
RA Kay M.P., Kinberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Kay M.P., Kinberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Swann R.M., Sycamore N., Fathalingam S.R., Plumb R.W., Ramsay H.,
RA Wilming J., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Wilming J., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-97336072; PubMed-9192867;
Mengus G., May M., Carre L., Chambon P.,
"Human TAF(II)135 potentiates transcripti
of the retinoic acid, vitamin D3, and thy
mammalian cells.";
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15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transcription initiation factor TFIID 135 kDa
(TAFII135) (TAFII-130) (TAFII130).
TAF4 OR TAF4A OR TAF2C1 OR TAF2C OR TAFII135 (
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Mammalia; Eutheria;
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Primates;
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Catarrhini;
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hormone rec
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or send a
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"Molecular cloning and analysis of two subunits of the human TFIID complex: hTAFIII30 and hTAFIII00.";

Proc. Natl. Acad. Sci. U.S.A. 93:13611-13616(1996).

-I- FUNCTION: MAKES PART OF TFIID IS A MULTIMERIC PROTEIN COMPLEX THAT PLAYS A CENTRAL ROLE IN MEDIATING PROMOTER RESPONSES TO VARIOUS ACTIVATORS AND REPRESSORS. POTENTIATES TRANSCRIPTIONAL ACTIVATION BY THE AF-2S OF THE RETINOIC ACID, VITAMIN D3 AND THYROID HORMONE.

-I- SUBUNIT: TFIID IS COMPOSED OF TATA BINDING PROTEIN (TBP) AND A
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                                        NE-PNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL
                                                                                                   AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS
                                                                                                                                                                                          LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL
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re 414:865-871(2001).
                                                                                                                                                       MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
                                                                                                                                                                                                                               PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL
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an email to license@isb-sib.ch).
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RESULT
T2D3_D
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Barlova D., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Goveya D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu 2., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu 2., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Lai Z.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
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01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 initiation factor TFIID 110 kDa
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MEDLINE-93145326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kokubo T., Gong D.-W., Roeder R.G., Horikoshi M., Nakatani Y.; "The Drosophila 110-kDa transcription factor TFIID subunit directly interacts with the N-terminal region of the 230-kDa subunit."; Proc. Natl. Acad. Sci. U.S.A. 90:5896-5900(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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SUBURIT: TFIID IS COMPOSED OF TATA BINDING
SUBURIT: TBP-ASSOCIATED FACTORS (TAFS).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE TAF2C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: TFIID IS A MÜLTIMERIC PROTEIN COMPLEX THAT PLAYS CENTRAL ROLE IN MEDIATING PROMOTER RESPONSES TO VARIOUS ACT AND REPRESSORS. MAY FUNCTION AS A COACTIVATOR BY SERVING AS OF PROTEIN-PROTEIN CONTACT BETWEEN ACTIVATORS LIKE SP1 (OR
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58; Mismatches
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POLY-GLN.
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InterPro; IPR001798; Kelch.
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Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).

SUBUNIT: COMPOSED PREDOMINANTLY OF SIX POLYPEPTIDES RANGING F
110 TO 150 KDA AND A MIMOR 300 KDA POLYPEPTIDE. THE MAJORITY
AND C-TERMINAL CLEAVAGE PRODUCTS REMAIN TIGHTLY, ALBEIT
NONCOVALENTLY, ASSOCIATED (BY SIMILARITY).
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SIMILARITY: CONTAINS 5 KELCH REPEATS.
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DOMAIN: THE HCF REPEAT IS A HIGHLY SPECIFIC
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PF01344; Kelch; 5.
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01 (Rel. 40, Last annotation update)
factor C1 (HCF) (VP16 accessory protein) (HFC1) (VCAF)
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Chordata; Craniata; Vertebrata; Euteleostomi;
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Wilson A.C., Peterson M.G., Herr W.;
"The HCF repeat is an unusual proteolytic cleavage signal.";
Genes Dev. 9:2445-2458(1995).
-I- FUNCTION: UPON LYTIC INFECTION OF PERMISSIVE CELLS, THE HSV
TRANSACTIVATOR PROTEIN VP16 ASSOCIATES WITH HCF. BINDING TO HC
ACTIVATES VP16 FOR ASSOCIATION WITH THE OCTAMER MOTIF-BINDING
                                                                                                                                   Frattini A., Faranda S., Redolfi E., Zucchi I., Vipatrosso M.C., Strina D., Susani L., Vezzoni P.; "Genomic organization of the human VP16 accessory housekeeping gene (HCFC1) mapping to Xq28."; Genomics 23:30-35(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Host cell factor C1 (HCF) (VP16 accessory protein) (HFC1) (VCAF)
                                                                                                                                                                                                    MEDLINE-95130107; P
                                                                                                                                                                                                                                                                from a large precursor Cell 74:115-125(1993).
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                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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P51610;
                                                                            MEDLINE=96033796; PubMed=7590226; Wilson A.C., Peterson M.G., Herr
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                                                                                                                                                                                                                                                                                                             Wilson
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Catarrhini;
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Pfam; PF01344; Kelch; 5
SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003961; InterPro; IPR001798;
                                                                                                                                                                          10
                                                                                      70
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ASSOCIATE.

TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL TISSUES AND THE ADULT KIDNEY. PRESENT IN ALL TISSUES TESTED.

ADULT KIDNEY. PRESENT IN ALL TISSUES TESTED.

DOMAIN: THE HCF REPEAT IS A HIGHLY SPECIFIC PROTEOLYTIC CLEAVAGE DOMAIN: THE HCF REMAILY OF POLYPEDTIDES THAT ARISE THROUGH SIGNAL.

SIGNAL.

PTM: EXISTS AS A FAMILY OF POLYPEDTIDES THAT ARISE THROUGH CLEAVAGE AT ONE OR MORE CENTRALLY LOCATED SITES. CLEAVAGE OCCURS AT A DEFINED SITE, PPCE/THET, WITHIN THE HCF REPEAT.

PTM: GLYCOSYLATED; CONTAINS O-LINKED N-ACETYLGLUCOSAMINE RESIDUES.

SIMILARITY: CONTAINS 5 KELCH REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Exercise Bioinformatics Institute. There are no restricted the state of the stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN OCT-1, TO FORM A MULTIPROTEIN-DNA COMPLEX RESPONSIBLE FO ACTIVATING TRANSCRIPTION OF THE HSV IMMEDIATE EARLY GENES.
SUBUNIT: COMPOSED PREDOMINANTLY OF SIX POLYPEPTIDES RANGING FROM 110 TO 150 kDa AND A MINOR 300 kDa POLYPEPTIDE. THE MAJORITY OF AND C-TERMINAL CLEAVAGE PRODUCTS REMAIN TIGHTLY, ALBEIT NONCOVALENTLY, ASSOCIATED.
SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING. IN THE SHORTER FORM THE N- AND THE C-TERMINAL FRAGMENTS FAIL TO
                                                                                                                                                                     VSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLVSPQQTV
                                                                                   TRAETTSNITSRPAVPANPQT-
                                                                                                                                IGSSPQMSGMAALAAAAAATQKIPPSSR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L20010; -; NOT_ANNOTATED_CDS
X79198; CAA55790.1; ALT_INIT
; HGNC:4839; HCFC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and this statement is not removed.
                                         -TVKVASSPVMVSNPATRMLKTAAAQVGTSVSSATNTSTRPIITVHKSGTVTVAQQ
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217
266
1010
1010
1072
                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                   Ä
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                                                                                                                                                                                                                                                                                                                       1164
1873
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1035
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1126
1126
1183
1311
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1339
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                                                                                                                                                                                                                                                                                                   208841
                                                                                                                                                                                                                                                                           HCF REPEAT 6.
HCF REPEAT 7 (DEGENERATE).
HCF REPEAT 8.
HCSING (IN SHORT ISOFORM).
R >> A (IN REF. 1).
S -> SVS (IN REF. 2).
P -> S (IN REF. 1).
A -> G (IN REF. 1).
A -> G (IN REF. 1).
                                                                                                                                                                                                                 57;
                                                                                                                                                                                                               Score 175; DB 1;
Pred. No. 0.0043;
7; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E E E E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KELCH 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KELCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 AA APPROXIMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT 4 (DEGENERATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                 ---VKICTVPNSSSQ---LIKKVAVTPVKKL
                                                                                                                             PTVLSVPAGTTIVKT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are no rest
                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                               148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Usage
                                                                                                                                                                                                                                                         Length 2035;
                                                                                                                                                                                                               Indels 134;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUC2_HUMAN STAN
Q02817; Q14878;
Q1-JUN-1994 (Rel. 2
Q1-NOV-1997 (Rel. 3
15-JUN-2002 (Rel. 4
                                                           and polymorphism.";

J. Clin. Invest. 88:1005-1013(1991).

-!- FUNCTION: COATS THE EPITHELIA OF THE INTESTINES,
OTHER MUCUS MEMBRANE-CONTAINING ORGANS. THOUGHT J
PROTECTIVE LUBRICATING BARRIER AGAINST PARTICLES
AGENTS AT MUCOSAL SURFACES.
-!- SUBUNIT: MULTIMERIC.
                                                                                                                                                                                                                                                  both
                                                                                                                                                                                                                                                                                                                                                                               Gum J.R. Jr., Hicks J.W., Toribara N.W., Siddiki B., Kim Y.S.; "Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of the amino terminus and overall sequence similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mucin 2 precursor MUC2 OR SMUC.
                                                                                                                                                                                                                                                                          Gum J.R. Jr., Hicks J.W.,
Kim Y.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Intestine;
MEDLINE-94132002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                           "MUC-2 human
                                                                                                                                                                    Toribara N.W., Gum J.R. Jr., Petersen G.M., Kim Y.S.;
                                                                                                                                                                                               SEQUENCE OF 1343-1895
MEDLINE=91358717; Publ
                                                                                                                                                                                                                                                              "The human MUC2 intestinal mucin has
                                                                                                                                                                                                                                                                                                     MEDLINE=93016075; PubMed=1400449;
                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    Identification of the amino terminus to prepro-von Willebrand factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                     Biol.
                                                                                                                                                                                                                                                                                                                                                      prepro-von Willebrand factor.";
Biol. Chem. 269:2440-2446(1994).
            TISSUE SPECIFICITY: COLON, SMALL BRONCHUS, CERVIX AND GALL BLADDER PTM: ALL CYSTEINE RESIDUES ARE IN
                                                   SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                    upstream a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAGPVGAKAGVVTLHSVGPTAATGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKIEAEEFTRKL-YVELKSSP-QP----HLVPFLKKSVVALRQLLPNSQSFIQQCVQQTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIIKTIPMSALITQAGATGVTSSPGIKSPITIITTKVMTSGTGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNLKAENSAAVQINLSPTMLENVKKCKNFLAML-IKLACSGSQSPEMGQNVKKLVEQLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQVVTTVVGGVTKTITLVKSPISVPGGSALISNLGKVMSVVQTKPVQTSAVTGQASTGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TA--ITVSAAQTTL----TAAGGLTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -TILVVKGTTGVTTLGTVTGTVSTSLAGAGGHSTSASLATPITTLGTIA--TLSSQVINP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDMVIATCTTTVTTSPVVTTTVSSSQS------EKSIIVSGATAPRTVSVQTLNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PKIATGHGQQGVTQVVLKGAPGQPGTILRTVP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TQIIQTKGPLPAGTILKLYTSADGKPTTIITTTQASGAGTKPTILGISSVSPSTTKPGTT
                                                                                                                                                                                                                                                                                                                               OF 626-1895 AND 4196-5179
                                                                                                                                                        small intestinal mucin
                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                    and downstream of its c
267:21375-21383(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29,
35,
                                                                                                                                                                                              1895 AND 4176-4195 FROM PubMed=1885763;
                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=8300571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Intestinal mucin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---VVTVTPGKPLNTVTT
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Last annotation updat
testinal mucin 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                     Toribara N.W., Rothe
                                                                                                                                                                                Culhane P.J., Lagace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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INVOLVED IN INTRACHAIN OR SIMILARITY).
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                                                                                                                                                        gene
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                                      INTESTINE,
                                                                                                                                                                                                                                                               cysteine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                                                                                                                                        structure.
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                                                                                         PARTICLES
                                                                                                                                                                                                                                                  repetitive
                                                                                                                                                                                                                                                                                      E.-M.,
                                       COLONIC TUMORS
                                                                                                                                                                                  R.E.,
                                                                                                                                                                                                                                                subdomains
tive region
                                                                                                      TO PROVIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                        Repeated
                                                                                                                                                                                                                                                                                      Lagace R.E.,
                                                                                        AND INFECTIOUS
                                                                                                                                                                                  Hicks
                                                                                                                                                        arrays
                                                                                                                                                                                  J.W.,
                                                                                                                                                                                                                                                             located
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BONDS

(BY

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PRINTS; PRO0438; GECYSKNOT.
SMART; SM00214; VWG; 2.
SMART; SM00216; VWD; 4.
SMART; SM00216; VWD; 4.
PROSITE; PS001022; EGE_1; UNK
PROSITE; PS01128; CTCK_1; 1.
PROSITE; PS01208; VWFC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L21998; AAB95295.1
EMBL; M74027; AAA59875.1
EMBL; M94131; AAA59163.1
EMBL; M94132; AAA59164.1
Genew; HGNC:7512; MUC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00007; Cys_kr
Pfam; PF00093; vwc; 1
Pfam; PF00094; vwd; 4
Pfam; PF01826; TIL; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein;
SIGNAL
CHAIN
    REPEAT
RE
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REPEAT
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (SC or send an email to license@isb-sib.ch).
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SIMILARITY: THE N-TERMINAL DOMAIN SHOWS SOME SIMILARITY TO THAT OF SILKWORM HEMOCYTIN.
SIMILARITY: CONTAINS 2 VWFC DOMAINS.
SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE (CTCK) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p; IPR000359; Cys_knot.
p; IPR0020561; EGF-like.
p; IPR002400; GF_cysknot.
p; IPR002919; TIL_cysrich.
p; IPR001007; VWF_C.
p; IPR001046; VWF_D.
pr00107; Cys_knot; 1.
pr00093; vwc; 1.
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                  P08068;
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22.0%;
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T-> S (IN REF. 3)
L-> P (IN REF. 3)
M-> T (IN REF. 3)
M-> S (IN REF. 2)
S MW; 85CD7571FB9A5663
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Pred. No. 0.
                               PRT;
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16-OCT-2001 (Rel. 40, Last annotation update)
Glucoamylase S1/S2 precursor (EC 3.2.1.3) (Glucan
glucosidase) (1,4-alpha-D-glucan glucohydrolase).
STA1 OR STA2 OR MAL5 OR YIR019C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi: Ascomycota: Saccharomycotina: Sa
                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-S288c / AB972;
Barrell B.G., Badcock K., Bankler A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Couis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.,
                                                                                                                                                                                                                                                                                                    EMBL;
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                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SPX101-1C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
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LI; ML6164; AAA35014.1;
LL; ML6165; AAA35015.1;
LL; X13857; CAA32069.1;
LB26877; B26877.
LA26877; A26877.
L; A26878; S48478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                glucose residues successively frowith release of beta-D-glucose.
SIMILARITY: TO S.POMBE SPBC215.13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n Saccharomyces cerevisiae.",
5 Lett. 239:179-184(1988).
CATALYTIC ACTIVITY: Hydrolysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: SOME, TO S.POMBE SPCC285.13C.
TTESSSAPVTSSTTESSSAPVPTPSSSTTESSSAPVPTPSSSTTESSSAPVPTPSSSTTE 677
                        TLVTKVAPVSAPPKVSSGPRLPAP-----QIVAVKAPNTTTIQEPANLQLPPGTVLIK 54
                                                                                                                                                                                                                   S0001458; MUC1.
                                                                  Similarity
                                                                                                                                                                                        Multigene family.
                                                                                                                                                                                                                                                                                                                                            an email to license@isb-sib.ch).
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                                                               9.18;
21.28;
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                                                                                                                                                                                                    Polysaccharide degradation;
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GLUCOAMYLASE S1/S2.
SER/THR-RICH.
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
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                                                     62;
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                                                   Score 162; DE
Pred. No. 0.01
52; Mismatches
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          Pfam; PF00520; ion_trans;
Pfam; PF01477; PLAT; 1.
Pfam; PF01825; GPS; 1.
SMART; SM00303; GPS; 1.
SMART; SM00308; LH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YS89_CAEEL STANKALL,
Q09624; Q09625; Q969D4;
Q1-NOV-1995 (Rel. 32, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-therical protein ZK945.9 in chromosome II.
                                                                                 InterPro;
InterPro;
                                                                                                                                                     EMBL; Z48544; CAB70192.1;
EMBL; Z48582; CAB70192.1;
EMBL; Z48582; CAB70201.1;
EMBL; Z48544; CAB70201.1;
                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilkinson-Sproat
Submitted (FEB-19
                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                           Durbin R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nemata
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: Integral membrane protein-1- SIMILARITY: CONTAINS 1 GPS DOMAIN.
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                                                                                                              InterPro;
                                                                                                                                        WormPep; ZK945
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                                                                                                                          InterPro;
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                                                                             zk945.9; CE25697.

IPRO01211; Cat_channel_TrpL.

IPRO01024; Lipoxygenase_LH2.

IPRO00636; M+channel_nlg.

IPRO00203; PKD_cys_rich.
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Caenorhabditis.
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Best Local S
Matches 84
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Q00130;
01-DEC-1992
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01-OCT-1996
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      between
                                              Virology 186:9-14(1992)
                                                                                  Davison A.J.
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Viruses; dsDNA viruses, no RNA stage;
Ictalurid Herpes-like viruses.
NCBI_TaxID=10401;
                                                                                                                STRAIN-Auburn
                                                                                                                             SEQUENCE FROM N.A.
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                                                                                              MEDLINE=92087490; PubMed=1727613;
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een the Swiss Institute of Bio
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                                                                catfish virus:
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(Rel. 24, Last sequence up
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l gene 50 protein.
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MEDLINE-93331716; PubMed-
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"Cloning of GT box-binding proteins: a novel:
"cloning of GT box-binding proteins: a novel:
"regulating T-cell receptor gene expression.";
Mol. Cell. Biol. 12:4251-4261(1992).
-I- FUNCTION: BINDS TO GC BOX PROMOTERS ELEME
ACTIVATES MRNA SYNTHESIS FROM GENES THAT
           This SWISS-PROT entry is copyright. It is produce between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There as use by non-profit institutions as long as it modified and this statement is not removed. Use
                                                                                                                                                                                                                                                                             MEDLINE-96051398; PubMed=7584044;
Nomura N., Nagase T., Miyajiam N., Sazuka T., Tanaka A., Seki N., Kawarabayasi Y., Ishikawa K.-I., Tabata S.;
"Prediction of the coding sequences of unidentified human The coding sequences of 40 new genes (KIAA0041-KIAA0080) canalysis of cDNA clones from human cell line KG-1.";
DNA Res. 1:223-229(1994).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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01-NOV-1997 (Rel.
16-OCT-2001 (Rel.
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                                                                                                          RECOGNITION SITES.
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE SP1
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Rel. 40,
i factor (
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                                                                                                          FAMILY OF
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THAT CONTAIN
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Best Local
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                   Eukaryota; Metazoa; (Mammalia; Eutheria; Eutheria; NCBI_TaxID=9606; [1]
                                                                                                                                               MTG8_HUMAN STANDARD; PRT; 604 AA. 006455; Q06456; Q16339; Q92479; Q16346; Q16347; Q1-100V-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) MTG8 protein (ETO protein) (E19th twenty one in the control of the contr
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ZN_FING
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CBFA2T1 OR MTG8 OR ETO
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                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
Transcription regulation; Activator; Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00096; zf-C2H2; 3.
PRINTS; PR00048; ZINCFINGER.
ProDom; PD000003; Znf_C2H2;
SMART; SM00355; ZnF_C2H2; 3.
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Pfam; PF00096; zf-C2H2;
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                                                                                                                                                                                                                                                                                                                                                                                     NPLAGPVGAKAG-VVTLHSVGPTAA
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M97190; AAA36629.1;
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518 54
548 57
578 60
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600 ZINC FING
542 C2H2-TYP
572 C2H2-TYP
600 C2H2-TYP
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Primates;
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24.9%;
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H2; 3
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C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                       Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                    425
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                                                       Vertebrata;
i; Hominidae;
                                                                                                                                                                                                                                Q16347;
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                                                                           Euteleostomi;
                                                         Homo
 IN AML-M2
                                                                                                                                                   (Cyclin
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MEDLINE-98326315; PubMed-96
MEDLINE-98326315; PubMed-96
Wolford J.K., Prochazka M.;
"Structure and expression o
Gene 212:103-109(1998).
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor.";
                                                       ARE PRODUCED BY ALTERNATIVE SPLICING.

1 TISSUE SPECIFICITY: MOST ABUNDANTLY EXPRESSED IN BRAIN. I
LEVELS IN LUNG, HEART, TESTIS AND OVARY.

1 DISEASE: INVOLVED IN ACUTE MYELOID LEUKEMIA (AML-M2) BY I
CHROMOSOMAL TRANSLOCATION T(8;21)(Q26;Q22) THAT INVOLVES
                                                                                                                   Cancer Genet. Cytogenet. 63:81-88(1992).
-I- FUNCTION: PUTATIVE TRANSCRIPTION FACTOR.
-I- SUBCELLULAR LOCATION: Nuclear (Potential).
-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; MTGBA AND
                                                                                                                                                                                                                                                                                                                                                                  Genes
[7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 334-432 FROM N.A., AN MEDLINE-95002916; PubMed-7919324; Tighe J.E., Calabi F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (APR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miyoshi H., Kozu T., Shimiz
Kamada N., Ohki M.;
"The t(8:21) translocation
production of an AMLI-WTG8
EMBO J. 12:2715-2721(1993).
                                                                                                                                                                                   MEDLINE-93046086; PubMed-1423235;
Nisson P.E., Watkins P.C., Sacchi N.;
"Transcriptionally active chimeric gene deriv
the AML1 gene and a novel gene on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                  Era T. Asou N., Kunisada T., Yamasaki H., Asou
Nishikawa S.-I., Yamaguchi K., Takatsuki K.;
"Identification of two transcripts of AMLI/ETO-
leukemic cells and expression of wild-type ETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Alternative, out-of-frame runt/MTG8 transcripts are encoded by th derivative (8) chromosome in the t(8;21) of acute myeloid leukemia
                                                                                                                                                                          cells."
                                                                                                                                                                                                                                      VARIANT AML1-MTG8/ETO FUSION IN
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                                                                                                                                                                                                                                                                                        myeloid leukemia
                                                                                                                                                                                                                                                                                                                 Kamada N.,
                                                                                                                                                                                                                                                                                                                          MEDLINE-93357484; PubMed-8353289; Kozu T., Miyoshi H., Shimizu K.,
                                                                                                                                                                                                                                                                                                                                       VARIANT AML1-MTG8/ETO FUSION IN AML-M2.
MEDLINE-93357484; PubMed-8353289;
                                                                                                                                                                                                                                                                                                                                                                                          cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95329434;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blood 84:2115-2121(1994).
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MEDLINE=93327761; PubMed=8334990;
                                                                                                                                                                                                                                                                                     "Junctions of the AML1/MTG8(ETO) fusion myeloid leukemia detected by reverse tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
   AND PROTEIN AML1.

SIMILARITY: CONTAINS 1 MYND-TYPE ZINC FINGER.

DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Hnematol.;

WWW-"http://www.infoblogen.fr/services/chromcancer/Genes/ETO.
                                                                                                                                                                                                                                                               82:1270-1276(1993).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial

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         PLNTYTTLKPSSL-GASSTP---SNEPNLKAENSAAVQINLSPTM-LENVKKCKNFLAML
                                             QTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTYVTTVPKPSSVQSVAVPTSVVTVTPGK 148
TLTNGTSHSPTALNGAPSPPNGFSNGPSSSSSSSSLANQ-QLPPACGARQLSKLKRFLTTL
                              RTEKHSTMPDSPVDVKTQSRLTP-----PTMPPPPTTQG-APRTSSFTPT---
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D13979; BAA03089.1;
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Saccharomycetales;
NCBI_TaxID=4932;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacci
Saccharomycetales; Saccharomycetaceae; Saccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A Drosophila photoreceptor cell-specific protein, calphotic cellcium and contains a leucine zipper.";

Proc. Natl. Acad. Sci. U.S.A. 90:1536-1540(1993).

-1- FUNCTION: MIGHT FUNCTION AS A CALCIUM-SEQUESTERING "SPORTER CYTOPLASMIC CALCIUM. IT BIN OF ERECULATE THE AMOUNT OF FREE CYTOPLASMIC CALCIUM. IT BIN OF CA+2 PER MOL OF PROTEIN.

-1- SUBGULIT: HOMODIMER (PROBABLE).

-1- SUBGULIULAR LOCATION: CYTOPLASMIC; HYPODENSE COMPARTMENT -1- SUBCELLULAR LOCATION: CYTOPLASMIC; HYPODENSE COMPARTMENT -1- SUBCELLULAR LOCATION: CYTOPLASMIC; HYPODENSE COMPARTMENT -1- SUBCELLULAR LOCATION: CYTOPLASMIC; HYPODENSE COMPARTMENT -1- DEVELOPMENTAL STAGE: EXPRESSED EARLY IN PHOTORECEPTOR CELLULAR LOCATION: CELLULAR LOCATION: CHARLES AND AXONS OF PHOTORECEPTOR CELLULAR LOCATION: SOMA MOL AXONS OF PHOTORECEPTOR CELLULAR LOCATION: SOMA MOL AXONS OF PHOTORECEPTOR CELLULAR LOCATION: STAGE: EXPRESSED EARLY IN PHOTORECEPTOR CELLULAR LOCATION: CELLULAR LOCATIO
                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
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01-OCT-1993
01-OCT-1993
01-FEB-1994
Elybase, Calcium-binding.
                                                                                                        EMBL;
PIR; A
                                                                                                                                          EMBL; L02111; AAA28405.1; EMBL; L05080; AAA28420.1;
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Martin J.H., Benzer S., Rudnicka M.,
"Calphotin: a Drosophila photoreceptu
"Calphotin: a Drosophila photoreceptu
Proc. Natl. Acad. Sci. U.S.A. 90:1531
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                      FlyBase; FBgn0010218; Cpn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
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CPN OR CAP.
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Ballinger D.G., Xue N., Harshman K.D.;
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Best Local
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01-NOV-1997
01-NOV-1997
16-OCT-2001
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                                                                                              STRAIN-ICR; TISSUE-Brain;
MEDLINE-96121389; PubMed-8575770;
Niwa-Kawakita M., Miyoshi H., Got
                                                     "Cloning and gene mapping of the mouse homologue associated with human acute myeloid leukemia."; Genomics 29:755-759(1995).
   This
                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                               MTG8 protein.
CBFA2T1 OR CBFA2T1H OR MTG8
                   -i- SUBCELLULAR LOCATION: Nuclear (Potential).
-i- SIMILARITY: CONTAINS 1 MYND-TYPE ZINC FINGER.
                                             -'I - FUNCTION: PUTATIVE TRANSCRIPTION
                                                                                      Shisa H., Ohki M.;
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                MTG8_MOUSE
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I -> V (IN REF. 2).
T -> A (IN REF. 2).
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A -> E (IN REF. 2).
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9; Mismatches
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Sciurognathi;
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thi; Muridae; Murinae; Mus
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Search completed: February 16, 2003, 21:56:21 Job time: 15.9186 secs
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MCD: MGI:104793; Cbfa2tlh,
InterPro; IPR003894; TAF_hom.
InterPro; IPR002893; Znf_MYND.
Pfam; PF01753; Zf-MYND; 1.
SMART; SM00549; TAFH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DOMAIN 30 33 POLY-PRO.

DOMAIN 75 81 POLY-SER.

DOMAIN 263 270 POLY-PRO.

DOMAIN 380 386 POLY-SER.

ZN_FING 488 524 MYND-TYPE.

SEQUENCE 577 AA; 64337 MW; 2656F185318C4B11 CRC64;
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                                                                                                                                                                                                                    264 L-RQLLPNSQSFIQ---QCVQQTSSDMVIATCTTTVTTSPVV 301
                                                                                                                                            107 QQF--GNDISPEIGERVRTLYLGLVNSTLTIEEFHSKLQEATNFPLRPFVIPFLKANLPL 164
                                                                                                                                                                 89 QTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGK 148
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                                                                      LQRELLHCARLAKQNPAQYLAQHEQLLLDASTTSPVDSSELL 206
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Q8wwq4 homo sapien
Q9n487 caenorhabdi
Q61191 mus musculu
Q9qwh2 mus musculu
Q61707 caenorhabdi
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O76894 drosophila
O76602 caenorhabdi
O99nd0 mus musculu
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Best Local Similarity
Matches 133; Conserva
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Exp. Cell Res. 0:0-0(2001).
EMBL; AY038601; AAK94779.1; -.
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STRAIN-BALB/C; TISSUE-PO BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                     Metsis M., Brunkhorst A., Neuman T.; "Cell Type Specific Expression of the TFIID Component TAFII135 in the
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
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SVAVPTSVVTVTDGKPLNTVT--TLKPSSLGASS-----TPSNE-PNLKAENSAAVQINL 185
                                          PQSTMAPRPATPTGAPPVQISTVQAPGTPIIAR-QVTP-----TTIIKQV---SQAQ 107
                                                                        TTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTVVTTVPKPSSVQ 133
                                                                                                       PRLPQPP----QKPN--NIQ---NEQLPPGMVLVRSENGQLLMI-PQQALAQMQAHAQAQ 59
                                                                                                                                                                                                                            662 AA; 71398 MW; 91A75F38CB0D0DA4 CRC64;
                                                                                                                                                                   Conservative
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53; Mismatches 102;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY069807; AAL39952.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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26.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 194.5;
Pred. No. 3.4e
52; Mismatches
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Last sequence up
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ว.บ.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
RESULT
076894
                                                                                                                                                                                                                                                                                                                                                RX MEDILING-2019606; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Babayani A., An. Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Babayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Durbin K.J., Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann W.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., McLeod M.P., McPherson D.,
RA Lisko P., Lei Y., Levitsky A.A., Li J., Li J., Li J., Li J. Z., Liang Y., Lin X.,
RA Lisko P., Lei Y., Levitsky A.A., Li J., Li, Lung Y., Lia Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S., M., Moy M., Murphy B., Murphy L., Muray D.M., Neshrefi A.,
Mount S., M., Moshrefi A.,
RA Pales R., N., Nicon K., Nicon K., Nicon K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            076894;
01-NOV-1998 (TrEMBLrel. 1
01-NOV-1999 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
EG:56G7.1 protein.
EG:56G7.1 OR CG14796.
                                                    Submitted (APR-1999) to the EMBL/GenBa
EMBL; AE003421; AAF45644.1; -.
EMBL; AL031028; CAA19845.2; -.
FlyBase; FBgn0025390; EG:56G7.1.
InterPro; IPR002557; Chitin_bind_PerA.
InterPro; IPR002955; P_rich_extensn.
                                                                                                                                                                                                                                                      "Sequencing
Submitted (
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Cadieu E., Dreano
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Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tarcheata; Hexapoda; Insecta; Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Musc. Ephydroidea; Drosophilidae; Drosophila.
                   PRINTS;
                                                                                                                                                                                           Benos
                                                                                                                                                                                                               SEQUENCE FROM N.A.
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               PF01607; CBM_14; 2.
S; PR01217; PRICHEXTENSN.
  SM00494; ChtBD2;
                                                                                                                                                                                                                                                    , Dreano S., Lelaure V., Mottler S., Gallbert F.; ng the distal X chromosome of Drosophila melanogaster."; (JUL-1998) to the EMBL/GenBank/DDBJ databases.
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12,
21,
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Last sequence update)
Last annotation updat
                                                                                                                                                                     EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                 Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Darrimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Barsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Wathstook L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  076602;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 122.9 kDa protein.
                                                        Geisel C., Harmon G., "The sequence of C. e Submitted (JUL-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
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Rhabditidae; Pelode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
   SEQUENCE
                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                         Nature 368:32-38(1994).
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EMBL/GenBank/DDBJ databases.
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Waterston R.;
Submitted (OCT-1
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01-JUN-2001
.01-JUN-2002
                                                                                                                                                                      Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P., Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C., Miller W., Koop B.F.;
Miller W., Koop B.F.;
"Comparative analysis of the gene-dense ACHE/TFR2 region on human chromosome 7q22 with the orthologous region on mouse chromosome 5.";
Nucleic Acids Res. 29:1352-1365(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-1998) to the EMBL; AF077538; AAC64622.1; Hypothetical protein. SEQUENCE 1275 AA; 122924
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ-
-- SIMILARITY: CONTAINS 3 MAM DOMAINS.
EMBL; AF312033; AAK28824.1; -.
EMBL; AY046056; AAL04416.1; -.
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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                                                                                                        STRAIN=129/SV;
Cheung T.L., W
                                                                                                                                                                                                                                                                             STRAIN=129/SV;
MEDLINE=21138439; PubMed=11239002;
                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
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                                                                    Domain Structure.";
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                                                                                      Genomic Basis of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                        Wilson
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                                                                                    on M.D.,
Inter- a
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Rodentia;
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                                                                                    and Intra-species
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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EGF-like.

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RESULT
Q9JK31
ID K31
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Best Local S
Matches 95
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Pfam; F
Pfam; F
SMART;
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                                                                                                                                                                                          01-OCT-2000 (Tremblrel 15, 01-OCT-2000 (Tremblrel 15, 01-DEC-2001 (Tremblrel 19, ATFa-associated factor.
                                                                                                                                                                                                                                                                                                                                                                                                             1157
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InterPro;
                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
                        SEQUENCE FROM N.A.
DeGraeve F., Bahr
                                                                                                                                                                         ATFa-associated ATF7IP OR ATF.
                                                                                                                                                                                                                                                                                                    Q9JK31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1103
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SEQUENCE 5374 /
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      murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; PF00094; Vwd; 4.
17; SM00001; EGF like;
17; SM00274; FOLN; 21.
17; SM00137; MAM; 3.
17; SM00214; VWC; 25.
17; SM00216; VWD; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASEETTVSTQETTLLTEQSAVTQTSI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPAEVTTVP-PVSIPSEETTIPTEVTTVPPEETTIPAEVTTVPPVSI-----PSEETTI-
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; PS01186; EGF_2;
; PS50060; MAM_2;
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      F., Bahr A., Chatton ATFa-associated fact
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IPR001007: VWF_C.
IPR001846: VWF_D.
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IPR003328; TILa_Cysrich.
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AA; 579536 MW;
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                                                                                                           Chordata;
Rodentia;
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      factor v
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Last annotation updat
                                                                                                                                                                                                                                                        Created)
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Pred. No. 0
                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                      PRT;
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, Kedinger C.;
with transcriptional
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.0025;
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  repressing
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            SEQUENCE FROM N.A.
ISOGAI T., Ota T., Hayashi K., Sugiyam Isogai T., Ota T., Hayashi K., Sugino S., Aot Nishikawa T., Nagai K., Sugano S., Aot Matsunawa H., Ishii S., Kawai Y., Sait Nakamura Y., Nagahari K., Masuho Y., S.
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBa.
EMBL; AKO01550; BAA91751.1;
InterPro; IPRO02965; P.rich, extensn.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                              Q9NVJ9;
01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-CCT-2000 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CDNA FLJ10688 fis, clone NT2RP3000320, highly similar to
                                                                                                                                                                                                                                                                                                     Q9NVJ9;
                                                                                                                                                                                                                                                                                                                                                                                    1143
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Oncogene 10:1807-1819(2000).
EMBL; AJ132702; CAB77024.1; -.
MGD; MGI:1888965; Atf71p.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                         1088
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  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -PNTTTIQFPANLQLPPGTVLIKSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTV
                                                                                                                                                                                                                                                                                                                                                                                      VNNGLTLGSAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -VSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKVAPVSAPPKVS------SGPRLPAPQIVAVKA----------
                                                                                                                                                                                                                                                                                                                                                                                                                                       PVPRAPANHQVVYTTLPAPTTQA-----PLRGTVMQAPAVRQVNPQNSVTVRVPQTTTYV 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLQPSGVPTSGPS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSSSSRGPTQMKIPISTFSPPS-SAEQNSSATPRIVAENQTNKTVDSSIN-----KKAAD
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                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                       (Human).
  AA;
                                                                                                                                                                                                                                                                                                                                                                                                              351
                                                                                                                                                                             Chordata;
Primates;
  75979
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  ¥.
                                                                Masuho Y., (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41;
                                                     EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 177.5;
Pred. No. 0.
                                                                                                                                                                          Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                       Sugiyama T.,
S., Aotsuka (
F2C43814F6B241C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                Saito K.,
Y., Sasaki
                                                                                          lyama T., Otsuki T., Su
Aotsuka S., Yoshikawa
Saito K., Yamamoto J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -QATIHVLPTAPTTVNVTHRPVTQVTTRL
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                                                                                                                                                                                         Euteleostomi;
                                                                                                                      Suzuki
                                                                                                                                                                                                                                partial
factor
                                                                                             Wakamatsu
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                                                                                             Α.,
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Query Match

9.98;

175

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4

Length

709;

Best Loc Matches

Local Similarity 25.4 nes 106; Conservative

25.48;

Pred. No. 0.00053;
3; Mismatches 166;

Indels

93;

20;

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                                                                                Query Match
Best Local S
Matches 106
                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                 corresponding region of human Xq28.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9QY35
                                                                                                                                                                            Pfam;
                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                Platzer M.,
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               Host cell factor C1 (Fragment). ABCD1 OR HCFC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9QY35;
                                                                                                                                          NON_TER
                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                       Rosenthal A.;
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-10090;
                                                                                                                                                                                                                                                             Comparative sequence analysis of the mouse Licam locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            445
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TRAETTSNITSRPAVPANPQT------VKICTVPNSSSQ---LIKKVAVTPVKKL 115
                                  IGSNPQMSGMAALAAAAAATQKIPPSSA---PTVLSVPAGTTIVKT-----VAVTPGTTT
                                                       VSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLVSPQQTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P--TKPNNVPSVPSPSIQR---NPTASAAPLGTTLAVQAVPTAHSIVQ-ATRTSLPTVGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVILHVPVAVSSQPQLLQSHPGTLVTNQPSGNVEFISVQSPPTVSGLTKNPVSLPSLP-N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:1349215; Abcd1.
                                                                                                                                                                                                                          MGI:105942; Hcfc1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVVYTTLPAPPAQAPLRGTVMQAPAVRQVNPQNSVTVRVPQTTTYVVNNGLTLGSTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELKSSP-QPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CKNFLAMLIKLACSGSQS------PEMG--QNVKKLYEQLLDAKIEAEEFTRKLYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGLYSPSTNRGPIQMKIPISAFSTSSAAEQNSNTTPRIENQTNKTIDASVSKKAADSTSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVTPPAVVSSQPKLQTPVTSG-SLTATSV--LPAPNTATVVATTQVPSGNPQPTISLQPL
                                                                                                                                                     PF00041; fn3; 2.
PF01344; Kelch; 4.
; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -VVTTTVSSSQSEKSI--IVSGATAPRTVSVQTLNPLAGPVGAKAGV---VTLHSVGP 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IQPAPPLQPSGVPTSGPSQTTI-HLLPTAPT----TVNVTHRPVTQVTTRLPVPRAPANH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTV-VTTVPKPSSVQSVAVPTSVVTVTP 146
                                                                                                                                                                                                                                      AF133093; AAF22156.1;
                                                                                             Similarity
                                                                                                                                                                                      IPR003961; FN_III. IPR001798; Kelch.
                                                                                                                                1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----ATGSDSSGVIDLTMDDEESGASQDPKKLNHTPVSTMSSSQPVSRPLQP 444
                                                                                                                                                                                                                                                                                                Brenner V.,
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                               Ã,
                                                                                           9.8%;
                                                                                                                               203436 MW;
                                                                                                                                                                                                                                                                                              Reichwald
                                                                                  60;
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                                                                                           Pred.
                                                                                                      Score 174.5;
                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                Mismatches
                                                                                                                               ABE998C5DDE688A9 CRC64;
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                                                                                           0.0021;
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                                                                                Indels
                                                                                                      Length
                                                                                139;
                                                                                                                                                                                                                                                                                                                                             Mus.
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                                   522
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                                                                                                                                                                                            Query Match
Best Local S
Matches 97
                                                                                                                                                                                                                                                                                          NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                      "Pig gastric mucin: isolation and c
with a novel tandem repeat.";
Gastroenterology 106:200-200(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=YORKSHIRE/CHESTER WHITE/HAMPSHIRE CROSS; MEDLLINE=94102478; PubMed=7506218; Turner B.S., Bhaskar K.R., Hadzopoulou-Cladaras LaMont J.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Turner B.S., Bhaskar LaMont J.T.;
                                                                                                                                                                                                                                                                                                                                                                  EMBL; U10281; ĀĀC48526.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-YORKSHIRE/CHESTER WHITE/HAMPSHIRE CROSS; MEDLINE-95275264; PubMed-7755593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gastric mucin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    029071;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mucin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Isolation and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        851
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167
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                                             NSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVK--
                                                                                           APISSTTSVQPSSSGSVPTTSATSVQSSSSSSAPTTSATSVQ-PSSSSSPPISSTVSVQP 166
                                                                                                                            APVSAPPKV--SGPRLPAPQIVAVK-----APNT--TTIQFPANLQLPP--GTVLIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATLSSQVINPTAITVSAAQTTLTAAGGLT 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTLHS -- VGPTA -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIIKTIPMSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAP-----AKIITAV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNLKAENSAAVQINLSPTMLENVKKCKNFLAML-IKLACSGSQSPEMGQNVKKLVEQLLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -TTLVVKGTTGVTTLGTVTGTVSTS-----LAGAGAHSTSA-----SLATPITTLGTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKIATGHGQQGVTQVVLKGAPGQPGTILRTVP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKIEAEEFTRKL-YVELKSSP-QP----HLVPFLKKSVVALRQLLPNSQSFIQQCVQQTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TQIIQTKGPLPAGTILKLVTSADGKPTTIITTTQASGAGTKPTILGISSVSPSTTKPGTT
                                                                                                                                                                                          l Similarity
97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>.</u>
                                                                                                                                                                                                                                                                                        528 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308:89-96(1995).
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
---- SSAPTTSATSVQPSSSSSPPISSTVSVQTSSSSSVPTTSTTSVQPS
                                                                                                                                                                                                                                                                                     528
; 49907 MW;
                                                                                                                                                                                                                   9.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K.R.,
                                                                                                                                                                                            61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hadzopoulou-Cladaras M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -ATGGTT
                                                                                                                                                                                          Score 173.5; DB 6;
Pred. No. 0.00051;
51; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                          OBF0F6879203B2EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of
                                                                                                                                                                                                                                                                                                                                                                                                                                            characterization of a cDNA clone
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Best Local S
Matches 94
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MEDLINE-21426417; PubMed-11535137;
Escande F., Aubert J.P., Porchet N.,

"Human mucin gene MUCSAC: organizati
repetitive region.";
Biochem. J. 358:763-772(2001).

EMBL; AJ298318; CAC83675.1; -.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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1349 AA;
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01-JUN-2001 (TremBLrel.
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STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
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STRAIN-BRISTOL N2;
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STRAIN-BRISTOL N2;
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EMBL/GenBank/DDBJ
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Query Match
Best Local
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Interpro; IPR003961; FN_III.
Interpro; IPR001798; Kelch.
Pfam; PF00041; fn3; 2.
Pfam; PF01344; Kelch; 5.
SMART; SM00060; FN3; 1.
SEQUENCE 2045 AA; 210537 MW; 1
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Q61191;
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Mus musculus (Mouse).
Arvota; Metazoa; Chordata;
Aberia; Rodentia;
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Kristie T.M., Dashner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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01-JUN-2002
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                 ATLSSQVINPTAITVSAAQTTLTAAGGLT
                                          VTLHS--VGPTA-----ATGGTT
                                                                                     SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGV
                                                                                                                  PKIATGHGQQGVTQVVLKGAPGQPGTILRTVP----MGGVRLVTPVTVSAVKPAV----
                                                                                                                                                                     TIIKTIPMSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAP-----AKIITAV--
                                                                                                                                                                                             PNIKAENSAAVQINISPTMLENVKKCKNFLAML-IKLACSGSQSPEMGQNVKKLVEQLLD 229
                                                                                                                                                                                                                                                                           AQVVTTVVGGVTKTITLVKSPISVPGGSALISNLGKVMSVVQTKPVQTSAVTGQASTGPV 706
                                                                                                                                                                                                                                                                                                    AQIGTTVV-----TTVPKP-----
                                                                                                                                                                                                                                                                                                                                                    TRAETTSNITSRPAVPANPQT-----VKICTVPNSSSQ----LIKKVAVTPVKKL 115
                                                                                                                                                                                                                                                                                                                                                                             IGSNPQMSGMAALAAAAAATQKIPPSSA---PTAWSVPAGTTIVKT-----VAVTPGTTT 588
                                                                                                                                          AKIEAEEFTRKL-YVELKSSP-QP----HLVPFLKKSVVALRQLLPNSQSFIQQCVQQTS
                                                                    -TTLVVKGTTGVTTLGTVTGTVSTS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                            9.6%;
Similarity 23.4%;
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(TrEMBLrel. 01, Last sequence up
(TrEMBLrel. 21, Last annotation
on factor C1 (HCF).
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 169.5; DB Pred. No. 0.0048;
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; Murinae; Mus.
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AC 06170
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Best Local Similarity
Matches 105; Conserv
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BMCD; MGI:10542;

InterPro; IPR003961; Fw_-

TherPro; IPR001798; Kelch.

TherPro; IPR001798; Z.

TherPro; IPR001798; Kelch.

TherPro; IPR001798; Kelch.
  01-AUG-1998
01-AUG-1998
01-MAR-2002
                                        061707
061707;
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Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
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Pfam; PF01344; Kelch;
SMART; SM00060; FN3;
SEQUENCE 2045 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kristie T.M.;
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 (TrEMBLrel.) (TrEMBLrel.)
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                                                     PRELIMINARY;
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07,
20,
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Created)
Last sequence update)
Last annotation update)
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; Murinae; Mus.
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GN 621.
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OS HOMO
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OC Eukar
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AC MCBI_
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Best Local S
Matches 63
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STRAIN-BRISTOL N2;

Clarke K., Bauer C., O'Neal !

"The sequence of C. elegans
"The sequence of C. elegans
                                                                                                                                                                                                                                                                                 01-NOV-1999 (TremBLrel.
01-NOV-1999 (TremBLrel.
01-DEC-2001 (TremBLrel.
MEDLINE=20431278; PubMed=10976766; Gunther M., Laithier M., Brison O.;
                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                           P621 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                   Q9Y4X8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Direct Submission.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ
EMBL; AF063007; AAC16427.1; -.
InterPro; IPR004822; Histone_core.
InterPro; IPR003894; TAF_hom.
SMARR; SM00549; TAFH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the nematode C. el investigating biology. The C. elegans Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                           Plasmid
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STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
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Rhabditidae; Peloderinae;
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                                                                                                                                                                                   Homo sapiens (Human).
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                                                                    EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKAARVKELIRGVIYLETTAEEFTRNLQQVLKSQAQPHLLPFLQNTLPALRNAVRNGTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VGARPMIRPMGPGGPSPMGLQ--GPVRGPMGHQ--MVQMHPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSEKSII-VSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEGVNPPPGYVFNNGRTPGPPQPPPPQQQSQQQPPLEMRQIPNPNQIPPQMVQGGPHMVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --GQNVKKLVEQLLDAKIEAEEFTTKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSPMAPQGPPGT-----PQNSAAAAAASDD--KNVTKCVRFLKTLINL--SNNDDPEMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27;
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27; Mismatches
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cosmid R119.";
EMBL/GenBank/DDBJ
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Last annotation
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                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local
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EMBL; AJ242978; CAB45135.1;
InterPro; IPR002965; P.rich_extensn.
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Plasmid.
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                                     462 IQPAPPLQPSGVPTSGPSQTTI-HLLPT
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                    TT
                                                         ELKSSP-QPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPVVT
                                                                                               CKNPLAMLIKLACSGSQS-----PEMG--QNVKKLVEQLLDAKIEAEEFTRKLYV
                                                                                                                                                                                                                           CGK-----ATGSDSSGVIDLTMDDEESGASQDPKKLNHTPVSTMSSSQPVSRPLQP
                                                                                                                     SGLYSPSTNRGPIQMKIPISAFSTSSAAEQNSNTTPRIENQTNKTIDASVSKKAADSTSQ
                                                                                                                                          GKPLNTVTTLKP------SSLGASSTPSNEPNLKAENSAAVQINLSPTMLENVKK
                                                                                                                                                               P--TKPNNVPSVPSPSIQR---NPTASAAPLGTTLAVQAVPTAHSIVQ-ATRTSLPTVGP
                                                                                                                                                                                 PQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTV-VTTVPKPSSVQSVAVPTSVVTVTP
                                                                                                                                                                                                        PVILHVPVAVSSOPQLLQSHPGTLVTNQPSGNVEFISVQSPPTVSGLTKNPVSLPSLP-N
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514 AA;
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Listing first 45 summaries
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AAW31494
ABG09468
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AAW06084
AAW25019
AAU825019
AAU82954
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Novel human diagno
Transcription fact
TATA-binding prote
Human TATA-binding
                                         TATA-binding prote Human homologue of TATA-binding prote Drosophila TATA-bi
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Drosophila melanog	ABB65440	22	1057	7.5	169.5	45
C parvum GP900 pro	ABJ04045	23	1721	7.6	171.5	44
Portion of Cryptos	AAB11727	21	1721	7.6	171.5	43
Cryptosporidium pa	AAW48299	19	1721		171.5	42
C. albicans Rbt1 p	AAY05477	20	750	7.6	172	41
Caenorhabditis ele	AAY95556	21	3178	7.7	173.5	40
Human transcriptio	AAY57452	21	2907	7.7	173.5	. 39
Caenorhabditis ele	AAY95559	21	2870	7.7	173.5	38
Human transcriptio	AAY57453	21	2781	7.7	173.5	37
	AAW06725	17	849	7.7	173.5	36
Human proteir	AAB94078	22	557	7.7	173.5	35
Drosophila mel	ABB67620	22	1658	7.8	175	34
Human SRCAP.	AAB50362	22	3118	7.8	176.5	3 3
Human SRCA	AAB50363	22	2972	7.8	176.5	32
	ABB60186	22	1714	7.8	176.5	ω
Drosophila	ABB71837	22	662	7.9	177.5	30
Human	AAB95541	22	1127	7.9	178	29
	AAB42650	21	1322	8.0	180.5	28
Human	ABG66756	23	1296	8.0	181	27
Human novel polyp	ABG66702	23	1296	8.0	181	26
Human polypepi	AAM93811	22	881	8.1	181.5	25
Human protein	AAB94334	22	709	8.1	181.5	24
Human protein	AAB93063	22	709	8.1	181.5	23
Human protein	AAM78994	22	709	8.1	181.5	22
Human protein s	AAM79978	22	708	8.1	181.5	21
Human EXMAD-2	AAB27242	22	571	8.1	181.5	20
Human	AAE21714	23	2135	8.5	191	19
Novel	AAB65656	22	1920	8.5	191	18
C899P predi	AAM24516	22	5179	8.7	195.5	17
Drosophila	ABB71319	22	864	8.9	199.5	16
Drosophila	ABB66631	22	842	8.9	199.5	15
Drosophila melano	ABB69806	22	1795	9.0	202	14
Host cell f	-	15	2035	9.1	0	13
Drosophila	ABB66055	22	921	10.7	41	12
Drosophila melanog	\sim	22	921	10.7	241.5	11

ALIGNMENTS

RESULT 1 AAW31494 IID AAW3 XX AAW31494 AC AAW3 XX AAW31494 AC AAW4 XX TATT AC TATT KW TATT KW TATT KW ATATT KW ATATT KW ATATT KW ATATT KW ATATT COS Home XX Home XX Home XX Home XX Home XX AC TATT XX WPI; 1998-109818/10. N-PSDB; AAV02872. TATA-binding protein associated binding factor 105; human; activator; hTAFII105; transcription factor; TFIID; transcriptional activation; antibodies; diagnosis; therapy; biopharmaceutical industry. AAW31494 standard; Protein; 801 Dikstein R, 02-OCT-1996; 20-JAN-1998 US5710025-A. 02-OCT-1996; Homo sapiens. Human hTAFII105 protein 28-APR-1998 (first entry) (REGC) UNIV CALIFORNIA Tjian R; 96US-0725012 96US-0725012. A

TATA-binding

prote

DNA encoding human tata-binding protein associated producing recombinant protein

factor -

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                                                                                                                                                                                                                                              RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This cDNA sequence represents a human tata-binding protein associated factor, hTAFTI105, isolated from Daudi cell nuclear extracts. Tightly associated subunits ("AF's) are components of the transcription factor TFIID and are thought to mediate transcriptional activation. This encoc protein may be produced recombinantly from transformed host cells or purified from human cells. hTAFTI105 specific binding agents such as specific antibodies could be used for diagnosis (e.g. genetic hybridisation screens for hTAFTI105 transcripts), therapy (e.g. gene therapy to modulate hTAFTI105 gene expression) and in the
                                                                                              Human;
food si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biopharmaceutical industry (e.g. as immunogens, reagents for isolating cell specific activators or other transcriptional regulators).
                                                                                                                                     Novel
              11-OCT-2001
                                                                                                                                                              13-FEB-2002
                                                                                                                                                                                                                    ABG09468 standard;
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                                                                  sapiens
                                                                                                                                                                                                                                                                                                VVSFCWDHICKPVIGTPVQIKLAQPGPVLSQP 452
                                                                                           supplement;
                                                                                                                                                                                                                                                                                                                                                    GTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAVTEGETSGAAICLPSVKP
                                                                                                                                                                                                                                                                                                                                                                                                        VTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPV
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                                                                                                                                                                                                                                                                                    VVSFCWDHICKPVIGTPVQIKLAQPGPVLSQP
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                                                                                                                                    human diagnostic
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                                                                                        chromosome mapping; gene mapping; gene therapy; upplement; medical imaging; diagnostic; genetic o
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                                                                                                                                  protein #9459
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Pred. No. 8.3e-159;
; Mismatches 0;
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fire wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 452; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-639362/73.
N-PSDB; AAS73655.
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated polynucleotide (I) and
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GTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAVTEGETSGAAICLPSVKP
                                                                                                                                               LYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTYTTSPV
                                                                           VTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTA
                                                                                                                                                                                                                      VQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRK 240
                                                                                                                                                                                                                                                                                                                                                                   MLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGT 120
                                                      VTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTA
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2000US-0649167
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Pred. No. 8.3e-159;
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                                                                                                                                                                                                                                This represents a polypeptide comprising a (modified) fragment (I) a TATA box-binding protein associated factor II 105 (TAFII105). A pharmaceutical composition comprising (I) or the polynucleotide or inhibitor or antagonist of (I) is useful for treating cancers and inducing apoptosis in pathological cells. The composition is also u for treating autoimmune diseases, inflammatory processes and viral bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptide encoding TATA box binding protein associated factor II 105 useful for treating e.g. cancers and inducing apoptosis has a dominant negative effect on the normal biological activity of the binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATA box-binding protein associated factor II 105; TAFII105; cancer; transcription factor; apoptosis; cytostatic; immunosuppressive; antiinflammatory; virucide; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                                      VVSFCWDHICKPVIGTPVQIKLAQPGPVLSQP
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)B; AAZ90465.
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Pred. No. 9e-159;
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                                  The TATA-binding protein associated factor hTAFII130 (including specific antibodies and fusion products) are used in drug screeni diagnostics and therapeutics. They are used in the development o specific blochemical assays for screening compounds that agonise antagonise selected transcription factors involved in regulating gene expression associated with human pathology.
                                                                                                                                                         Disclosure;
                                                                                                                                                                                        TATA-binding protein associated protein factors corresponding nucleotide sequence and deriv. and in screening, diagnostics and therapeutics
Sequence
                                                                                                                                                                                                                            TATA-binding
                                                                                                                                                                                                                                                               N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR56494 standard;
                                                                                                                                                                                                                                                                                                                                                                                                     28-JAN-1993;
30-JUN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRK
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                                                                                                                                                                                                                                                               AAQ70731.
                                                                                                                                                                                                                                                                                                                Dynlact
Wang E,
                                                                                                                                                         Page 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapeutic; gene transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein associated factor; hTAFII130;
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93US-0087119.
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, Weinzierl ROJ;
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28-JAN-1993;
30-JUN-1993;
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Tjian
    Screen
                         N-PSDB; AAT42217
                                   WPI; 1996-333245/33
                                                                                                                                                                               09-JUL-1996
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                                                                                                                                                                                                                                                                  Human; TATA-binding
                                                                                                                                                                                                                                                                                        Human TATA-binding
                                                                                                                                                                                                                                                                                                                                                          AAW06084 standard;
                                                                                       (REGC ) UNIV CALIFORNIA
                                                                                                                                                         28-JAN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                               TLTQT--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPKVSSG------PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM
                                                                                                                                                                                                                                                                                                                                                                                                                                 TFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKL--AQPGPVL 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDGKTEAEDFTSRLYRELNSSPQPYLVPFLKRSLPALRQLTPDSAAFTQQSQQQPPPPTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTVPGATTTSSAATE-----TMENVKKCKNELSTLIKLASSGKQSTETAANVKELVQNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NE-PNIKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----TTIIKQV----SQAQTTVQPSATLQRSPGVQPQLVLGGAAQTASLGTATAVQTGTPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS
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   for
                                                     Dynlacht BD, Hoey
Wang E, Weinzierl F
   cpds. that
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                                                                                                                                                                                                                                             expression library.
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                                                                                                            94US-0188582.
93US-0013412.
93US-0087119.
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                                                                                                                                                                                                                                                                                       protein associated factor hTAFII130 protein.
                                                                                                                                                                                                                                                        transcription;
                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                  protein;
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34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                             PMVALROPH-NRIMLTTPQQIQLNPLQPVPVV
   bind
human TATA-binding protein associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61;
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                                                                                                                                                                                                                                                       TBP associated tion; messenger
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Pred. No. 3.2e-30;
1; Mismatches 128;
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                                                                 Ruppert
                                                                  Ś
                                                                                                                                                                                                                                                      factor; TFIID; holoenz
RNA; nuclear fraction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        -QPPKP----GALTRPPQV
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                                                                                                                                                                                                                                                                                                                                                                                                             446
                                                                                                                                                                                                                                                                holoenzyme;
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This is the amino acid sequence of the human TATA-binding protein (TBP) C associated factor (TAF) designated TAFIIJO. The protein is a component of the TFIID fraction required for reconstituting RNA polymerase II in vitro transcription activity. The encoded protein has an estimated mol. C vitro transcription activity. The encoded protein has an estimated mol. C the invention relates to purified proteins involved in transcription by RNA polymerase II, the RNA polymerase which transcribes messenger RNA. RNA polymerase II transcription proceeds in vitro upon addition of several nuclear fractions designated TFIIA, B, D, F, H, I and J to RNA polymerase II holoenzyme. Fraction TFIID has been shown to contains a TBP and other TAPs. purification of TFIID and separation of the corresp. Scrum raised against the TFIID fraction allowed cloning of the corresp. C genes from lambda-gtll expression libraries.
                                            Query Match
                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Examples; Column 105-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor - by testing ability to bind to polypeptide fragments of the factor, useful as (ant)agonists of transcription factors involved in
                                                                                           737
                                                                                           Å
                       23.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86pp;
Score 521; DB 17;
Pred. No. 3.2e-30;
1; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English
                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                   component
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밁 Ъ 밁 Ş . B 밁 Š 밁 Š 밁 Qy 411 404 344 284 280 228 226 169 173 119 62 8 13 Local Similarity wes 159; Conserv TLTQT-----TFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKL--AQPGPVL 449 VTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAV 403 Q----ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL---LDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ----TS RTVPGATTTSSAATE-----TMENVKKCKNFLSTLIKLASSGKQSTETAANVKELVQNL NE-PNIKAENSAAVQINISPTMIENVKKCKNFIAMIKLACSGSQSPEMGQNVKKIVEQL LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115 PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL PPKVSSG-----SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGV ----TTIIKQV----SQAQTTVQPSATLQRSPGVQPQLVLGGAAQTASLGTATAVQTGTPQ AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----LDGKIEAEDFTSRLYRELNSSPOPYLVPFLKRSLPALRQLTPDSAAFIQQSQQQPPPPPTS -----TQPTQVGVGKQGQPTPLVIQ-----QPPKP-----GALIRPPQV Conservative ----PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM PMVALRQPH-NRIMLTTPQQIQLNPLQPVPVV 61; Indels 120; 446 Gaps 343 339 283 279 227 225 168 172 118 61 20;

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AAW25019
ID AAW2
XX AAW2
XX AAW2
XX OB-O
DT OB-O
DE TATA
KW TATA
KW TNATA
  RNA polymerase initiation.
                      TATA-binding
                                        TATA-binding
                                                                08-OCT-1997
                                                                                     AAW25019;
                                                                                                         AAW25019 standard;
      protein associated factor; TAF; nuclear
se transcription; TATA-binding protein;
                                          protein associated
                                                                                                         Protein;
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                  TAF; nuclear protein;
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28-JAN-1993;
30-JUN-1993;
09-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Comai L,
Tjian R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW25018 represents TATA-binding protein associated factor (TAF) polypeptide, hTAFII100 (mol. weight 100kD). TAF peptides derived from hTAFII30 alpha, hTAFII130 beta, hTAFII140, hTAFII170, hTAFII100, hTAFII130 hTAFII30 hTAFII30 hTAFII30, hTAFII30 hTAFII10 and nucleic acids encoding them, are used to modulate transcription, including transcription initiation. TAFS are nuclear proteins involved in RNA polymerase I, if and III transcription. The peptides act by binding to a different TAF, an activator, or TBP (TATA-binding protein) or competitively inhibiting association of a TAF domain with another compound, typically a protein like TBP or another TAF, an activator, or DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Column 111-116; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for modulating transcription of TAFs
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nes 159; Conserv
                                                                         SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGV 343
                                                                                                                                                                                        NE-PNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL
                                                                                                                                                                                                                                                                                        MI-POQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
                                                                                                                                                                                                                                                                                                                                                                            PPKVSSG------PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM 61
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                         VTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAV 403
                                                                                                                              LDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ----TS 283
                                                                                                                                                                       RTVPGATTTSSAATE-----TMENVKKCKNFLSTLIKLASSGKQSTETAANVKELVQNL
                                                                                                                                                                                                                                                           AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS
                                                                                                                                                                                                                                                                                                                     LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
                                                                                                                                                                                                                                                                                                                                                PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL 118
                                                                                                               LDGKIEAEDFTSRLYRELNSSPOPYLVPFLKRSLPALRQLTPDSAAFIQQSQQQPPPPPTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ic acids encoding human TATA-binding peptide(s) - for production of recon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dynlact BD, Hoey
Wang E, Weinzierl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      737
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                      ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0188582.
93US-0013412.
93US-0087119.
96US-0646715.
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TQPTQVGVGKQGQPTPLVIQ---
                                                                                                                                                                                                                                SQAQTTVQPSATLQRSPGVQPQLVLGGAAQTASLGTATAVQTGTPQ 225
                                                                                                                                                                                                                                                                                                                                                                                                                        23.28;
                                                                                                                                                                                                                                                                                                                                                                                                             61;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 521; DB 18;
Pred. No. 3.2e-30;
61; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruppert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nding protein associated factor
recombinant peptide(s), used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tanese
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 737;
                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                          120;
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                       279
                                                                                                                                                                                                                                                                                          172
                                                                                                                                                                                                                                                                                                                                                                                                          20;
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Query Match Best Local Sim Matches 154;

Similarity

22.8%;

Score 513; DB 2 Pred. No. 2e-29; Mismatches

DB 23; 127;

Length 1023;

118;

Gaps

19

Conservative

62;

Sequence

1023

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                        The invention describes a method of screening a candidate antifungal CC compound for interaction with essential proteins (EP) or for modulation of EP activity e.g fungal gene transcription. The proteins tested in the CC invention include RPC34, POP3, TFA2, NAB2, MPT1, MTT2, BOS1, POL30, RSA2, CC SQT1, MTW1, TFB1, SPC98, BRR2, RNA1, GCD7, SKI6, NIP1, LCP5, NCE103, CC ECO1, ORC2, CNS1, YPD1, TIM10 and SR84 from S. cerevisiae, C. albicans CC and human homologues. The method involves contacting a culture with one CC viability of the culture of cells which preferably comprises fungal cells or yeast cells. Preferably the identified compounds interact with, or CC modulate (preferably inhibit) activity of C. albicans EP. The inhibitor CC compounds identified by the method are useful for preventing or CC inhibiting fungal agents interact with essential fungal elements CC mammal. The antifungal agents interact with essential fungal elements CC that can be used to treat fungal infection by preventing the growth and CC preferentially killing the fungal, but does not inhibit the biological activity of mammalian homologues. This amino acid sequence represents a CC method of the invention.
                                                                                                                                                                                                                                                                                                                                                                       protein,
protein,
effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moore J,
Mendillo
                                                                                                                                                                                                                                                                                                                                                                            Screening candidate antifungal compound for interaction with essential protein, modulation of essential protein activity, binding to essentia protein, by contacting protein with test compound and determining effects -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antifungal; fungal gene transcription; RPC34; POP3; TFA2; NAB2; MPT1; MTR2; BOS1; POL30; RSA2; SQT1; MTW1; TFB1; SPC98; BFR2; RNA1; GCD7; SKI6; NIP1; LCP5; NCE103; ECO1; ORC2; CNS1; YPD1; TIM10; SRB4;
                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-147962/19
N-PSDB; ABK32842.
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10-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human homologue of MPT1 protein target
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M, Moore D,
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2000US-224457P
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                                                                                                                                                                                                                                                                                                                                          79; 522pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
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Mccoy M, Sanderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1023
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anderson K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for antifungal compound
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Hag T, Zhu S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               449
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RESULT 8
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                                                                                                                                        Comai L, L
 The TATA-binding protein associated factor dTAFIII10 specific antibodies and fusion products) are used in
                                                        TATA-binding protein associated protein factors -corresponding nucleotide sequence and deriv. antiin screening, diagnostics and therapeutics
                                                                                                                                                                                                     28-JAN-1993;
30-JUN-1993;
                                                                                                                                                                                                                                                                                                            Drosophila.
                                                                                                                                                                                                                                                                                                                                             TATA-binding
                                                                                                                                                                                                                                                                                                                                                                  TATA-binding
                                    Disclosure; Page 56-61; 180pp; English.
                                                                                                                                                                                                                                        28-JAN-1994;
                                                                                                                                                                                                                                                               04-AUG-1994.
                                                                                                                                                                                                                                                                                     WO9417087-A.
                                                                                                                                                                                                                                                                                                                                 diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                  AAR56487;
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR56487 standard; Protein;
                                                                                                                                                                              (REGC ) UNIV CALIFORNIA.
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                                                                                                           1994-264019/32.
DB; AAQ70724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q----ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLTQT------PMVALRQPH-NRIMLTTPQQVNLSE 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TEGETSGAAICLESVKPVVSFCWDHICKEVIGTEVQIKLAQ 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS
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                                                                                                                                          Dynlact I
, Wang E,
                                                                                                                                                                                                                                                                                                                                protein associated factor; dTAFIII10; screening;
therapeutic; gene transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                  protein-associated
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                     93US-0013412
93US-0087119
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                                                                                                                                            BD, Hoey T, R
                                                                                                                                                                                                                                                                                                                                                                                                                                         921
                                                                                                                                                     Ruppert
                                                                                                                                                                                                                                                                                                                                                                  factor dTAFII110
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 (including drug scree
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screening,
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RESULT 9
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    PAN PRESENTATION OF THE PR
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Matches
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                                                                                           28-JAN-1994;
28-JAN-1993;
30-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostics and therapeutics. They are used in the development of specific biochemical assays for screening compounds that agonise or antagonise selected transcription factors involved in regulating gene expression associated with human pathology.
    Coma 1
                                             (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                           28-JAN-1993;
                                                                                                                                                                                                                                       09-JUL-1996
                                                                                                                                                                                                                                                                                    US5534410-A
                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; TATA-binding protein; TBP associated factor; RNA polymerase II; transcription; messenger RNA; nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila TATA-binding protein associated factor dTAFII110 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JAN-1997
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Pred. No. 2.8e-09;
5; Mismatches 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC (TBP) associated factor (TAF) designated TAFIII10. The protein CC (TBP) associated factor (TAF) designated TAFIII10. The protein is a CC component of the TFIID fraction required for reconstituting RNA CC polymerase II in vitro transcription activity. The encoded protein CC has an estimated mol. wt. of 110 kD by SDS-PAGE, a calculated mol. wt. CC based on sequence of the gene of 99.4 kD and an estimated pI of 10.1. CC The invention relates to purified proteins involved in transcription CC by RNA polymerase II, the RNA polymerase which transcribes messenger CC RNA. RNA polymerase II transcription proceeds in vitro upon addition CC of several nuclear fractions designated TFIID has been shown to CC contains a TBP and other TAFs. Purification of TFIID and separation of the components reveals 7 proteins ranging in size from 30-250 kD. CC serum raised against the TFIID fraction allowed cloning of the corresp.
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                                 AAW25028 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screen for cpds. that bind human TATA-binding protein associated factor - by testing ability to bind to polypeptide fragments of the factor, useful as (ant)agonists of transcription factors involved
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                                                                                                               VVSGTAVTLSLPAVTFGETSGAAICLPSVKP 420
                                                                                                                                      QIP-SLQVPGQANIVQIR--GPQHAQLQRTGSVQIRATTRP----PNSVPTAN---
                                                                                                                                                           LNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKP
                                                                                                                                                                                                      ----QCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVS----VQT
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                                                                                                                                                                                                                                                                                                                           APQLPQITQIQTIPAQQSQQQQVNNVSSAGGTATAVSSTTA-
                                                                                                                                                                                                                                                                                                                                              KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSP 187
                                                                                                                                                                                                                                                                                                                                                                      NTTSTTNHPTTTQ-IRLQTVPAAASMTNTTATSNIIVNSVASSGYANSSQPPHLTQLNAQ
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                                                                                                                                                                                  PSQTTTIGQTQVRMI--TPNALGTPRPTIGHTTISKQPPN---IRLPTAPRLVNTGGIRT
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Pred. No. 2.8e-09;
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Tjian R,
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       ASPQPCLIGFLKKSLPLLRQALYTKELVIEGIKPPPQHVLGLAGLSQQLPKIQAQIRPIG
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28-JAN-1993;
30-JUN-1993;
'09-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acids encoding them, are used to modulate transcription, including transcription initiation. TAFS are nuclear proteins involved in RNA polymerase I, II and III transcription. The peptides act by binding to a different TAF, an activator, or TBP (TATA-binding protein) or competitively inhibiting association of a TAF domain with another compound, typically a protein like TBP or another TAF, an activator,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nawzowa representation and the polypeptide, draffill10 (mol. weight 110kD). TAF peptides derived from draffi30 alpha, draffi30 beta, draffi40, draffi60, draffi80, draffill10, draffi1150, and draffi250, their human equivalents and nucleic acids encoding them, are used to modulate transcription,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATA-binding protein associated factor; TAF; nuclear protein; RNA polymerase transcription; TATA-binding protein; TBP; initiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 compound, typically or DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding human TATA-binding (TAF) peptide(s) - for production of record for modulating transcription of TAFs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Column 35-40; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATA-binding
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DB; AAT79604.
                                                                                                                                                                                                                           NTTSTTNHPTTTQ-IRLQTVPAAASMTNTTATSNIIVNSVASSGYANSSQPPHLTQLNAQ
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SSPQPHLVPFLKKSVVALRQL-----
                                                                                                                                      APQLPQITQIQTIPAQQSQQQQVNNVSSAGGTATAVSSTTA---
                                                                                                                                                                              KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSP
                                            TQQGNTKEKCRKFLANLIEL--STREPKPVEKNVRTLIQELVNANVEPEEFCDRLERLLN
                                                                    TMLENVK-KCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELK
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Wang E,
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Pred. No. 2.8e-
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recombinant peptide(s),
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N-PSDB;
                                                  HCF is required for the transcription of a number of viral genes, such as the immediate early herpes simplex virus-1 genes. Epitopes of the encoded protein can be used in defining functional domains of HCF, identifying compounds that associate with HCF or designing compounds capable of modifying transcription. Such agents can be used to treat viral infection
                                                                                                                                                                                                                                                              New Host Cell Factor polypeptide(s) and nucleic acid - are us to develop agents for diagnosis or treatment of disease associated with expression of a HCF-modulated gene e.g. viral
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Best Local Similarity
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  New isolated nucleic
                                                             Venter JC,
                                                                                                               23-MAR-2000;
11-JUL-2000;
                                                                                                                                                 23-MAR-2001; 2001WO-US09231
                                                                                                                                                                           27-SEP-2001
                                                                                                                                                                                                  WO200171042-A2
                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                    pharmaceutical.
                                                                                                                                                                                                                                                                                      Drosophila
                                                                                                                                                                                                                                                                                                               26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                ABB69806 standard; Protein; 1795
                         N-PSDB;
                                                                                     (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                             Drosophila; developmental biology; cell signalling; insecticide;
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                         2001-656860/75.
DB; ABL13909.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --KAENSAAVQINLSPTMLENVKKCKNFL--AMLIKLACSGSQSP------EMGQNVK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPA--TVKVASSPVMVSNPAT------RMLKTAA-----AQVGTSVSSATNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DHICKPVIGTPVQIKL-AQPGPVLSQP 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASLATPITTLGTIATLSSQ----VINPTAITVSAAQTTLTAAGGLTTPTITMQPV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPLYTSVA---NTYTTVSLQPEKPYVSGTAVTLSLPAVTFGETSGAAICLPSVKPYVSFCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRTVPMGGVRLVTPVTVSAVKPAVTTLVVKGTTGVTTLGTVTGTVST--SLAGAGGHSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTSSPGIKSPITIITTKVMTSGTGAPAKIITAVPKIATGHGQQGVTQVVLKGAPGQPGTI 845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---VTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLK-PSSL-GASSTPSNEPNL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGSSPQMSGMAALAAAAAATQKIPPSSA---PTVLSVPAGTTIVKT-----MAVTPGTTT 588
                                                                                                                                                                                                                                                                                                                                                                                                                          -----SQPTQVTLITAPSGVEAQP
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                                                                                                                                                                                                                                                                                      melanogaster
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                                                             Adams M,
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2000US-0614150
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23.5%;
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Pred. No. 5.1e-06;
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                                                             Myers
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reagent for detecting 1000 or
                                                                                                                                                                                                                                                                                      SEQ ID NO 36210
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Disclosure; SEQ ID NO 36210; 21pp + Sequence Listing; English
                                                                                                            genes from Drosophila and for elucidating cell signalling and interactions -  \\
                                                                                                                    cell-cell
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences. cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). ftp.wipo.int/pub/published_pct_sequences. 1795 AA; WIPO 18

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RESULT 15
ABB66631
ID ABB66
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AC ABB66
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            759 TTLTVTPKTSTTTTTEKPITSSPK-PTTTTQKTTSTAPNTT-----KVAITTQKETTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     700 PTSSTGKPTTTPK-PSTRTTPTTTKVTTTTQITTTPLRSSTETTSTQPPTTTTPQPTTT 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 PVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQL------PPGTVLIKSNSG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 PLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQI 118
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                                                                                                                                                                                                                                                                                                                                        SQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGA--TAPR--TVS 326
                                                                                                                                                    QNSTSSTDLTTVTRP
                                                                                                                                                                                      EKPVVSGTAVTLSLP 401
                                                                                                                                                                                                                                                                                                     TTS------VTATTRITTTISESSTETTSTQKPKSTTPTSTTRTTPKVTTVI 1017
                                                                                                                                                                                                                                                                                                                                                                              TQEATTSTQKVSTVTITTKKATESSPLTTLSTEEPNTTPKP------LRTTTPT 970
                                                                                                                                                                                                                                                                                                                                                                                                                  SPEMGQNVKKLVEOLLDAK--IEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPN 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSTENPTTNSVKTSALTSSTQRA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQ 212
                                                                                                                                                                                                                             VSTQNPTT -- TTSKTSTVTITTPNPSPSTQRPTTTTRQPTSITASTTSIGTTRIPTTTNP
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95; Conserv
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Pred. No. 6e-06;
58; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -TSTTSEPTKTTQNITTTTPKPTTLKTS 922
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pharmaceutical. Drosophila; Drosophila melanogaster polypeptide

developmental biology; cell signalling; insecticide;

SEQ

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26-MAR-2002 ABB66631;

(first entry)

ABB66631 standard; Protein;

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Drosophila melanogaster.

WO200171042-A2

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Best Local Similarity 22.5
Matches 124; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
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                                                                                                                                                                                                                                                                                                                                                                                                           117 PPVAATPTPVAPIPVAAPVIATPPVAASAPTPAAVTPVVSP--VIATPPVVPANTTV--- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 IPAPAPIAAASVAPVASVAP--PVVAAPTPP----AASPVSTPPVAVAQIPVAVSAPVA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GTLVTKV-APVSAP-----PKVSSGPRLPAP----QIVAVKAPNTTTIQFPANLQ 45
                                                                                                                                                                                                                                    RQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIV----SGAT 320
                                                                                                                                                                                                                                                                                                                                           PVAAPVAAVPAAVPVVAPVLAPAVAPAVAPVVAETPAPPPVAETPVATTPEC---VAPLI
                                                                                                                                                                                                                                                                                                                                                                 PSSLGASSTPSNEPNLKAENSAAVQINLSPTMLE------NVKKCKNFLAMLI 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTIPSPVSAPVAAPVTPSAVAAPVQVVSPAAVAPAAPIAVTPVAPPPTLASVQPATVT 63
AEETPETPAPASAPVTIAALDIPEVAPVIAAPSDAPAEAPSAAAPIVSTPPTTASVPETT 488
                                 FGET-----SGAAICLPSVKPVVSFCWD-----HICKPVIGTP-----VQIKL 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKVAVT-----PVKKLAQIGTT--VVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPPGTVLIKSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNS-SSQLI 104
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DB; ABL10734.
                                                                                                   QTSKPLVTSVANTVTTVSLQPEKP-----VVSGTAVTLS-----LPAVT 404
                                                                                                                                       EPETIAPPVVAETPEVASVAVAETTPPVVPPVAAES-----IPAPVVAT------
                                                                                                                                                                    APRTVS------VQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLL 365
                                                                                                                                                                                                     ----PVSAS-----TEPPVAAATLTTAPET-PALAPVVAESQVAANTVVATPPTPAP 325
                                                                                                                                                                                                                                                                         ------PEVSVVATKPLAAAEPVVVAPPATETPVVAPAAASPHVSVAPAVETAVVA- 278
                                                                                                                                                                                                                                                                                                         KLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVAL 264
                                                                 -TPVPATLAVTDPDVTASAVPELPPVIAPSPVPSAVAETPVDLAPPVLPPVAAEPVPAVV 428
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22.58;
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Qy 443 AQPGPVLSQP 452 | | | | ::| | Db 489 APPAAVPTEP 498

Search completed: February 16, 2003, 21:54:59 Job time: 42.6501 secs

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Run on:
                                                                                                 OM protein - protein search, using sw model
February 16, 2003, 20:54:50; Search time 8.71092 Seconds (without alignments) 2152.161 Million cell updates/sec
                                                                                                                                                                     GenCore version 5.1.3 Compugen Ltd
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Title: Perfect score:

Sequence: US-09-763-909-2_COPY_1_452
2249
1 GTLYTKVAPYSAPPKVSSGP.....VIGTPVQIKLAQPGPVLSQP 452

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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QY 1 GTLYTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQEPANLQLPPGTVLIKSNSGPL 60

Query Match 100.0%; Score 2249; DB 1; Length 801; Best Local Similarity 100.0%; Pred. No. 7.8e-122; Matches 452; Conservative 0; Mismatches 0; Indels 0;

Gaps

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1 801 AA;

85658 MW; D12B4932FE4A9CD2 CRC64;

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P15822	Q02496						P75211	Q60528	P32768	P14859	Q29076
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ALIGNMENTS

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Transcription regulation; Nuclear protein.	SMART; SM00549; TAFH; 1.	MIM; 601689; -	11538; TAF4B.	321; CAA70499.1;	CA COM AN CHARLE TO ELECTRONICATION CONT.	or and an email to license distaint (see nuth://www.isb-sib.ch/dimounce/	is not removed	itions as long as	European Bioinformatics Institute. There are no restrict	between the Swiss Institute of Bioinformatics and the EMBL outstation -	This SWISS-PROT entry is copyright. It is produced through a collaboration		-!- SIMILARITY: BELONGS TO THE TAF2C FAMILY.			SUBCELLULAR IOCATION: NICCIONE	NUMBER OF THE ASSOCIATED FACTORS (TAFS). TAFILLUS MAY FORM	-I- SUBURIT: TFIID IS COMPOSED OF TATA BINDING PROTEIN (TBP) AND A	PROMOTER RESPONSES TO VARIOUS ACTI	MULTIMERIC PROTEIN COMPLEX THAT PLAYS A CENTRAL ROLE IN MEDIATING	A GENE-SELECTIVE COACTIVATOR IN CERTAIN CELLS. TFIID IS A	-I- FUNCTION: CELL TYPE-SPECIFIC SUBUNIT OF TFIID THAT MAY FUNCTION AS	Cell 87:137-146(1996).	numan tari too is a ceri type specific friib subunit ferated to	10s to a coll turn consists matte subject to lated	MEDITINE 9/OLITAS; PUDMED = 8858150;	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	[1]		Buxaryota; metazoa; thotaata; trantata; vertebrata; fuceteoscomi; Mammalia: Buthoria: Drimatos Catarrhini: Hominidao, Homo		TAF4B OR TAF2C2 OR TAFII105.		Transcription initiation factor TFIID 105 kDa subunit (TAFII-105)	15-IIN-2002 (Ref. 50, East sportstion undste)	(Rel. 36, Creat		T2DT_HUMAN STANDARD; PRT; 801 AA.	T2DT_HUMAN	T 3 1

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RX MEDLINE-21638749; PubMed-11780052;
RA DeLoukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA DeLoukas P., Matthews L.H., Ashurst J.P., Babbage A.K., Bagguley C.L.,
RA Jones M., Stavrides G., Almeida J.P., Beard L.M., Beare D.M.,
RA Balley J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.D., Dunn M.,
RA Clegs S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegs S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Cloulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Bunn M.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., HO S., Holden J.L., Howden P.J.,
RA Hammond S., Harley J.L., Heath P.D., HO S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., King A., Knights A., Laird G.K., Lawlor S.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehvaslahho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97336072; PubMed-9192867;
Mengus G., May M., Carre L., Chambon
"Human ThF(II)135 potentiates transcr
of the retinoic acid, vitamin D3, and
mammallan cells.";
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[2]
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Mammalia; Eutheria;
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Catarrhini; Hominidae;
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                                                         LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
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"MOLECULAR CLOTING and analysis of two subunits of the human TFIID complex: hTAFTII30 and hTAFTII100.",
Proc. Natl. Acad. Sci. U.S.A. 93:13611-13616(1996).
-I- FUNCTION: MAKES PART OF TFIID IS A MULTIMERIC PROTEIN COMPLEX THAT PLAYS A CENTRAL ROLE IN MEDIATING PROMOTER RESPONSES TO VARIOUS ACTIVATORS AND REPRESSORS. POTENTS TRANSCRIPTIONAL ACTIVATION BY THE AF-2S OF THE RETINOIC ACID, VITAMIN D3 AND THYROID HORMONE.
-I- SUBUNIT: TFIID IS COMPOSED OF TATA BINDING PROTEIN (TBP) AND A NUMBER OF TBP-ASSOCIATED FACTORS (TAFS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for come entities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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SIMILARITY: BELONGS TO THE TAF2C FAMILY.
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POLY-HIS.
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G -> GPG (I
Score 521;
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SING (IN REF. 3).
> L (IN REF. 3).
a6453827572A0752 CRC64;
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MEDINE-2016/06 pubMed=10731132;

MEDINE-20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

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Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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Cell 7:
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Eukaryota; Metazoa; Arthropoda; Mandibulata;
Insecta; Pterygota; Neoptera; Endopterygota;
Muscomorpha; Ephydroidea; Drosophilidae; Dros
MCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kokubo T., Gong D.-W., Roeder R.G., Horikoshi M., Nakatani Y.; "The Drosophila 110-kDa transcription factor TFIID subunit directly interacts with the N-terminal region of the 230-kDa subunit."; Proc. Natl. Acad. Sci. U.S.A. 90:5896-5900(1993).
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MEDLINE-93145326;
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ota; Diptera; Brachycera;
Drosophila.
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RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart M.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hastin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McIson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McIson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Weinson S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhao Q., Zheng L.,
RA Wang Z.-Y., Kublin G.M., Venter E., Wang A.H., Smith H.O.,
RA Williams S.M., Rublin G.M., Venter J.C., Shao Q., Zheng L.,
RA Yellor R.H., Zhong W., Rublin G.M., Venter J.C.,
RT The genome sequence of Drosophila melanogaster.*;
RC C. CENTRAL ROLE IN MEDIATING PROWOTEN RESPONSES TO VARIOUS ACTIVATORS
C. AND REPRESSORS MAY FUNCTION AS A COACTIVATOR BY SERVING AS A SITE
C. SUBGILUAR LOCATION: NICelear.
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Matches 112
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Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., I
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hes 112;
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een the Swiss Institute of Bioinformatics and the Ex
European Bioinformatics Institute. There are no restr
by non-profit institutions as long as its content
                               KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSP 187
                                                                                                        NITSRPAVPANPQTVKICTVPNSSSQ-----
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S63550; AAB27433.1; -.
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99338 MW;
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Host cell factor C1 (HCF) (VP16 accessory F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Fetal brain; MEDLINE-95130107; p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS), AND MEDLINE-93327419; PubMed-8392914; Wilson A.C., Lamarco K., Peterson M.G., Herr W.; "The VP16 accessory protein HCF is a family of pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Me
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96033796; PubMed=7590226;
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Mammalia; Eutheria;
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                                                                                                                                                                  FUNCTION: UPON LYTIC INFECTION OF PERMISSIVE CELLS, THE HSV TRANSACTIVATOR PROTEIN VP16 ASSOCIATES WITH HGF. BINDING TO HGF ACTIVATES VP16 FOR ASSOCIATION WITH THE OCTAMER WOTIF-BINDING PROTEIN OCT-1, TO FORM A MULTIPROTEIN-DNA COMPLEX RESPONSIBLE FOR ACTIVATING TRANSCRIPTION OF THE HSV IMMEDIATE EARLY GENES.
SUBUNIT: COMPOSED PREDOMINANTLY OF SIX POLYPEPTIDES RANGING FROM 110 TO 150 KDA AND A MINOR 300 KDA POLYPEPTIDE. THE MAJORITY OF MAD C. TERMINAL CLEAVAGE PRODUCTS REMAIN TIGHTLY, ALBEIT NORCHAL THE MAJORITY OF NORCHAL THE M
                        ASSOCIATE.
                                                          NONCOVALENTLY, ASSOCIATED.
SUBCELLULAR LOCATION: Nuclear.
SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND SHORT FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING. IN THE SHORTER FORM THE N- AND THE C-TERMINAL FRAGMENTS FAIL TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a large precursor protein."; 74:115-125(1993).
                                                                                                                                                                                                                                                                                                                                               on A.C., Peterson M.G., Herr W.;
HCF repeat is an unusual proteolytic cleavage signal.";
s Dev. 9:2445-2458(1995).
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  KIDNEY.
SPECIFICITY: HIGHLY EXPRESSED KIDNEY. PRESENT IN ALL TISSUES
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Primates;
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Vezzoni P.;
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                                                                                                                                                                      446 TLLPQAAP--APPTTTTIQVLPTVPGSSISVPTAARTQGVPAVLKVTGPQATTGTPLVTM
                                       166
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                                                                                                                                                     40 FPAN------LQLPPGTVLI---KSNSGPLMLVSPQQT-----VTRAETTSNI--TS
                                                                                                                                                                                         2 TLVTKVAPVSAPPKVSSGPRLP-----
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                                       TPSNEPNL----
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                   LISNLGKVMSVVQTKPVQTSAVTGQASTGPVTQIIQTKGPLPAGTILKLVTSADGKPTTI
                                                        VGTSVSSATNTSTRPIITVHKSGTV-TVAQQAQVVTTVVGGVTKTITLVKSPISVPGGSA
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PF01344; Kelch;
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  Pfam; PF00041; fn3; 2.
Pfam; PF01344; Kelch; 5.
SMART; SM00060; FN3; 2.
Nuclear protein; Repeat.
REPEAT 44 89
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P51611;
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the Euro
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Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
-i- FUNCTION: UPON LYTIC INFECTION OF PERMISSIVE CELLS, THE HSV
TRANSACTIVATOR PROTEIN VP16 ASSOCIATES WITH HCF. BINDING TO HCF
ACTIVATES VP16 FOR ASSOCIATION WITH THE OCTAMER MOTIF-BINDING
PROTEIN OCT-1, TO FORM A MULTIPROTEIN-DNA COMPLEX RESPONSTBLE RO
ACTIVATING TRANSCRIPTION OF THE HSV IMMEDIATE EARLY GENES (BY
                                                                                                                                EMBL; D45419; BAA0825
InterPro; IPR003961;
InterPro; IPR001798;
                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                     This
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16-0CT-2001 (Rel. 40, Last annotation update)
Host cell factor C1 (HCF) (VP16 accessory protein) (HFC1) (VCAF)
(CFF).
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01-OCT-1996 (Rel. 34,
16-OCT-2001 (Rel. 40,
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Exercise Bioinformatics Institute. There are no restricted the state of the stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: EXISTS AS A FAMILY OF POLYPEPTIDES THAT ARISE THROUGH CLEAVAGE AT ONE OR MORE CENTRALLY LOCATED SITES. CLEAVAGE AT A DEFINED SITE, PPCE/THET, WITHIN THE HCF REPEAT (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: COMPOSED PREDOMINANTLY OF SIX POLYPEPTIDES RANGING FROI 110 TO 150 kDa AND A MINOR 300 kDa POLYPEPTIDE. THE MAJORITY OF AND C-TERMINAL CLEAVAGE PRODUCTS REMAIN TIGHTLY, ALBEIT
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SUBUNIT: CON
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Chordata; Craniata; Vertebrata; I
Rodentia; Sciurognathi; Muridae;
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01-AUG-1988 (Rel. 08, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-UCCT-2001 (Rel. 40, Last annotation update)
11-OCT-2001 (Rel. 40, Last annotation update)
12-OCT-2001 (Rel. 40, Last annotation update)
13-OCT-2001 (Rel. 31, Last sequence update)
13-OCT-2001 (Rel. 31, Last sequence update)
13-OCT-2001 (Rel. 31, Last sequence update)
14-OCT-2001 (Rel. 31, Last sequence update)
15-OCT-2001 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 31, La
                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyc
                              SEQUENCE FROM N.A.
                                                                                  NCBI_TaxID=4932;
                                                                                                                   Saccharomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKIEAEEFTRKL-YVELKSSP-QPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMV
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KELCH 5.
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EMBL; M16164; AAA35014.1; --
EMBL; M16165; AAA35015.1; --
EMBL; X13857; CAA33069.1; --
PIR; B26877; B26877.
                                                                                                                                                                                                                                                                                                                                               SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     entitles requires a license agreement (Some send an email to license@isb-sib.ch).
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use by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pardo J.M., Ianez E., Zalacain "Similar short elements in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=89031230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: Hydrolysis of termina glucose residues successively from non-rewith release of beta-D-glucose. SIMILARITY: TO S.POMBE SPBC215.13.
SIMILARITY: SOME, TO S.POMBE SPC285.13C.
                                                                                                                                                                                                                                                                                                                                            A26877; A26877.
S48478; S48478.
S0001458; MUC1.
SSSTTESSVAPVPTPSSSSNITSSAPSSTPFSSSTESSSVPV---PTPSSSTTESSS---
                                                                                                                                              TTESSSAPVTSSTTESSSAPVPTPSSSTTESSSAPVPTPSSSTTESSSAPVPTPSSSTTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae.";
Lett. 239:179-184(1988).
                                               PTPSSSTTESSSAPVTSSTTESSSAPVPTPSSSTTESSSAPVPTPSSSTTESSSAPVPTP
                                                                      -TPVKKLAQIGTTVVTT------VPKPSSVQS-----VAVPTSVVTVTPGKPLNT-
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Multigene family.
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Nakamura M., Fukui
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BER/THR-RICH.

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                 degradation;
                                                                                                                                                                                                          DB 1;
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ne STA2 and
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                                                                                                                                                                                                                    Length 1367;
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RESULT 7
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J. Clin. Invest. 88:1005-1013(1991).

-I- FUNCTION: COATS THE EPITHELIA OF THE INTESTINES, AIRWAYS, AND OTHER MUCUS MEMBRANE-CONTAINING ORGANS. THOUGHT TO PROVIDE A OTHER MUCUS MEMBRANE-CONTAINING AGAINST PARTICLES AND INFECTI
                                                                                                                                                                                                                                                                                                                                                                                                               Gum J.R. Jr., Hicks J.W., Toribara N.W., "Molecular cloning of human intestinal mu identification of the amino terminus and to prepro-von Willebrand factor.", J. Biol. Chem. 269:2440-2446(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q02817; Q14878;
01-JUN-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                   MEDLINE=91358717; PubMed=1885763;
Toribara N.W., Gum J.R. Jr., Culhane P.J., Lagace
Petersen G.M., Kim Y.S.;
                                                                                                                                                                                                                                                                                                         both
                                                                                                                                                                                                                                                                                                                                   Gum J.R. Jr., Hicks
Kim Y.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Intestine;
MEDLINE=94132002;
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Mammalia; Eutheria;
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                                                                                                                                                                                                          "MUC-2
                                                                                                                                                                                                                                                             SEQUENCE OF 1343-1895 AND 4176-4195 FROM
                                                                                                                                                                                                                                                                                                      "The human MUC2 intestinal mucin has cysteine-rich both upstream and downstream of its central repetit
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93016075; PubMed=1400449;
                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Colon;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 626-1895 AND 4196-5179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
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        AGENTS AT MUCOSAL SURFACES.

- SUBCELLULAR LOCATION: Secreted.

- TISSUE SPECIFICITY: COLON, SMALL INTESTINE, (
BRONCHUS, CERVIX AND GALL BLADDER.

- PTM: ALL CYSTEINE RESIDUES ARE INVOLVED IN II
INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).

- POLYMORPHISM: THE NUMBER OF REPEATS IS HIGHLY
VARIES AMONG DIFFERENT ALLELES.
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                                                                                                                                                                                                       human small intestinal
                                                                                                                                                                                                                                                                                           Chem.
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                                                                               INTESTINE,
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SIMILARITY

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Pfam; PF00094; vwd; 4.
Pfam; PF01826; TIL; 1.
PF1NTS; PR00438; GFCYSKN
SMART; SM00214; VWC; 2.
SMART; SM00216; VWD; 4.
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InterPro; IPR000561; EGF-11ke
InterPro; IPR002400; GEF-Cyskn
InterPro; IPR002919; TIL_Cyst
InterPro; IPR001007; VWF_C.
InterPro; IPR001846; VWF_D.
Pfam; PF000007; Cys_knot; 1.
Pfam; PF000093; VWc; 1.
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PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS01208; VWFC; 2.
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Eukaryota; Metazoa; Arthropoda; Mandibulata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                   use by non-profit institutions as long modified and this statement is not remove entities requires a license agreement (Se
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-Auburn 1;
                                                                                                                                                                                                                                                                                                                                  Ictalurid herpesvirus 1 (Channel catfish virus) (CCV). Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Ictalurid Herpes-like viruses.
EMBL;
                                      or send
                                                                                                                                                                                    Virology 186:9-14(1992)
                                                                                                                                                                                                                       Davison A.J
                                                                                                                                                                                                                                          MEDLINE-92087490; PubMed-1727613;
                                                                                                                                                                                                                                                         STRAIN-Auburn
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                                    an email to license@isb-sib.ch)
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. 24, Last sequence up.
. 34, Last annotation :
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Q05049;
01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Integumentary mucin C.1 (FIM-C.1) (Fragment).
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Xenopus laevis (African Clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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-i- TISSUE SPECIFICITY: SKIN.
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-i- SIMILARITY: CONTAINS 6 P-TYPE (7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "P-domains as shuffled cysteine-rich modules in integumentary C.1 (FIM-C.1) from Xenopus laevis. Polydispersity and genetic
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J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00088; trefoil; SMART; SM00018; P; 6.
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L02115; AAA74725.1; -. PIR; A45155; A45155.
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TISSUE=Skin;
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Glycoprotein; Alternative splicing
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Matches 100;
YS89_CAEEL S
Q09624; Q09625;
Q1-NOV-1995 (Rel
15-JUN-2002 (Rel
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                                                                                                                                       GPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAVTFGETS
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                                                                                                                                                                                                                                                                              EEFTRKLYVELKSSPQPHLVPFLKKSVVA--LRQ---LLPNSQSFIQQCVQQTSSDMVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                        CFDPKGHGGIHCFHRKPKGHSHEEHTTTTTKAPTTIQIATT--TTTPTTTTTTTKATPTT
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                                                                                                                                                                                                  SQ----
                                                                                                                                                                                                                                                                                                                     ECKMEPSKREDCGYSGITESQCRT-----KGCCFDSSIPQTKWCFYTL-SQVADCKVEP
                                                                                                                                                                                                                                                                                                                                               QINLSPTMLENV-----KKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEA
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   9625; Q969D4;
5 (Rel. 32, Created)
2 (Rel. 41, Last sequents 2 (Rel. 41, Last anno
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                                                              STANDARD;
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67774 MW;
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BY SIM
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Pred. No. 0.003
56; Mismatches
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-> R.
-> A.
F085277F1ED2FD40 CRC64;
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Query Match
Best Local Sin
Matches 100;
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EMBL; Z48582; CAB70192.1; JOINED.
EMBL; Z48582; CAB70201.1; -.
EMBL; Z48544; CAB70201.1; JOINED.
WormPep; ZK945.9; CE25697
InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR001024; Lipoxygenase_LH2.
InterPro; IPR000638; M+channel_n1g.
InterPro; IPR000203; PKD_cys_rich.
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SEQUENCE
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TRANSMEM
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Durbin R.;
Submitted
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ZK945.9/ZK945.10.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Enkaryota; Peloderinae; Cae
                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01477; PLAT; 1
Pfam; PF01825; GPS; 1.
SMART; SM00303; GPS; 1
SMART; SM00308; LH2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (see or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Bristol N2;
Wilkinson-Sproat J.;
Submitted (FEB-1995)
                                                                                                                                                                                                                                                                                                                               Hypothetical
DOMAIN
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           TTVVTTVPKPSSVQSVAV-PTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENS
                                                                                                     TLVTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM
 SSSSTTVTTPTSTESTSTSPSSTVTTSTTAP
                                       VTSTSSTVTTTEPTTTLTTSTASTSTTEPSTSTVTTSPSTS-----
                                                            LVSPQQTVTRAETTSNITSRPAVPA--NPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIG
                                                                                 TLSTSIPTTTPEITSTLSSLPDNAICSYLDETTTSTTFTTTMLTSTTTEEPSTSTTTTE
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00; Conservative
                                                                                                                                                                     l protein; 1.
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105 1241
107 2120
13 30
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2858
2958
3060
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                                                                                                                                                                     344726
                                                                                                                                                                                                                                                                                                                   Transmembrane.

SER/THR-RICH.

GLY/SER-RICH.
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Caenorhabditis.
                                                                                                                           62;
                                                                                                                                                                     MW;
                                                                                                                          Score 175.5;
Pred. No. 0.02
52; Mismatches
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POTENTIAL.

POTENTIAL.
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STSTTGPSS
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                                                                                                                                      .025;
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                                                                                                                           215;
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                                        PVTSTVTSS
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L outstation -
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                                                                                                                     Query Match
Best Local :
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01-DEC-1992
01-DEC-1992
01-DEC-1992
                                                                                                                                                     TRANSMEM
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                            "The DNA sequence of equine herpesvirus-1."; Virology 189:304-316(1992).
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                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=92295566; PubMed=1318606;
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                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                       Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Alphaherpesvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Equine herpesvirus type 1 (strain Ab4p)
Viruses; dsDNA viruses, no RNA stage; He
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                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                    ; M86664; AAB02506.1;
H36802; VGBEX1.
TVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAA 180
                                                                                   GTLVTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPL
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                                          MLVSPQQTVTRAETTSNITSRPAVPANPOTVKICTVPNSSSQLIKKVAVTPVKKLAQIGT
                                                                 GTTNSSSSPTTSPPTTSSSP----PTSTHTSSPSSTSTQ
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(Rel.
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797
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80342 MW;
                                                                                                                                                                                                                        Transmembrane;
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                                                                                                                      7.7%;
19.0%;
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POTENTIAL.
GLYCOPROTEIN X
SER/THR-RICH.
                                                                                                                                                                                                                                                                                        is not removed.
                                                                                                                     Score 172.5; DB Pred. No. 0.0069
                                                                                                                                                     POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL).
50C9ED9211F5E5B2 CRC64;
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RESULT 13
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Q07284;
                                                                                                                                                                                                                                                                Klein K., Mueller-Lantzsch N.;
Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: RESPONSIBLE FOR EBV BINDING TO THE CR2 RE
                                                                                                                                                                                                                                                                                                                                   "The Epstein-Barr virus candidate vaccine antigen conserved between virus types A and B."; Virology 195:578-586(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Epstein-barr virus (strain AG876) (Hum Epstein-barr virus (strain P3HR-1) (Hum Epstein-barr viruses, no RNA stage; Viruses; dsDNA viruses, no RNA stage; Gammaherpesvirinae; Lymphocryptovirus. NCBI_TaxID=82830, 82829;
                                                                                                                                                                the European Bioinformatics Institute. Thuse by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                  Lees J.F., Arrand Arrand J.R.;
                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-AG876, and MEDLINE-93331716;
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                                                                                       Membrane;
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3; AAA02787.1; -.
6; CAA47986.1; -.
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J.E., Pepper S.
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ID YAG3_Y
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AC P39712
DT 01-FEB
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DT 12-FEB
DT EB
DE Hypoth
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Best Local S
Matches 111
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P39712;
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                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacci
Saccharomycetales; Saccharomycetaceae; Saccharomyces
NCBI_TaxID=4932;
   STRAIN-S288c / AB972;
MEDLINE-95249563; Pub
                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Hypothetical 138.1 kDa protein in FLO9-GDH3 i
                                         SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
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S--SDMVIATCTTT--VTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVG
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----GLISTTEPWTGTFTSTSTEMTTVTGTNGQPTDETVIVIRTPTSEGLVTT-TTEP
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STRONG, TO YEAST PROTEIN FLO1.
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RESULT 15

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DT 16-OC

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16-OCT-2001 (Rel. 40, I
16-OCT-2001 (Rel. 40, I
                                                                                                                          EMBL; U83191; AAC51208...
Genew; HGNC:12857; ZAN.
                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                               Interpro; IPR000561; EGF-11:
Interpro; IPR000998; MAN_doi
Interpro; IPR002919; TIL_Cy;
Interpro; IPR003328; TILa_C;
Interpro; IPR001846; VWF_D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Chromosome localization of the mouse zonadhesin zonadhesin gene (ZAN).";
Genomics 41:119-122(1997).
-i- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNI
                                                                                                                                                                                                                                                                        between
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Tsui L.C., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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Homo sapiens (Human).
Metazoa; Chordata;
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MEDLINE-99018118; E
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                                                                                                                                                                                                                                     European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                 DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDICTAL ISTHMUS. DOMAIN: THE VWFD DOMAINS 2 AND 3 MAY MEDIATE COVALENT OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2). SIMILARITY: CONTAINS 3.5 MAM DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVE APICAL REGION OF THE SPERM HEAD (BY SIMILARITY).
TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPER DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION ZONA PELLUCIDA.
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                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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TIPTEKLTALRPPHP
                                                                             TSVANTVTTVSLQPEKPVVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKP 432
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                                                             SPEKLTIPT - - - - - EKPTISTEKPTIPTEKLT
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Search completed: February 16, 2003, 21:56:12 Job time : 19.7109 secs

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A;Experimental source: intestine
F;1-59,60-118,119-177,178-236;237-295/Region: repeat
F;296-565/Region: semi-unique #status predicted
F;566-582,583-599,600-616,617-633,634-647/Region: repeat
                                                                                                                                                                                                                                                                                                                                                                                             R;Van Klinken, B.J.W.; Van Dijken, T.C.; Oussoren, E.; Bueller, H.A.; Dekker, J.; Einerh Blochem. Blophys. Res. Commun. 238, 143-148, 1997
A;Title: Molecular cloning of human MUC3 cDNA reveals a novel 59 amino acid tandem repea A;Reference number: PC4395; MUID:97445141; PMID:9299468
A;Accession: PC4395
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A;Gene: MUC5B
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A; Residues: 1-648 < VAN>
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Best Local Similarity 20...
100; Conservative
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Best Local Similarity
Matches 102; Conserv
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T----TVPKPSSVQSVAVPTSVVTVTPGKPLNTVT----TLKPSSLGASSTPSNEDNL 173
                                                                                                                        VDRSTPVTTSTQSNSTP--TPPEVITLPMSTPSEVSTPLTI-MPVSTTSVTISEAGTAST
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                                                                                                                                                                                            Score 185; DB 2; I
Pred. No. 0.00092;
3; Mismatches 188;
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                                                                                                                                                                                                                                 Length 648;
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                                  414 CLPSVKPVVSFCWD--HICKPVIGTPV 438
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                                                                                                                                              390 SFSIPAEVTTIRISITSERS----TPLTTLLVST-----
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                                                                                                                                                                             TVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTA 353
                                                                                                                                                                                                                     TLEGTTTMPMSTTSERSTLLTTVL---ISPISVMSPSEASTLSTPPGDTSTPLLTSTKAG 389
                                                                                                                                                                                                                                          AEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTT
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                                                                       FPGASIASTPPLDTSTTFTPS-----TDTASTPTIPV----ATTISVSVITEGSTPGTTI 475
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Search completed: February 16, 2003, 22:00:40 Job time: 25.2925 secs

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probable Myb-family transcription factor F16M22.4 [imported] -
c;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change
c;Accession: F96615
                                                                                                                                    RESULT
F96615
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C; Superfamily: Eps
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A; Residues: 1-825 < NHA>
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1ly: Epstein-Barr virus men
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; Pred. No. 0.00059;
44; Mismatches 169;
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Chin, C.W.; Chung, M.K.; Coun, C., Chin, C.W.; Chung, M.K.; Coun, C., Chin, C.W.; Hughes, B.; Huizar, L. ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000

Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khayk C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rozzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Shinn, P.; Southwick, A.M.; S. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; S. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                        J. Biol. Chem. 272, 3168-3178, 1997
A;Title: Human mucin gene MUC5B, the 10.7 kb large ca;Reference number: Z22899; MUID:97166151; PMID:9013 A;Acression: T45025
                                                                                                                                                                                                    mucin MUC5B, tracheobronchial [imported] - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_ch
C;Accession: T45025
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A;Cross-references: EMBL: Z72496; A;Experimental source: placenta
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A; Gene: F16M22.4
                                        A; Molecule type: DNA
A; Residues: 1-3570 <DES>
                                                                                A; Status: preliminary; translated
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112; Conser
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Chung, M.K.; Conn, L.;
Hughes, B.; Huizar, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB:AE005173; NID:g11055843; PIDN:AAG28311.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.3%; Score 186.5; DB
23.8%; Pred. No. 0.0011;
tive 58; Mismatches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alm, C.J.; Federspiel, N.A.; Kaul, S.; White, (L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.;
                     NID:g1834502; PIDN:CAA96577.1;
                                                                                  from
                                                                                  GB/EMBL/DDBJ
                                                                                                                                                                                                                           21-Jan-2000 #text_change
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                                                                                                                          PMID: 9013550
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                                                                                                                                                                                     Aubert,
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                                                                                                                                                                                                                                                                                                                                                                                                               427
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                     PID:g1834503
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Marzia
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A;Molecule type: DNA
A;Residues: 1-1777 <FAV>
A;Cross-references: EMBL:U41263; PIDN:AAC24428.1; GSPDB:GN00020; CESP:T19D12.
A;Experimental source: strain Bristol N2; clone T19D12
C;Genetics:
C;Genetics:
C;Genetics:
A;Gene: CESP:T19D12.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T19D12.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #te C;Accession: T34369 R;Favello, A.
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                                                                                                                                                                                                                                                                                                                                                                                      A; Introns: 36/1; 134/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, Novemb
A;Description: The sequence of C. elegans
A;Reference number: Z21513
A;Accession: T34369
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                                                                                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                QLIKKVAVTPVKKLAQIGTTVVTTVPKPSSVQ-SVAVP---TSVVTVTPGKPLNTVTTLK
                                                                                                                                            TTTVGKTTTTAQNSTWAATTTASNTTTQPVVTTSTSTQGISTTTAQATPSSSVIPTTT
                                                                                                                                                                                                                         VTTTVAQTTTAPIVTTAN--TTTQGVTTTAGVTTTVTRAQNSTLAATTTAPSTNTTTQGV
                                                                                                                                                                                                                                                                 LVTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNS----GP
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    PSSLGA-SSTPSNEPHLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEM
                                                              QTTQRPTSTGIPSTVSTSQGTSSTSPIPSTTQTSSSAPSTYTSNFTPSPTTTLLT-STIA
                                                                                                                                                                                 LMLVSPQQTVTRAE-----TTSNITSRPAVPANPQTVKICT----VPNSS-----S
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                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                  180/1; 622/3; 691/2; 754/1; 1111/2; 1174/1; 1271/3;
                                                                                                                                                                                                                                                                                                                           8.5%; Score 192; DB 2; Length 1777; 24.3%; Pred. No. 0.0013;
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                                                                                                                                                                                                                                                                                                        59;
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legans cosmid T19D12.
                                                                                                                                                                                                                                                                                                        Mismatches 176;
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A; Title: Channel catfish vir
A; Reference number: A39447;
A; Contents: annotation
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C; Superfamily:
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A; Residues: 1-670 <DAV>
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A; Accession: F36791
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Best Local S
Matches 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                            248
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                                                                                                                                                                                                                                                                                                    TTVVTTVPKPSSVQSVAVPT----SVVTVTPGKP---LNTVTTLKPS-SLGASSTPSNEP
                                                                                                                                                                                                                                        NLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAK 231
                                                                                                                                                                                                                                                                                                                                                                                                  RAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTP------VKKLAQIG
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  SVGPTAATGGTTA----
                                     ATVKPTGATGTVTTTTAKPTGANDTANVTKPTGATGTVTTTT----AKPTGA-TGTVTVA
                                                                         CTT--TVTTSPVVTTTVSSSQSEKSIIVSGAT-APRTVSVQTLNPLAGPVGAKAGVVTLH
                                                                                                                                                        IEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQT-SSDMVIAT
                                                                                                                                                                                                      PAKPAGANGTVVTTTPAM----
                                                                                                                                                                                                                                                                               DTVVTTTP-----AMPTGATDTVVTTTPAMPTGATDTVVTTTPAMPTGATDTVVTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSTQGVPTSSKSSSPN-----STPTTTTTP-----
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-GTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTL 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 191; DB 2;
Pred. No. 0.00042;
                                                                                                                     -DTVVTTAPATPAGANDTANVTKPTGATDTVVTT
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RESULT 8
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A;Gene: SGD:MUC1; STA2; MAL5; DEX2; SGD:S0001458
A;Cross -references: MIPS:YIR019c; SGD:S0001458
A;Map position: 9R
C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase C;Superfamily: yeast glucan 1,4-alpha-glucosidase C;Superfamily: yeast glucan 1,4-alpha-glucosidase C;Superfamily: yeast glucan 1,4-alpha-glucosidase F;S-21/Domain: transmembrane #status predicted <TML>
F;S-21/Domain: transmembrane #status predicted <TML>
                                                                                                                                                                                                               calphotin - fruit fly (Drosophila melanogaster)
C; Species: Drosophila melanogaster
C; Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_ch
C; Accession: A47283
R; Ballinger, D.G.; Xue, N.; Harshman, K.D.
Proc. Natl. Acad. Sci. U.S.A. 90, 1536-1540, 1993
A; Mitle: A Drosophila photoreceptor cell-specific protein, A; Reference number: A47283; MUID:93165730; PMID:8434015
                                                     A;Cross-references: GB:L05080; NID:g157071; PIDN:AAA28420.1; A;Note: sequence extracted from NCBI backbone (NCBIN:124958, C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen
                                                                                                                A; Molecule type: nucleic acid
A; Residues: 1-873 <BAL>
                                                                                                                                                                            A;Contents: photoreceptor cells A;Accession: A47283
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    22
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  . 88
  Score 197.5; DB 2; Pred. No. 0.00024;
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A;Gene: FlyBase:Cpn
A;Cross-references: FlyBase:FBgn0010218
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen
C;Keywords: calcium binding
                                                                                                                                                                                                                                     A;Cross-references: GB:L02111; NID:g157031; PIDN:AAA28405.1; A;Experimental source: photoreceptor cells
A;Note: sequence extracted from NCBI backbone (NCBIN:124955,
                                                                                                                                                                                                                                                                                                                                               R;Martin, J.H.; Benzer, S.; Rudnicka, M.; Miller, C.A. Proc. Natl. Acad. Sci. U.S.A. 90, 1531-1535, 1993
A;Title: Calphotin: a Drosophila photoreceptor cell calcium-binding A;Reference number: A47282; MUID:93165729; PMID:8094559
A;Accession: A47282
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A; Residues: 1-865 < MAR>
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GTIPSPVSAPVAAPVTPSAVAAPVQVVSPAAVAPAPAAPIAVTPVAPPPTLASVQPATVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNS-SSQLIKKVAVT-----PVKKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117;
                                                                                        Similarity
                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                       8.6%;
                                ----PKVSSGPRLPAP----QIVAVKAPNTTTIQFPANLQ 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71;
                                                                      Score 194; DB 2;
Pred. No. 0.00038;
1; Mismatches 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----NVKKCKNFLAMLIKLACSGSQSPEMGQNVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                        Length
                                                                       Indels
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                                                                                                                                                                carboxyl-terminal homolo
                                                                                                                                                                                                                                      NCBIP: 124956)
                                                                                                                                                                                                                                                                        PID:g157032
                                                                      144;
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63
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                                                                      23;
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IPAPAPIAAASVTPVASVAP--PVVAAPTP---

PAASPVSTPVAVAQIPVAVSAPVA 115

LPPGTVLIKSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNS-SSQLI 104

A; Molecule 1 A; Residues:

Molecule type: mRNA

1-639 <GU1>

Lagace,

R.E.;

Kin,

Y.S.

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A:Molecule type: DNA
A:Residues: 1343-1350, 'L',1352-1411,'S',1413-1448,'P',1450-1503,'T',1505-1915 <TOR
A;Cross-references: GB:M74027; NID:g188863; PIDN:AAA59875.1; PID:g188864
A;Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:55749, NCBIP:55750)
R;Gum, J.R.; Byrd, J.C.; Hicks, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.S.
J. Biol. Chem. 264, 6480-6489, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.S.
J. Biol. Chem. 264, 6480-6489, A;Title: Molecular cloning of human intestinal mucin cDNAs. Sequence analysis and A;Reference number: A33532; MOID:89197956; PMID:2703501
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                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A: Molecule type: protein
A: Residues: 2328-2342, 'K', 2344-2354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Xu, G.; Huan, L.; Khatri, I.; Sajjan, U.S.; McCool, D.; Wang, D.; Jones, C.; Forstner Biochem. Biophys. Res. Commun. 183, 821-828, 1992
A;Title: Human intestinal mucin-like protein (MLP) is homologous with rat MLP in the C-A;Reference number: PQ0328; MUID:92198477; PMID:1550588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: sequence extracted from NCBI backbone (NCBIP:116698)
R;Toribara, N.W.; Gum Jr., J.R.; Culhane, P.J.; Lagace, R.E.; Hicks, J.W.; Petersen, G.I J. Clin. Invest. 88, 1005-1013, 1991
A;Title: MUC-2 human small intestinal mucin gene structure. Repeated arrays and polymorphise ference number: A43932; MUID:91358717; PMID:1885763
A;Accession: A43932
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R;Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Rothe, E.M.;
J. Biol. Chem. 267, 21375-21383, 1992
A;Title: The human MCC2 intestinal mucin has cysteine-rich
A;Reference number: A45106; MUID:93018075; PMID:1400449
A;Accession: A45106
                                                                                                                                                                                          C;Keywords: glycoprotein; intestine; tandem repeat F;2766-2834/Domain: von Willebrand factor type C repeat homology
                                                                                                                                                                                                                                                                                            A; Cross-references: GDB:120203; OMIM:158370
A; Map position: 11p15.5-11p15.5
                                                                                                                                                                                                                                                                                                                                                                    A; Gene: GDB: MUC2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: small intestine
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A; Residues: 2328-2468 <XUG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Human bronchus and intestine express the A;Reference number: A61257; MUID:91086481; PMID:19 A;Accession: A61257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Jany, B.H.; Gallup, M.W.; Yan, P.S.; Gum, J.R.; Kim, Y.S.; J. Clin. Invest. 87, 77-82, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M22405; NID:g188873; PIDN:AAA36334.1; A;Experimental source: intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1916-2193 <GU4>
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A; Residues: 2037-3020 <GU3>
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A; Accession: B45106
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                                                                                                                                                                                                                            Superfamily: von Willebrand factor; von Willebrand factor type A repeat Keywords: glycoprotein; intestine; tandem repeat
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Residues: 'T', 1
                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Experimental source: bronchus
                                                                                                         Local
2 TLYTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM
                                                                                                     Similarity
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                                                                                              9.0%;
22.3%;
                                                                       45;
                                                                                                  Score 202;
Pred. No. 0
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                                                                   Mismatches
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                                                                                              DB 2;
                                                                                                                             Length 3020;
                                                                   Indels 114;
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                                                                                                                                                                                                    <VWC>
                                                                Gaps
61
                                                                                                                                                                                                                                                              homology;
                                                                   17;
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                                                                                                                                          R;Yamashita, I.; Nakamura, M.; Fuku
J. Bacteriol. 169, 2142-2149, 1987
A;Title: Gene fusion is a possible
A;Reference number: A91831; MUID:87
A;Accession: A26877
                                                                                                                                                                                                                                                                                                                                                                glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae N;Alternate names: extracellular glucoamylase; mucin-like protein MUC1; proc;Species: Saccharomyces cerevisiae C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Nov-1999 C;Accession: S48478; A26877; B26877; S27281; JC6123 R;Rowley, K.
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                    A; Molecule type: DNA
A; Residues: 762-1331
                                                              A;Cross references:
A;Accession: B26877
                                                                                                  A; Molecule type: DNA
A; Residues: 1-242 < YAM>
                                                                                                                                                                                                                                      A; Residues: 1-1367 < ROW>
A; Cross-references: GB: Z47047;
                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: S48478
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                                                                                                                                                                                                                                                                                      DNA
                                                                               EMBL:M16164; NID:g172522; PIDN:AAA35014.1;
                         <YA2>
                                                                                                                                                           possible mechanism underlying
1; MUID:87194600; PMID:3106330
                                                                                                                                                                                                                                                                                                                                             Library, October 1994
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                                                                                                                                                                                                                        EMBL: Z38061; NID: g603997; PID: g763364; GSPDB: GN00009; Fuku1, S.
                                                                                                                                                                                  the
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PID:g172526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cerevisiae)
                                                                                                                                                                                  of STA1
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A;Cross-references: EMBL:M16165; NID:g172523; PIDN:AAA35015.1; R;Pardo, J.M.; Ianez, E.; Zalacain, M.; Claros, M.G.; Jimenez, FEBS Lett. 239, 179-184, 1988
A;Title: Similar short elements in the 5' regions of the STA2 a;Reference number: S27281; MUID:89031230; PMID:3141213
A;Accession: S27281
                                                                                                                             A;Cross-references: EMBL:X13857; NID:g4551; PIDN:CAA32069.1; R;Lambrechts, M.G.; Bauer, F.F.; Marmur, J.; Pretorius, I.S. Proc. Natl. Acad. Sci. U.S.A. 93, 8419-8424, 1996
                                                A; Reference number: JC6123; A; Accession: JC6123
                                                                                                         A; Title: Mucl,
                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-31 <PAR>
                            nucleic
                                                                         a mucin-like protein that in ther: JC6123; MUID:96323237;
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                      not shown
                                                                         is regulated by 7; PMID:8710886
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A; Note: sequence extracted from NCBI backbone (NCBIP:135349)
R; Platzer, M.; Bauer, D.; Drescher, B.
submitted to the EMBL Data Library, March 1995
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                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; not compared with A;Molecule type: mRNA; protein A;Residues: 1-2035 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 74, 115-125, 1993
A;TITLe: The VP16 accessory protein HCF is a family of polypeptides A;Reference number: A40718; MUID:93327419; PMID:8392914
A;Accession: A40718
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                                                                                                              A; Molecule type: DNA
A; Residues: 1-2035 < PLA>
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  A; Title: The
                                                          R; Kristie,
                                                                                 A;Cross-references: EMBL:U52112; NID:g1302657; PIDN:AAC51751.1; PID:g1302663
                                                                                                                                                                                               A; Accession: G02511
                                                                                                                                                                                                                             A; Reference number: H01368
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                          e, T.M.; Pomerantz, J.L.; Tv
Chem. 270, 4387-4394, 1995
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mucin 2 precursor, intestinal - human (fragments)
N;Alternate names: mucin SMUC-41
C;Species: Homo sapiens (man)
C;Date: 110-Mar-1993 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C;Accession: A49963; A45106; B45106; A43932; B33522; A61257; PQ0328; PQ0329
R;Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Siddiki, B.; Kim, Y.S.
J. Biol. Chem. 269, 2440-2446, 1994
A;Title: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identifical A;Reference number: A49963; MUID:94132002; PMID:8300571
A;Accession: A49963
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A;Residues: 100-563,'R',565-603,'VS',604-1163,'P',1165-1872,'A',1874-2035
A;Cross-references: EMBL:X79198; NID:g558348; PIDN:CAA55790.1; PID:g558349
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R;Frattini, A.; Faranda, S.; Redolfi, E.; Zucchi, I.; Villa, A.; Patrosso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A56088; MUID:95181425; PMID:7876203 A; Accession: A56088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: Xq28-Xq28
A; Introns: 65/1; 114/3; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: GDB: HCFC1; HFC1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPLVTSVA--NTVTTVSLQPEKPVVSGTAVTLSLPAVTFGETSGAATCLPSVKPVVSFCW
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119; Conserv
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; Pred. No. 0.00029;
66; Mismatches 188
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(MUC2) cDNA. Identification

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RESULT 2
A45183
TBP-associated factor TFIID - fi
TSpecies: Drosophila sp.
TSP-1993 #sequence_r
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T33369
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A.Reference number: A45183 MUID:93145326; PMID:7678780 A.Residues: preliminary; not compared with conceptual translation A.Molecule type: nucleic acid A.Residues: 1-921 <HOED A.Experimental source: embryo
                           C;Accession: T33369
R;Geisel, C.; Harmon, G.
submitted to the EMBL Da
                                                                                                    hypothetical protein H02F09.3 - Caenorl
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision
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C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-19:
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-19:
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-19:
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-19:
C;Date: 10-Jun-1995 #sequence_revision 18-Nov-1995 #sequence_revision 18-Nov-1995 #sequence_revision 18-Nov-1995 #sequence_revision 18-Nov-1995 #sequence_revision 18-Nov-1995 #sequence_revision 
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Data Library, July 1998 guence of C. elegans cosm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.7%; Score 241.5;
24.8%; Pred. No. 5.6e
tive 65; Mismatches
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                                                                                                       29-Oct-1999
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     H02F09
                                                                                                    #text_change
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R:Turner, B.S.; Bhaskar, K.R.; Hadzopoulou-Cladaras, Gastroenterology 106, 200, 1994
A;Title: Pig gastric mucin: isolation and characteri; A;Reference number: I47141; MUID:94102478; PMID:75063
A;Accession: I47141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-1275 GEI>
A; Cross references: EMBL:AF077538; PIDN:AAC64622.1; GSPDB:GN00028; CESP:H02F09.3
A; Experimental source: strain Bristol N2; clone H02F09
C; Genetics:
A; Gene: CESP:H02F09.3
A; Map position: X
A; Introns: 42/1; 78/3; 106/3; 135/2; 161/2; 224/1
A; Introns: 42/1; 78/3; 106/3; 135/2; 161/2; 224/1
A; Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-528 <TU;
                                                        A;Title: Isolation and characterization of A;Reference number: S55315; MUID:95275264; A;Accession: S55315
                                                                                                                    A;Cross-references: EMBL:U10281; NID:g915205; PIDN:AAC48526.1; R;Turner, B.S.; Bhaskar, K.R.; Hadzopoulou-Cladaras, M.; Specia Biochem. J. 308, 89-96, 1995
                                                                                                                                                                                 A;Status: preliminary; translated
A;Molecule type: mRNA
A;Residues: 1-528 <TUR>
                                                                                                                                                                                                                                                                                                                                                 gastric mucin (clone PGM-2A) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 03-Nov-2000
C;Accession: I47141; S55315
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Best Local
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Accession: T33369
Status: prelimina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STVTG-STVTEASTISGSTESSTIPGSTESTVSEASTVSGSSVSTVS
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Pred. No. 3.4e-05;
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                                                                             cDNA clones encoding PMID:7755593
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Result
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
       241.5
241.5
21.5
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200.5
197.5
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3: pir3:*
4: pir4:*
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1 GTLVTKVAPVSAPPKVSSGP......VIGTPVQIKLAQPGPVLSQP 452
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       GenCore version 5.1.3 Compugen Ltd
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pir2:*
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S52863
T34513
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C87719
A53577
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S29605
T45462
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F96615
T45025
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T33369
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A407181
A40733
S48478
S48478
A47283
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host cell factor C
mucin 2 precursor,
glucin 1,4 alpha-g
calphotin - fruit
calcium-binding pr
hypothetical prote
membrane glycoprot
DNA-binding protei
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protein R119.6 (im
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7C4566	A406/0 S14871 T22061 S60896 T31113	T42215 T22696 S56032 A57784	T18535 S51959 A41258
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ALIGNMENTS

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TVTTVSLQPEKP 389	APRTVSVQT 329 : :: APRLVNTGGIRT 460	LPNSQSFIQ 276 : : QQLPKIQAQIRPIG 405	EEFTRKLYVELK 246	ENSAAVQINLSP 187	AQIGTTVVTTVP 127 : SQPPHLTQLNAQ 243	VSPQQTVTRAETTS 76 	Length 921; Indels 111; Gaps 17;		3, NCBIP:134864)	atani, Y. subunit directly intera	(Drosophila melanogaste hange 15-Oct-1999

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Search completed: February 16, 2003, 22:04:22 Job time : 20.3897 secs

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APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative sp
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 63923
LENGTH: 775
TYPE: PRT
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 RESULT 14
US-09-724-676A-63923;
Sequence 63923, App.;
GENERAL INFORMATION
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Best Local S
Matches 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 32.9
e 63923, Application INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                LDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ----TS 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAV 403
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                                                                                                                                                  TFGETSGAAICLPSVKPVVSFCWDHICKPVI--GTPV------QIKLAQPG 446
                                                                                                                                                                                                                                                                   Q----ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL------
                                                                                                                                                                                                                                                                                                                                                                                                                        RTVPGATTTSSAATE-----TMENVKKCKNFLSTLIKLASSGKQSTETAANVKELVQNL 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----TTIIKQV----SQAQTTVQPSATLQRSPGVQPQLVLGGAAQTASLGTATAVQTGTPQ 539
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                                                                                                                -----GALIQLNPLQPV-----PVVKPAVLPGTKALSAVSAQAAAAQKNKLKEPG 760
                                                                                                                                                                                          -----QPTQVGVGKQGQPTPLVIQ-----QPPKP------
                                                                                                                                                                                                                             VTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAV 403
                                                                                                                                                                                                                                                                                                         SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGV 343
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                     US/09724676A
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; APPLICANT: Compugen LTD;
; TITLE OF INVENTION: VARIANTS of alternative spl
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTMARE: PatentIn version 3.2
; SEQ ID NO 63923
; ELNGTH: 775
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-63923
                                                                                                                                                                                 APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative sp
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 63926
LENGTH: 807
TYPE: PRT
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US-09-724-676-63926
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Best Local :
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13 PPKVSSG------PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM 61
                                                              Local Similarity
les 157; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
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                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09724676
                                                           22.6%; Score 507.5; DB·5; 32.9%; Pred. No. 1.3e-20; Itive 58; Mismatches 121;
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                     -PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM
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CURRENT APPLICATION NUMBER: US/09/
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 63929
LENGTH: 679
TYPE: PRT
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US-09-724-676-63920
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                                                   ; ORGANISM: Homo sapiens
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US-09-724-676A-63929
                                                                                                                                                        Sequence 63920, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 199181.4 Compugen
                                                                                                  CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 63920
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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
  Matches
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  Local Similarity
nes 157; Conserv
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           22.6%; Score 507.5; 32.9%; Pred. No. 1.1
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Pred. No. 1.1e-20;
58; Mismatches 121;
  Mismatches
            .1e-20
                        DB 5;
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US-09-724-676A-63920
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US-09-724-676A-63920
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.2
SEQ ID NO 63920
LENGTH: 711
TYPE: PRT
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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LDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ----
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                                                                           RTVPGATTTSSAATE-----TMENVKKCKNFLSTLIKLASSGKQSTETAANVKELVQNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 507.5; DB 5
Pred. No. 1.1e-20;
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US-09-724-676A-63924
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NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 63924
LENGTH: 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 63924, Application US/09724676A GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 129181.4 Compugen FILE REFERENCE: 129181.4 COMPUGEN: US/09/724,676A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative
                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115 :: | | | : | : | | : | | |
                                                                                                                                                                                                                                                                            PPKVSSG-----PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGV 343
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                      NE-PNIKAENSAAVQINISPTMIENVKKCKNFLAMLIKIACSGSQSPEMGQNVKKLVEQI
                                                                           ----TTIIKQV----SQAQTTVQPSATLQRSPGVQPQLVLGGAAQTASLGTATAVQTGTPQ
                                                                                                                  AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS 168
                                                                                                                                                           MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
                                                                                                                                                                                                                                     PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL
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      RTVPGATTTSSAATE - - -
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                    Score 521; DB 5;
Pred. No. 2.4e-21;
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 63929
LENCTH: 679
TYPE: PRT
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US-09-724-676-63929
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INERAL INFUNCTION: UNITED APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative FILE REFERENCE: 129181.4 Compugen US/09/724,676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
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                                                                                                                                                                        VTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAV
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                                                         -GALIQLNPLQPV---
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32.9%;
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Pred. No. 1.1e-20;
8; Mismatches 121;
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RESULT 5
US-09-724-676-63921
Sequence 63921, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
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Best Local
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LENGTH: 805
TYPE: PRT
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TLTQT
                           TFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKL--AQPGPVL 449
                                                                                               VTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAV
                                                                                                                                Q----ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL---
                                                                                                                                                               SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGV 343
                                                                                                                                                                                                  LDGKIEAEDFTSRLYRELNSSPQPYLVPFLKRSLPALRQLTPDSAAFIQQSQQQPPPPPTS
                                                                                                                                                                                                                 LDAKIEAEEFTRKLYYELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ----TS 283
                                                                                                                                                                                                                                                                  RTVPGATTTSSAATE----TMENVKKCKNFLSTLIKLASSGKQSTETAANVKELVQNL
                                                                                                                                                                                                                                                                                                 NE-PNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL 227
                                                                                                                                                                                                                                                                                                                               ----TTIIKQV----SQAQTTVQPSATLQRSPGVQPQLVLGGAAQTASLGTATAVQTGTPQ 539
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PMVALROPH-NRIMLTTPQQIQLNPLQPVPVV 760
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Pred. No. 2.3e-21
1; Mismatches 128
                                                              -QPPKP----GALIRPPQV
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; ORGANISM: Homo sapiens US-09-724-676-63924

TYPE: PRT

CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 63924
LENGTH: 837

US-09-724-676-63924; Sequence 63924, Application US/09724676

GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen

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RESULT 6
US-09-724-676A-63921
Sequence 63921, Application US/09724676A
SEQUENCE LIMEORATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
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ORGANISM: Homo sapiens
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     725
                                 404 TFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKL--AQPGPVL 449
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                                                                                                                                              Q----ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL------
TLTQT------PMVALRQPH-NRIMLTTPQQIQLNPLQPVPVV
                                                                                                           VTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAV 403
                                                                                                                                                                                                                    LDGKIEAEDFTSRLYRELNSSPQPYLVPFLKRSLPALRQLTPDSAAFIQQSQQQPPPPTS
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                                                                       -TOPTOVGVGKQGQPTPLVIQ-
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Pred. No. 2.3e-21
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RESULT 3
US-09-724-676-63930
Sequence 63930, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 63927
LENGTH: 709
TYPE: PRT
               CURRENT APPLICATION NUMBER: US/99/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 63930
LENGTH: 741
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Best Local Similarity
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TITLE OF INVENTION: Variants of alternative splicing
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TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ----TS 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159;
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Matches 159
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SEQ ID NO 63930
LENGTH: 741
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 97222
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                                                                                                             62 LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
                                                                                                                                                                                          13 PPKVSSG------PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM 61
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----TTIIKQV----SQAQTTVQPSATLQRSPGVQPQLVLGGAAQTASLGTATAVQTGTPQ
                                  AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS 168
                                                                           MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
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76-63927 NEFORMATION: TI Compugen LTD INVENTION: Variants of ERENCE: 129181.4 Compug APPLICATION NUMBER: US/ FILING DATE: 2000-11-2 F SEQ ID NOS: 97222 : Patentin version 3.2 63927 709 RT M: Homo sapiens 76-63927 76-63927 799 RT TATTSGIRATLIPTVLAPRLPAP : TATTSGIRATLIPTVLAPRLPAP : TATTSGIRATLIPTVAPRLPAPTTIIKQVSQAQTTVQPS C-PHIKAENSAAVQINLSPTMLE TVPGATTTSSAATETME DAKIEAEEFTRKLYVELKSSPQP DMVIATCTTTVTTSPVVTTTVSS DMVIATCTTTTTSPVVTTTVSS DMVIATCTTTTTSPVVTTTVSS DMVIATCTTTTTSPVVTTTVSS DMVIATCTTTTTSPVVTTTVSS DMVIATCTTTTTSPVVTTTVSS	2135 2382 2382 2382 2382 2382 2382 2374 15374 15374 15374 15374 2576 2601 2601 2601 2601 2601 2761 2761 2761 2761 2761 2761 2761 276
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ACID MOLECULES ENCODING GPCR PROTEINS

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; TITLE OF INVENTION: NUCLEIC ACID MOLECULES E
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000173
; CURRENT APPLICATION NUMBER: US/60/173,464
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 30269
; SOFTMARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 9223
; LENGTH: 921
; TYPE: PAT
; ORGANISM: Drosophila
US-60-173-464-9223
                                                                    ; LENGTH: 921
; TYPE: PRT
; ORGANISM: Drosophila
US-60-173-464-20611
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL000173
CURRENT APPLICATION NUMBER: US/60/173,464
CURRENT FILING DATE: 1999-12-29
                                                                                                                                     NUMBER OF SEQ ID NOS: 30269
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20611
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Local Similarity 24.8%;
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                  10.8%;
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 65;
Score 243.5; DB 27,
Pred. No. 3.6e-10;
65; Mismatches 163;
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                           VVSGTAVTLSLPAVTFGETSGAAICLPSVKP 420
                                                      QIP-SLQVPGQANIVQIR--GPQHAQLQRTGSVQIRATTRP-----PNSVPTAN-----
                                                                                LNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKP
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Search completed: February 16, Job time : 165.507 secs 2003, 22:18:24

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; LOCATION: (1)...(1083)
; OTHER INFORMATION: Xaa
PCT-US02-30474-3271
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Matches
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PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
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PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
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PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
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CURRENT APPLICATION NUMBER: PCT/US02/30474
CURRENT FILING DATE: 2002-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 3476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Drmanac, Radoje TTITLE OF INVENTION: Novel Nucleic Acids TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/US00/35017 PRIOR FILING DATE: 2000-12-22
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TYPE: PRT
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                                                                    KLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ
                                                                                                                                        GASSTPSNEPNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVK
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                                                GATTTSS--
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----TSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPV
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US-60-167-217-11401
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APPLICANT: L1, Peter W. D.
TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLEUCLES ENCODING DROSOPHILA PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL000152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11401, Application US/60167217
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SOFTWARE: FastSEQ for Windows
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                                                                 QIP-SLQVPGQANIVQIR--GPQHAQLQRTGSVQIRATTRP-----PNSVPTAN-----
                                                                                                 LNPLAGPYGAKAGYYTLHSYGPTAATGGTTAGTGLLQTSKPLYTSYANTYTTYSLQPEKP
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----KLTAVKVGQTQIKAI-TPSLHP
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Pred. No. 3.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 163;
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RESULT 14
US-60-173-464-9223
US-60-173-464-9223
; Sequence 9223, Application US/60173464
; GENERAL INFORMATION:
; APPLICANT: L1, Peter W.D.
. TITLE OF INVENTION: ISOLATED G-PROTE:

ISOLATED G-PROTEIN COUPLED RECEPTORS

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RESULT 11
US-09-893-519A-14
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Best Local S
Matches 154
                                                                                                                                                                                                                                              Sequence 14, Application US/09893519A GENERAL INFORMATION:
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                                                                                   APPLICANT:
                                                                                                                                                       APPLICANT: ANADYS PHARMACEUTICALS, INC
APPLICANT: THOMPSON, Craig
APPLICANT: MOORE, Jeffrey
APPLICANT: BUURMAN, Ed T.
APPLICANT: BRADLEY, John
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CURRENT APPLICATION NUMBER: PCT/US01/20592A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,164
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-29
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PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 146
                                  APPLICANT:
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TYPE: PRT
APPLICANT
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                                                                                                                BUURMAN, Ed T.
BRADLEY, John
DESILVA, Thamara
HARRIS, Sandra
                                               MCCOY, Melissa
                                                                                 KOMARNITSKY, Svetlana MENDILLO, Marc
                                SANDERSON, Karen
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APPLICANT: LONG, Fan

APPLICANT: DAVIDOV, Eugene

TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND METHODS OF USE

FILE REFERENCE: 0342/16548-US2

CURRENT APPLICATION NUMBER: US/09/893,519A

CURRENT FILING DATE: 2001-06-28

PRIOR APPLICATION NUMBER: US 60/215,164

PRIOR FILING DATE: 2000-06-29

PRIOR FILING DATE: 2000-08-10

NUMBER OF SEQ ID NOS: 146

SOFTWARE: PATENTIAN VERSION 3.1

SEQ ID NO 14

FENDER 101
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GENERAL INFORMATION:
                      Sequence 3271,
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Best Local
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OTHER INFORMATION: Corresponds to
PUBLICATION INFORMATION:
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                                                                                                                                                                                                -----TQPTQVGVGKQGQPTPLVIQ------QPPKP--
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                      Application PC/TUS0230474
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Pred. No. 3.4e-32;
52; Mismatches 127;
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APPLICANT: Tang, Y. Tom APPLICANT: Zhang, Jie APPLICANT: Ren, Felyan

APPLICANT:
APPLICANT:
APPLICANT:

Ren, Feiyan Xue, Aidong J. Zhao, Qing A. Wang, Jian-Rui Wehrman, Tom 19;

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US-60-324-631-1665
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                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application PC/TUS0120592 GENERAL INFORMATION:
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Best Local
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SEQ ID NO 1665
LENGTH: 1051
TYPE: PRT
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APPLICANT:
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CURRENT APPLICATION NUMBER: PCT/US01/20592
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,164
PRIOR FILING DATE: 2000-06-29
                                                       APPLICANT: DAVIDOV, Eugene
TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS
FILE REFERENCE: 0342/10548-057
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                                                                                                                                                                                                                                                                                                                                   ANADYS PHARMACEUTICALS, INC
                                                                                                            HAQ, Tariq
ZHU, Shuhao
LONG, Fan
                                                                                                                                                                                                         HARRIS, Sandra
KOMARNITSKY, Svetlana
MENDILLO, Marc
                                                                                                                                                                                                                                                     BRADLEY, John
DESILVA, Thamara
                                                                                                                                                                                                                                                                                     MOORE, Jeffrey
BUURMAN, Ed T.
                                                                                                                                                            SANDERSON, Karen
                                                                                                                                                                          MOORE, Daniel
MCCOY, Melissa
                                                                                                                                                                                                                                                                                                                      THOMPSON, Craig
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Pred. No. 7.8e-33;
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                                                                              AND
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PCT-US01-20592A-14 RESULT 10

Sequence 14, Application PC/TUS0120592A GENERAL INFORMATION: APPLICANT: ANADYS PHARMACEUTICALS, INC

APPLICANT:

BRALL_ DESILVA, The TRIS, Sandra THOMPSON, Craig MOORE, Jeffrey BUURMAN, Ed T. BRADLEY, John DESILVA, Thamara

APPLICANT: APPLICANT APPLICANT APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:

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HAQ, Tariq ZHU, Shuhao LONG, Fan SANDERSON, Karer MCCOY, Melissa MENDILLO, Marc KOMARNĪTSKY, Svetlana

r: DAVIDOV, Eugene INVENTION: ANTIFUNGAL COMPOUNDS AND

METHODS

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Best Local Simi
Matches 154;
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
FRATURE:
FRATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: human genbank accession #: CAA72189
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                                                                                                                                                                                                                                    LDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ----TS
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TLTQT---
                                                                                                      VTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAV
                                                                                                                                                                                                                                                                                       RTVPGATTTSSAATE-----TMENVKKCKNFLSTLIKLASSGKQSTETAANVKELVQNL 625
                                  TFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQ
                                                                                                                                            Q-----ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL-----
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-----PMVALRQPH-NRIMLTTPQQVNLSE 785
                                                                      -TQPTQVGVGKQGQPTPLVIQ------
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PCT-US02-30474-1660
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SOFTWARE: pt_FL_genes
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TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 810CIP PCT
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APPLICATION NUMBER: US 09/496,914
FILING DATE: 2000-02-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-12-22
APPLICATION NUMBER: US 09/491,404
FILING DATE: 2000-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 09/488,725
FILING DATE: 2000-01-21
APPLICATION NUMBER: US 09/552,317
FILING DATE: 2000-04-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 09/560,875 FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/03800 FILING DATE: 2001-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/02623
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                                  VTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAV 403
                                                                                                                                             RTVPGATTTSSAATE-----TMENVKKCKNFLSTLIKLASSGKQSTETAANVKELVQNL
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                                                                                                         SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGV 343
                                                                                                                                                                                  LDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ----TS
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di, Vinod
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TQPTQVGVGKQGQPTPLVIQ--
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RESULT 8
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CURRENT APPLICATION NUMBER: US/60/324,631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 09/552,317
FILING DATE: 2000-04-25
APPLICATION NUMBER: PCT/US00/3501
FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NT FILING DATE: 2001-09-24
APPLICATION NUMBER: US 09/488,725
FILING DATE: 2000-01-21
                                  APPLICATION NUMBER: PCT/USO1/08656 FILING DATE: 2001-04-18
                                                                    APPLICATION NUMBER: US 09/770,160 FILING DATE: 2001-01-26
                                                                                                                          APPLICATION NUMBER: US 09/552,929
                                                                                                                                                                                                FILING DATE: 2000-03-31
APPLICATION NUMBER: US 09/649,167
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 09/577,409 FILING DATE: 2000-05-18
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FILING DATE: 2000-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 09/560,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 09/496,914
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APPLICATION NUMBER: PCT/US01/02623
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                                                                                                         FILING DATE: 2000-04-18
                                                                                                                                             FILING DATE: 2001-03-30
                                                                                                                                                              APPLICATION NUMBER: PCT/US01/08631
                                                                                                                                                                                 FILING DATE: 2000-08-23
                                                                                                                                                                                                                                    APPLICATION NUMBER: US 09/540,217
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                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 09/574,454
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INVENTION: Novel Nucleic Acids and
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Asundi, Vinod
Wang, Zhiwei
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Ghosh, Malabika
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Wang, Jian-Rui
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NUMBER: US 09/577,408: 2000-05-18
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PCT-US94-01114-16
; Sequence 16, Application PC/TUS9401114
; GENERAL INFORMATION:
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Matches
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CURRENT FILING DATE: 2000-10-27
NUMBER OF SEQ ID NOS: 2121
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 1271
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APPLICANT:
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   COMPUTER
                                                                                                                            TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS, TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS NUMBER OF SEQUENCES: 36
                                                                                                              CORRESPONDENCE ADDRESS:
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                               COUNTRY:
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                                                                                               ADDRESSEE:
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                     94111-4187
                                                                 San Francisco
    READABLE
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                                              California
                                                                              4 Embarcadero Center,
                                                                                                                                                                                                          Ruppert, Siegfried
Tanese, Naoko
                                                                                                                                                                                                                                         Dynlact, Brian D. Hoey, Timothy
                                    USA
                                                                                                                                                                           Weinzierl, Robert O.J.
                                                                                                                                                                                                                                                                          Comai, Lucio
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                                                                                                                                                                                         Wang, Edith
                                                                             FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT Embarcadero Center, Suite 3400
    FORM
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Pred. No. 3
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3.2e-153;
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                                                                                                                                                                       RESULT 7
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                                                                                                                         Sequence 1660, Applic GENERAL INFORMATION:
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Best Local 9
                                                                                            APPLICANT: Tang, Y. Tom APPLICANT: Zhang, Jie
                                               APPLICANT:
                                                                              APPLICANT:
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APPLICANT
                             APPLICANT:
                                                              APPLICANT:
                APPLICANT
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
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TOPOLOGY: linear
MOLECULE TYPE: pro
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LENGTH: 737 amino acids
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NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
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                                                                                                                                                                                                                                                     404 TFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKL--AQPGPVL
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                       TLTQT-----PMVALRQPH-NRIMLTTPQQIQLNPLQPVPVV
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                           Zhao, Qing A.
Wang, Jian-Rui
                                                           Ren, Feiyan
Xue, Aidong J.
Zhou, Ping
                                                                                        Zhang, Jie
              Wehrman,
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                                                                                                                                          Application PC/TUS0230474
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Pred. No. 4.5e-33;
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Matches
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
                                                            APPLICANT:
          APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic
TITLE OF INVENTION: POLYPOPTIGES
FILE REFERENCE: 809ACIP PCT
                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                         APPLICANT: Tang, Y. Tom
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TYPE: PRT
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OTHER INFORMATION: Incyte ID No: 4398735CD1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
mes 452; Conserv
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                                                                                                                                                           Zhang, Ji.
Zhao, Qing A.
Zhao, Jian-Rui
Wang, Jian-Rui
                                                                                                                       Xue, Aidong J.
Wang, Dunrui
Ghosh, Malabika
Asundi, Vinod
                                                         Weng, Gezhi
Haley-Vicente, Dana
                                                                                  Zhou, Ping
Goodrich, Ryle W.
                                                                                                           Wehrman, Tom
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NUMBER:
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PCT/US02/29964
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Pred. No. 1.1e-173;
0; Mismatches 0;
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RESULT 5
US-60-243-468-1271
Sequence 1271, Application US/60243468
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN DRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LENGTH: 843
; TYPE: PRT
; ORGANISM: Homo s
PCT-USO2-29964-410
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Best Local Similarity
Matches 445; Conservat
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SEQ ID NO 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 09/560,875 PRIOR FILING DATE: 2000-04-27
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PRIOR FILING DATE: 2000-02-03
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ER: US 60/323,739
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98.5%;
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Pred. No. 2.6e-169;
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Ellen ISOLATED HUMAN DRUG

TARGET

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GENERAL INFORMATION:

APPLICANT: Dikstein, Rivka

APPLICANT: Yamit-Hezi, Ayala

ITILE OF INVENTION: A TRANSCRIPTION FACTOR TFIID SUBUNIT,

ITILE OF INVENTION: TAFIIIO5, POLYPEPTIDES, DNA ENCODING THI

ITILE OF INVENTION: PHARMACEUTICAL COMPOSITIONS

FILE REFERENCE: 13005-002001

CURRENT APPLICATION NUMBER: US/09/763,909

CURRENT APPLICATION NUMBER: US/09/763,909

CURRENT FILING DATE: 2001-02-26

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 2
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; ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                           Local
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                                                                        VQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRK 240
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                                                                                                                                                                                        MLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGT 120
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APPLICANT: YUE, HOLLY
APPLICANT: YUE, HUIDIN
APPLICANT: ZEBARJADIAN, YEGANEH
TITLE OF INVENTION: NUCLEIC ACID ASSOCIATED PR
FILE REFERENCE: PF-1146 PCT
CURRENT APPLICATION NUMBER: PCT/US02/25829
CURRENT FILLNG DATE: 2002-08-14
PRIOR APPLICATION NUMBER: US 60/313,111
PRIOR APPLICATION NUMBER: US 60/314,682
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/314,756
PRIOR APPLICATION NUMBER: US 60/314,756
PRIOR FILING DATE: 2001-08-24
PRIOR PRIOR APPLICATION NUMBER: US 60/315,105
PRIOR FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: US 60/315,105
PRIOR APPLICATION NUMBER: US 60/315,751
PRIOR APPLICATION NUMBER: US 60/316,751
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BURFORD, Brendan M.
DUGGAN, Brendan M.
FT.LIOTT, Vicki S.
                                                                                                                                                                                                                                            WARREN, Bridget A
XU, Yuming
YAO, Monique G.
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LU, Dyung Aina M.
LU, Yan
LEHR-MASON, Patricia N
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BOROWSKY, Mark L.
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BECHA, Shanya D.
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Soo Yeun
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	697	equence 351,	equence 40374,	equence 4074	equence 21466,	equence 2685	ce 26685	ce 55, /	equence 108,	ce 108,	e 108,	equence	equence 362,	equence 314,	equence 28	equence 35	equence 36	equence 20	equence 56	Ø	equence 49	equence 56	equence 19	equence 8933,	equence 25058,	e 11408,	equence 24957	equence 11376	2, Ac	equence 2, Appl	e 20611	equence 9223,	Sequence	quence 327:	9	e 14,	equence 14, A	e 1665	e 166

ALIGNMENTS

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APPLICATI HYSEG, INC
APPLICANT: HYSEG, INC
ITITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/USO1/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
INUMBER OF SEG ID NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
INUMBER OF SEG ID NOS: 60736
SOFTWARE: CUSTOM
SEQ ID NO 39827
LENGTH: 801
TYPE: PRT
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PCT-US01-08631-39827
; Sequence 39827, Application PC/TUS0108631
; GENERAL INFORMATION:
                                                                                                                                                      ; ORGANISM: Homo sapiens
PCT-US01-08631-39827
                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 452; Conservative 0
0;
                                                                                              Score 2249; DB 1;
Pred. No. 1.1e-174;
                                                                              Mismatches
                                                                                                                Length 801;
                                                                              Indels
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                                                                           Gaps
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Sequence 16, Appl

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MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ
US-10-124-557-104
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US-10-124-557-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 44, Application US/10124557 Patent No. US20020137894A1 GENERAL INFORMATION:
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Best Local
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                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Megakaryocyte Stimulating NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1140 amino a
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIAT 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PNIKAENSAAVQINISPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKIVEQILDA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 6.9%; l Similarity 20.8%; 86; Conservative 4
                                                                     APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-Apr-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                               ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge
               APPLICATION NUMBER: US 07/643,502 FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                             STATE: Massachusetts
 APPLICATION NUMBER:
                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Turner, Katherine
Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                           Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
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Pred. No. 0.0054;
US 07/546,114
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Search completed: February 16, 2003, 22:02:21 Job time: 23.9045 secs

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MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-124-557-44
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Best Local Similarity
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                                                                                                                                                                                                                                                                                     662
                                                                       767
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                                                                                                                                            740
                                                                                                                                                                         231 KIEAEEFTRKLYVELKSSPOPHLVPFLKKSVVALROLLPNSOSFIOOCVOOTSSDMVIAT 290
                                                                                                                                                                                                                 717
                                                                                                                                                                                                                                                  171
                                                                                                                                                                                                                                                                                                                    114 KLAQIGTTVVTTVPKPSSVQSVAVPTS---VVTVTPGKPLNTVTTLKPSSLGASSTPSNE 170
                                                                                                                                                                                                                                                                                                                                                     604 --TKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPK 661
                                                                                                                                                                                                                                                                                                                                                                                                                          547 APTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTT--- 603
                                                                                                                                                                                                                                                                                                                                                                                      54 KSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 APVSAPPKVSSGPRLPAPQIVAVKAPNT-----TTIQFPANLQLPPGTVLI 53
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                                                                                                      CTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                     TKTPAATKPEMTTTAKDKTTERDL----RTTPETTT-----AAPKMTKETATTTEKTT
                                                                                                                                                                                                                                               PNLKAENSAAVQINLSPIMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDA 230
 ESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEE
                                  PTAATGGTTAGTGL---
                                                                                                                                            ----DEST----PELSAEPTP----
                                                                                                                                                                                                                PPTTSEVSTPTTTK-EPTTIH-----
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APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1270 amino acids
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APPLICATION NUMBER: US 07/457,196
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Pred. No. 0.0062;
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                                  -LQTSKPLVTSVANTVTTVSL--QPEK 388
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869
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                                                                                                                                                                           ; ORGANISM: Saccharomyces cerevisiae US-09-801-368-110
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SEQ ID NO 110
LENGTH: 1075
                                                                                                        Matches 101;
                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 110, Application US/09801368 Patent No. US20020128250A1
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Busby, Robert APPLICANT: Cali, Brian
                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
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                                                                  2 TLVTKVAPVSAPPKVSSGPRLPAPQIVAVKAPN----TTTIQFPANLQLPPGTVLIKSN 56
SGPLMLV---SPQQT-----VTRAETTSNITSRPAVP----ANPQTVKICTVPNSSSQLI 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEE 912
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                                  TEVTTITGTNGQPTDET-----VIVIRTPTSEGLITTTTE-----PWTGTFTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --TKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPK 704
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                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sherman, Amir
Silva, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Royer, John
Salama, Sofie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maxon, Mary
Milne, Todd
No. US20020128250Alman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Madden,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Holtzman, Doug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hecht, Peter
                                                                                                     6.9%;
ilarity 22.4%;
Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kevin
                                                                                                      63;
                                                                                                   Score 156; DB 10;
Pred. No. 0.005;
3; Mismatches 170;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Secondary Metabolite Production
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                                                                                                                                     Length 1075;
                                                                                                     Indels 116;
                                                                                                 Gaps
                                  470
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US-10-124-557-104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 104, Application US/10124557 Patent No. US20020137894A1 GENERAL INFORMATION:
INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 785 VTVTSCESHVCTESI -- SSAIVSTATVTVS 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       370 PLYTSVANTVTTVSLQPEKPVVSGTAVTLS 399
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               TELEFAX: (617)876-5851
                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: CSETT, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: CURSSIFICATION ONTA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Turner, Katherine Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSK 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -ALRQLLPNSQSFIQQCV-------QQTSSDMVIATCTTTVTTSPVVTTTVSSSQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPF-----LKKSVV- 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSSSISSESPKSP-TNSSSSLPPV---TSATTGQETASSL-PPATTTKTSE-----QTTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSVTSSLVTSSSFISSSVISSSTTTSTSIFSESSTSSVIPTSSSTSGSSESKTSSASSSS 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSSSSGQITSSI------TSSRPIITPFYPSNGTSVISSSVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEGLITATTEPWTGTFTSTSTEVTTITGTNGQPT-----DETVIVIATPTTAISSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGASSTPSNEPNLKAENSAAVQI-----NLSPTMLENVKKCKNFLAMLIK---LACSGS 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DETVIVIRTPTSE----GLITTTTEPWTGTFTSTSTEMTTVTGTNGQPTDETVIVIRTPT
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                                                                                                                                                                                       APPLICATION NUMBER: US 07/457,196 FILING DATE: 29-DEC-1989
                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/546,114 FILING DATE: 29-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                  APPLICATION NUMBER: US 07/390,901 FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                   FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/643,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02140
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                                                                         5190
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                                                                                                                                                                                                                                                                                                                                                                                               Version
                                                                                                                                                                                                                                                                                                                                                                                                 #1.25
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-10-124-557-74
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US-10-124-557-74
                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
                             662 KPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPT-TPKKP----APTTPETP 716
                                                                 114 KLAQIGTTYVTTYPKPSSYQSYAVPTS---VYTYTPGKPLNTYTTLKPSSLGASSTPSNE 170
                                                                                                          604 --TKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPK
                                                                                                                                                                                                 547
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                                                                                                                                              54 KSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVK 113
                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                 8 APVSAPPKVSSGPRLPAPQIVAVKAPNT-----TTIQFPANLQLPPGTVLI 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/10/124,557
ETLING DATE: 16-Apr-2002
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Megakaryocyte Stimulating NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                        APTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTT---
                                                                                                                                                                                                                                                                             86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
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STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1038 amino acids
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                                                                                                                                                                                                                                                                             Conservative
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Hewick, Rodney M.
Gesner, Thomas G.
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                                                                                                                                                                                                                                                                           40;
                                                                                                                                                                                                                                                                                              Score 156; DB 12
Pred. No. 0.0048;
                                                                                                                                                                                                                                                                           Mismatches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5190
                                                                                                                                                                                                                                                                                                               DB 12;
                                                                                                                                                                                                                                                                                                               Length 1038;
                                                                                                                                                                                                                                                                         Indels 124;
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                                                                                                          661
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ
US-10-124-557-58
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  Query Match
Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 58, Application U Patent No. US20020137894A1 GENERAL INFORMATION:
                                                                                                                                                                                                                               TELEPHONE: (617)876-11
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 58:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351 PTAATGGTTAGTGL--------LQTSKPLVTSVANTVTTVSL--QPEK 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   717 PPTTSEVSTPTTTK-EPTTIH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    767 TKTPAATKPEMTTTAKDKTTERDL----RTTPETTT-----AAPKMTKETATTTEKTT 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 CTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 KIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIAT 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 PNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDA 230
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/390,901 FILING DATE: 08-AUG-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: PATENTIN PRESENT APPLICATION DATA:
                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1049 amino acids
                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Turner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/643,502 FILING DATE: 18-CAN-1991 APPLICATION NUMBER: US 07/546,114 FILING DATE: 29-UN-1990 APPLICATION NUMBER: US 07/457,196 FILING DATE: 29-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                        NAME: Cserr,
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      Conservative
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Hewick, Rodney M.
Gesner, Thomas G.
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6.9%; Score 156; DB 12;
20.8%; Pred. No. 0.0048;
tive 40; Mismatches 164;
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Stephen C.
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    164;
                                        Length 1049;
  Indels 124;
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OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25

Gesner, Thomas G.

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RESULT 10
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                                                               Sequence 84, Application US/10124557 Patent No. US20020137894A1 GENERAL INFORMATION:
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                                                    APPLICANT:
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                                                                                                                                                                          ESKITATTTQVTSTTTQDTTPFKITTLKTTTLAPKVTTTKKTITTTEIMNKPEE 804
                                                                                                                                                                                                          PTAATGGTTAGTGL--
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                                                                                                                                                                                                                                                                                                                                  KIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIAT 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLAQIGTTVVTTVPKPSSVQSVAVPTS---VVTVTPGKPLNTVTTLKPSSLGASSTPSNE
                                                                                                                                                                                                                                      TKTPAATKPEMTTTAKDKTTERDL----RTTPETTT-----AAPKMTKETATTTEKTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/643,502 FILING DATE: 18-JAN-1991 APPLICATION NUMBER: US 07/546,114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-Apr-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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REFERENCE/DOCKET NUMBER: GI 5190
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TELEFAX: (617)876-5851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/390,901 FILING DATE: 08-AUG-1989
                                Turner, Katherine
Clark, Stephen C.
    Jacobs,
Hewick,
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   Kenneth
Rodney M.
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Best Local Similarity
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PTAATGGTTAGTGL-----
                                                                                           ----DEST----PELSAEPTP---
                                                                                                                                                                                                                                                                                                                                                                                                             86;
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MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: US-10-124-557-84
                                                783 TKTPAATKPEMTTTAKDKTTERDL----RTTPETTT-----AAPKMTKETATTTEKTT
                                                                                                                                                                                                                                                                                                                                                                                                           114 KLAQIGTTVVTTVPKPSSVQSVAVPTS---VVTVTPGKPLNTVTTLKPSSLGASSTPSNE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                              620 --TKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPK 677
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (617)876-1170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVK 113
                                                                                                CTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVG
                                                                                                                                                                                                       KIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIAT 290
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                                                                                                                                                                                                                                                                                                       PNIKAENSAAVQINISPTMIENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKIVEQIIDA 230
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FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 0
FILING DATE: 29-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/390,901 FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/643,502 FILING DATE: 18-JAN-1991 APPLICATION NUMBER: US 07/546,114
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-----LQTSKPLVTSVANTVTTVSL--QPEK 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 156; DB 12; Pred. No. 0.0047;
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                                                                                                                                                      -----KALENSPKEPGVPT
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                                                                     APPLICANT: Royer, John
APPLICANT: Salama, Sofile
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods fo
FILE REFERENCE: 109272.147
                                                                                                                                                                                                                                                                                                                                                                 GENERAL
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 106, Application US/09801368 Patent No. US20020128250A1
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Best Local :
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APPLICANT:
APPLICANT:
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           CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
                                                                                                                                                                                                                                                                                                     APPLICANT: Busby, Robert APPLICANT: Call, Brian APPLICANT: Hecht, Peter
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THER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.9

THER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.8

THER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4

THER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.2

THER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.2

THER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.5

THER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.3

THER INFORMATION: EXPRESSED IN HELA, SIGNAL = 9.3

THER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 7.7

THER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.2

THER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.2

THER INFORMATION: EXPRESSED IN HEL100, EVALUE 0.00e+00

THER INFORMATION: SWISSPROT HIT: PO8640, EVALUE 3.00e-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSP--VVT
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Similarity 24.1%;
87; Conservative 5
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Holtzman, Doug
Madden, Kevin
                                                                                                                                                                                                        Maxon, Mary
Milne, Todd
No. US20020128250Alman,
2000-01-19
                                                                                       for Improving
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Pred. No. 0.0088;
1; Mismatches 157;
                                                                                         Secondary
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RESULT 4
US-10-124-557-14
; Sequence 14, Application
; Patent No. US200201378948
; GENERAL INFORMATION:
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Best Local Similarity
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 COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp
COMPUTER: IBM PC c
                                                                                                                                            Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                           APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LACSGSOSPEMGQNVKKLVEQLLDAKIEAEE----FTR---KLYVELKSSPOPHLVPFLK 258
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                                                                 CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                  ZIP:
                                                                                                               ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
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21.0%;
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Pred. No. 0.0032;
2; Mismatches 18
                                                                                                                                                                               Stimulating Factors
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                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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TYPE: PRT
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PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/801,368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Summers, Eric TITLE OF INVENTION: Methods for Improving FILE REFERENCE: 109272.147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                               ----GLISTTTEPWTGTFTSTSTEMTTVTGTNGQPTDETVIVIRTPTSEGLVTT-TTEP
                                                                                                                             ATTAMTTTOPWNDTFTSTSTEMTTVTGTNGVPTD-ETVIVIRTPTSE------
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                                                                                                                                                                                                                                                          97;
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Silva, Jeff
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Salama, Sofie
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Milne, Todd
No. US20020128250Alman,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Madden, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Holtzman, Doug
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                              NIKAENSAAVQINISPTMLENVKKCKNFLAMLIK---LACSGSQSPEMGQNVKK 222
                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Robert
                                                                                                                                                                                                                                                                       7.6%;
                                                                                                                                                                                                                                                          73;
                                                                                                                                                                                                                                                                       Score 172; DB 10;
Pred. No. 0.00052;
                                                                                                                                                                                                                                                          Mismatches
-DETVIIVKTPTTAISSSLSSSSSGQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secondary Metabolite Production
                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                          164;
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                                                                                                                                                                                                                                                                                     Length 1322;
                                                                                                                                                                                                                                                        Indels 128;
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                                      SOFTWARE: Annom-
SEQ ID NO 34248
LENGTH: 2665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 34248, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K
                                                                                                     NUMBER OF SEQ ID NOS: 49117
                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1005 TSSLPPVTTTKTSEQTTLV----TVTSCESHVCTESISSAI 1041
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                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: GB 24263.6 FILING DATE: 2000-10-04
                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/0066
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                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00662
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                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00669
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sapiens
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1, David K.
                                                                                Sequence Listing Engine vers. 1.1
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; ORGANISM: Homo sapiens US-09-922-217-1068
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 Best Local Similarity 22.1 Matches 102; Conservative
                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1068
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Best Local Similarity 22.1
Matches 102; Conservative
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                       APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Xu, Jiangchun APPLICANT: Lodes, Michael J.
                                                                                                                                  LENGTH: 5179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QTSKPLVTSVANT--VTTVSLQPEKPVVSGTAVTLSLPAVT 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LACSGSQSP----EMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKS 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IKKVAVTPVKKLAQIGTTVVTTVPKPSSVQSVAVP----TSVVTVTPGKPLNTVTTLKPS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVSPQQTVTRAET-----TSNITSRPAVPANPQT-----VKICTVPNSSSQL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLYTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTTTPITTTT-TVTPTPTPTGTQTPTTTPITTTTTTTPTPTPTGTQTPTTTPITTTTVT 1977
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                                                                                                                                                                                                                                                                                                                   King, Gordon E.
Wang, Aljun
                                                                                                                                                                                                                                                                                                                                                                                        Wang, Tongtong
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Stolk, John A.
                                                                                                                                                                                                                                                                                                                                                         Jiang, Yuqiu
Smith, Carole Lynn
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secrist, Heather
Benson, Darin R.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Madeleine
8.7%; Score 195.5; DB 10; 22.1%; Pred. No. 7.7e-05; tive 44; Mismatches 208;
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                                    Length 5179;
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                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens US-09-833-263-1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-833-263-1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
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                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1068 LENGTH: 5179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1068, Application Patent No. US20020110547A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 210121.471C12
CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT FILING DATE: 2001-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Stolk, John A.

APPLICANT: Meagher, Madeleine J.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Aijun
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                                                                                                                                                                                                                                  y Match 8.7%; Score 195.5; DB 10; Local Similarity 22.1%; Pred. No. 7.7e-05; hes 102; Conservative 44; Mismatches 208;
                                                                                                                                                                    62 LVSPQQTVTRAET-----TSNITSRPAVPANPQT-----VKICTVPNSSSQL 103
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  SLGASSTP---
                                         ----TPSPPPTTMTTPSPTTTPSPPTTTMTTLPPTTTSSPLTTTPLPPSITPPTFSPF 1773
                                                                                                                                                                                                                                                      TLVTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTSKPLVTSVANT -- VTTVSLQPEKPVVSGTAVTLSLPAVT 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVALRQLLPNSQSFIQQCVQQTSSDMVIATCT---TTVTTSPVVTTTVSSSQSEKSIIVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STTTPTTPCVPLCNWTGWLDSGKPNFHKPGGDTELIGDVCGPGWAANI---
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                                                                                 IKKVAVTPVKKLAQIGTTVVTTVPKPSSVQSVAVP----TSVVTVTPGKPLNTVTTLKPS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SCRATMYPDVPIGQLGQTVVCDVSVGLICKNEDQ------KPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TPSPPPTTMTTPSPTTTPSPPTTMTTLPPTTTSSPLTTTPLPPSITPPTFSPF 1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clapper, Jonathan D.
Stolk, John A.
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SNEPNLKAENSAAVQIN--LSPIMLENVKKCKNFLAMLIK 205
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                                                                                                                                                                                                                                                                                                                                         Length 5179;
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US-09-893-519A-14

Length 1023;

Matches 113; Query Match

Conservative

69;

Local Similarity

8.9%;

Score 200.5; Pred. No. 6e-Mismatches

6e-06; DB 10; 225;

Indels Length 1367;

101;

Gaps

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                                                                                                                                       APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Se;
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
NUMBER OF SEQ ID NOS: 440
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US-09-801-368-108
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                                                                                  SEQ ID NO 108
LENGTH: 1367
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                         ORGANISM: Saccharomyces cerevisiae -09-801-368-108
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APPLICANT:
                                                                                                                          SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cali, Brian
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                                                                                                                                                                                                                                                                                                                                              Sherman, Amir
Silva, Jeff
                                                                                                                                                                                                                                                                                                                                                                                      Salama, Sofie
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No. US20020128250Alman,
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Holtzman, Doug
                                                                                                                                                                                                                                                                                                                                                                                                              Royer, John
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Pred. No. 1.3e-27;
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                   NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 1068
LENGTH: 5179
TYPE: PRT
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                                                                                                                                                        TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE FILE REFERENCE: 210121.471C14
                                                                                                                      CURRENT APPLICATION NUMBER: US/10/025,380 CURRENT FILING DATE: 2001-12-19
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSP---VVTTTVSSSQSE 311
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Vedvick Thomas S.
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Wang, Aijun
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Skeiky, Yasir A. W.
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Benson, Darin R.
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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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US-10-124-557-74
US-10-124-557-58
US-09-801-368-110
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sequence 108, App
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Sequence 114, App
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US-09-735-367B-2	US-09-735-367B-3	US-09-991-630-13	US-09-991-630-10	US-09-991-630-2	US-09-905-129-13	US-09-905-129-10	-905-129-	US-09-991-630-24	US-09-991-630-16	US-09-905-129-16	US-09-991-630-14	US-09-991-630-11	US-09-905-129-14	US-09-905-129-11	US-09-864-761-36047	US-09-801-368-104	US-10-161-510-10	US-09-864-761-35720	US-09-862-027-40	US-10-124-557-62	US-10-124-557-2	US-10-124-557-52	US-10-124-557-40	US-10-124-557-48	US-10-124-557-60
2,		13	10		13,	10,		24	16,	16,	14,	11,				Sequence 104, App	Sequence 10, Appl	357	40,		Sequence 2, Appli	52		Sequence 48, Appl	Sequence 60, Appl

ALIGNMENTS

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SEQ ID NO 14
LENGTH: 1023
TYPE: PRT
ORGANISM: Homo s
FEATURE:
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US-09-893-519A-14
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NAME/KEY: misc_feature
NAME/KEY: misc_feature
OTHER INFORMATION: Corresponds to SEQ ID NO: 87
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Human Genbank/CAA72189
PATTABASE ENTRY DATE: 197-06-25
                                                                                                                                                                                                                                                                                                             APPLICANT: DAVIDOV, Eugene
TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND METHODS OF USE
FILE REFERENCE: 0342/16540-US2
CURRENT APPLICATION NUMBER: US/09/893,519A
CURRENT FILING DATE: 2001-06-28
                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/224,457
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 146
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BUURMAN, Ed T.
BRADLEY, John
DESILVA, Thamara
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KOMARNITSKY, Svetlana
MENDILLO, Marc
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                                                                                                                                                                                                                                                                                                                                                                                                             LONG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOORE, Daniel
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SLEPNIEGTVYMYAGYYYPMKVVYSNAVSWGT
Query Match 7.3%; Score 163.5; DB Best Local Similarity 21.1%; Pred. No. 1.4e-05 Matches 102; Conservative 67; Mismatches 15 11 SAPPKYSSGPRLPAPQIVAVKADNTTTIQFPANLQLPP
70 12. 10. 10. 10. 10. 10. 10. 10. 10. 10. 10
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PLICATI
CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP PCT/JP94/00290 FILING DATE: 24-FEB-1994
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/325,267A FILING DATE: 18-NOV-1994
VA Y: USA 22202
PONI ESSE
APPLICANT: OWNELS, MALIA-LENA APPLICANT: KERAKEN, SIRKE TITLE OF INVENTION: YEAST AGGLUTINATION GENES TITLE OF INVENTION: CONTAINING THEM NUMBER OF SEQUENCES: 7
OGAWA, M
APPLICANT: WATARI, JUNJI APPLICANT: WATARI, JUNJI APPLICANT: TAKATA VOCUTUTEO
0 N
372 TSPVDSSELL 381
292 TTTVTTSPVV 301
EFHSKLQEATNFPLRPFVIPFLKANLPLLQ
255 SSLANO-OLPPACGAROLSKLKRELTTLOOFGNDTSPETGERVRTLVLGLVNSTLTTE

Search completed: February 16, 2003, 22:02:50 Job time : 20.6146 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 6
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 650-324-1677
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                 399 TTATTTTTSETESVIKPDEWCWLEKNGECEAKGATYVGVIGKDGRIENGMAFTMIPNDD
                                                                                                459 THVRFRFKVKDVGNTISVRCRKGAGKLEFP------DRSLDFTIPPVAGHNSCSII 508
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                                                                                                                                                                                                                                                                                                                                                                                                                           95 TVPNSSSQLIKKVAVTPVKKLAQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 TTTIQFPANLQLPPGTVLIKSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKIC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/928,361B FILING DATE: 12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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REFERENCE/DOCKET NUMBER: 48
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VELKSSPQPHLVPFLKKSVVALRQLLPNSQSF----IQQCV-------QQTSSDMVIA 289
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                                                                                                                                                               VKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIE--AEEFTRKLY 242
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Sherman Avenue, Suite 6
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THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Release #1.0,
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                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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177 NSAAVQINLSPTM-LENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAE 235
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                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 15-AUG
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STATE: Virginia
                                                                                                                                                    61 MLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGT 120
                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                   ---PTMPPPPTTQG-APRTSSFTPT---TLTNGTSHSPTALNGAPSPPNGFSNGPSSSSS
                                                                                   TVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSL-GASSTP---SNEPNLKAE 176
                                                                                                                     VFTNPPQVATYHRAIKITVDGPREPRN-RTEKHSTMPDSPVDVKTQSRLTP------ 201
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                                                                                                                                                                                        72;
                                                                                                                                                                                        Similarity 28.8
72; Conservative
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8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                              752 amino acids
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Miyoshi, Hiroyuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                         7.3%;
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                                                                                                                                                                                                      Score 164.5; DB 1;
Pred. No. 9.7e-06;
                                                                                                                                                                                         Mismatches 108;
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US-09-165-239A-4
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SOFTWARE: FastSEQ for
SEQ ID NO 4
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                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: JOHNSON, ALEXANDER
APPLICANT: BRAUN, BURKHARD R
TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES FROM CANDIDA
TITLE OF INVENTION: ALBICANS ENCODING POLYPEPTIDES ASSOCIATED WITH FILAMENTOUS
TITLE OF INVENTION: GROWTH
FILE REFERENCE: 220022000700
                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/165,239A
CURRENT FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/068,065
PRIOR FILING DATE: 1997-12-18
                                                                                                                                                                                                                                                                                                                                               LENGTH: 750
TYPE: PRT
ORGANISM: Candida
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hes 106;
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 DAKIEAEEFTRKLYVEL
                               SAPVTETPTGPVSTVTEQSKTIVTITSCSN-----NACSES--
                                                           NEPNIKAENSAAVQINISPTMIENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKIVEQIL 228
                                                                                                                                                   ---ETETETTPTAHLITTTA-----QTTTVITVTSCSNNACSKTEVT-----TGVVVV 440
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                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                      Score 172; DB 4; Length 750;
Pred. No. 2.2e-06;
3; Mismatches 176; Indels 1
-KSSPQPHLVPFLKKSVVALRQLLPNSQSFIQ
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Best Local S
Matches 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NELSON, RICHARD, C. APPLICANT: GUT, JIRI
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APPLICANT: LEECH, JAMES
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TYPE: PRT
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les 92; Conserv
            TTQKPTTTTTKVPGKPPIATTTTLKPIVTTTTTKATTTTTTTVPTTTTTKRDEMTTT 676
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TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPTOSPORIDIUM PARVUM TITLE OF INVENTION: INFECTIONS FILE REFERENCE: 480.19-4 (HV)

CURRENT APPLICATION NUMBER: US/08/700,651B

CURRENT FILING DATE: 1997-08-14

EARLIER APPLICATION NUMBER: 08/415,751

EARLIER FILING DATE: 1995-04-03

NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                              459 THVRFRFKVKDVGNTISVRCRKGAGKLEFP------DRSLDFTIPPVAGHNSCSII 508
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HSVGPTAATGGTTAGTGLLQTS----KPLVTSVAN--TVTTVSLQPEKPVVSG----TAV 396
                                                                                                                                                                                                                                   VELKSSPQPHLVPFLKKSVVALRQLLPNSQSF----IQQCV-----QQTSSDMVIA
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                                                                                                                                                                               VGVSGDGKIHVSPYGSKDVSLISAPIQPSELFNEVYCDTCTAKYGAIHSGYQTSADFVTT 568
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                                                             TTAKPTTTTTGAPGQPTTTTTGSPSKP--TTTTTTKATTTTTLNP
                                                                                                                     TC---TTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTL 346
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                                                                                                                                                                                                                                                                                                                                                            -VKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIE--AEEFTRKLY 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.6%; Score 171.5;
21.5%; Pred. No. 8.3e
tive 50; Mismatches
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PCT-US93-11721-5

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Sequence 2, Application US/09579181

Patent No. 6365372

GENERAL INFORMATION:
APPLICANT: Chrivia, John
APPLICANT: Yaciuk, Peter
TITLE OF INVENTION: SNF2 Related CBP Activator Protein (SRCAP)
FILE REFERENCE: 16153-4247

CURRENT APPLICATION NUMBER: US/09/579,181

CURRENT FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/136,620
PRIOR FILING DATE: 1999-05-27

NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGER OF SEC ID NOS: 17
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Best Local Similarity
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                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                    LENGTH: 2972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      629
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  48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 9.1%; Score 204; DB 5; Length 2035; Local Similarity 23.5%; Pred. No. 1.7e-08;
                                                                        PGTVL---IKSNSG--PLMLVSPQQTVTRAETTSNITSRPAV-----PANPQTVKICTV 96
                                    PVRPPP----GPELSAQPTPGPVPQVL------PASLMVSASPAGPPLIPASRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SQPTQVTLITAPSGVEAQP 973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSSDMVIATCTTTVTT------SPVVT-----TTVSSSQSEKSIIVSGA-----TA 321
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                                                                                                                  Conservative
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                                                                                                            7.8%; Score 176.5; DB 4; Length 2972; 22.4%; Pred. No. 6.9e-06; vative 56; Mismatches 196; Indels 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66;
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US-09-579-181-1
                                                                                                                                                                                                                                                                                                                                         ; NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ve
SEQ ID NO 1
LENGTH: 3118
; TYPE: PRT
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US-09-579-181-1
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APPLICANT: Chrivia, John
APPLICANT: Yaciuk, Peter
TITLE OF INVENTION: SNF2 Related CBP Activator Protein (SRCAP)
                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 123; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09579181 Patent No. 6365372
                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/136,620
PRIOR ETLING DATE: 1999-05-27
NUMBER OF FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 16153-4247
CURRENT APPLICATION NUMBER: US/09/579,181
CURRENT FILING DATE: 2000-55-25
   1069
                                                                          1016
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                                                                                                                                                                                      PPPGSSSLLKPLTVPPGYTFPPAAATTTSTTTATATTTAVPAPT---
                                 -PNSSSQLIKKVAVTPVKKLAQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTT 155
                                                                        PGPVLLPPLQPNSGSLPQVLPSPLGVLSG-----
                                                                                                           PGTVL---IKSNSG--PLMLVSPQQTVTRAETTSNITSRPAV-----PANPQTVKICTV 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQPGPVLSQP 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASALTLGLATAPSLSSSQTPGHPLLLAPTSSHVPGLNSTVA----PACSPVL-VPAS-AL 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTAVTLSL---PAVTFGETSGAAICL-----PSVKPVVSFCWDHICKPVIGTPVQIKL 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEKSIIVSGATAPRTVS-----VQTLNPLAGPVGAKAGV-----V 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPPSSGLPAVLN------PRPTLTPGRLPTPTLGTARAPMPTPTLVRPLLKLVHSPS 1123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPPGSSSLLKPLTVPPGYTFPPAAATTTSTTTATATTTAVPAPT-----PAPQRLI 973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTT-----VSSSQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -PNSSSQLIKKVAVTPVKKLAQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTT 155
                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Ver. 2.0
                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                       7.8%; Score 176.5; DB 4; 22.4%; Pred. No. 7.5e-06; tive 56; Mismatches 196;
                                                                        TSRPPTPTLSLKPTPPAPVRLSPA 1068
                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                              Length
----PAPQRLI 1119
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US-08-393-703-5
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                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                         TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Lamarc
                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                   TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wilson, Angus
APPLICANT: Herr, Winship
TITLE OF INVENTION: A NOVEL EXARYOTIC TRANSCRIPTION PROTEIN:
TITLE OF INVENTION: HOST CELL FACTOR
                                         537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        322
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                                                                                                              Local Sin
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CITY: San Francisco
     70
                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                     10 VSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLVSPQQTV 69
                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 24-FEB-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
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 TRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTV------
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                                     IGSSPOMSGMAALAAAAAATOKIPPSSA---PTVLSVPAGTTIVKT----MAVTPGTTT 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASLATPITTLGTIATLSSQ----VINPTAITVSAAQTTLTAAGGLTTPTITMQPV-----
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                                                                                                                             Similarity
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                                                                                                              Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                           66;
                                                                                                           Score 204; DB 1;
Pred. No. 1.7e-08;
6; Mismatches 188
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                                                                                                                                            Length 2035;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application:
                                                                                                       TELEFAX: (415) 398-324
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                          REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: FP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wilson, Angus
APPLICANT: Herr, Winship
TITLE OF INVENTION: A NOVEL
TITLE OF INVENTION: HOST CEL
                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                       FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/
FILING DATE: 03-DEC-1993
                  TOPOLOGY:
                               STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---VTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLK-PSSL-GASSTPSNEPNL---- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASLATPITTLGTIATLSSQ-----VINPTAITVSAAQTTLTAAGGLTTPTITMQPV-----
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
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LNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKP 389
                                                                                                                                    SSPQPHLVPFLKKSVVALRQL-----
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                                                                                                                                                                                                                                  APQLPQITQIQTIPAQQSQQQQVNNVSSAGGTATAVSSTTA--
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                                                                                                                                                                                                                                                                                                NTTSTTNHPTTTQ-IRLQTVPAAASMTNTTATSNIIVNSVASSGYANSSQPPHLTQLNAQ 243
                                                                                                                                                                                                                                                                                                                             NITSRPAVPANPQTVKICTVPNSSSQ-----LIKKVAVTPVKKLAQIGTTVVTTVP 127
                                                                                                                                                                                                                                                                                                                                                               PQSPSITLSTLNTGQTPA-----LLVKTDNGFQLLRVGTTTGPPTVTQTITNTSNNS 184
                                PSQTTTIGQTQVRMI--TPNALGTPRPTIGHTTISKQPPN---IRLPTAPRLVNTGGIRT
                                                               ----QCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVS----VQT
                                                                                                ASPQPCLIGFLKKSLPLLRQALYTKELVIEGIKPPPQHVLGLAGLSQQLPKIQAQIRPIG
                                                                                                                                                               TOOGNTKEKCRKFLANLIEL -- STREPKPVEKNVRTLIQELVNANVEPEEFCDRLERLLN
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F: 4 Embarcadero Center, Suite 3400
San Francisco
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Pred. No. 3.2e-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN: TITLE OF INVENTION: HOST CELL FACTOR
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                               70 TRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTV----- 122
                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0
FILING DATE: 12-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                QTKPVQTSAVTGQASTGPVTQIIQTKGPLPAGTILKLVTSADGKPTTIITTTQASGAGTK 747
                                                                                                TRPIITVHKSGTV-TVAQQAQVVTTVVGGVTKTITLVKSPISVPGGSALISNLGKVMSVV 687
                                                                                                                                 ---VTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLK-PSSL-GASSTPSNEPNL---- 173
                                                                                                                                                                LPA--TVKVASSPVMVSNPAT------RMLKTAA-----AQVGTSVSSATNTS 628
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KLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ 281
                                                               --KAENSAAVQINLSPTMLENVKKCKNFL--AMLIKLACSGSQSP------EMGQNVK 221
                                                                                                                                                                                                                                  IGSSPQMSGMAALAAAAAATQKIPPSSA---PTVLSVPAGTTIVKT-----MAVTPGTTT 588
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4 Embarcadero Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2035 amino acids
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Angus
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                                                                                                                                                                                                                                                                                                                 Score 204; DB 1; Pred. No. 1.7e-08;
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er, Suite 3400
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                                                                                                                                                                                                                                                                                                                                 Length 2035;
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US-08-188-582-2
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Patent No. 553441
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                            APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELLERAX: (415) 398-3249
TELLERAX: (415) 398-3249
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ATTORNEY/AGENT INFORMATION:
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Local :
159;
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 4 Embarcadero Center,
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Tanese, Naoko
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Comai, Lucio
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                    FLEHR,
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HOHBACH, TEST, ALBRITTON & HERBERT dero Center, Suite 3400
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                                                                     OF USE
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Patent No. Sequence 2,

, Application US/08646715 5637686

GENERAL INFORMATION:
APPLICANT: Tjian,
APPLICANT: Comai,

Tjian, Comai,

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RESULT 5
US-08-646-715-2
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Best Local Similarity
Matches 112; Conserv
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 921 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Osman, Richard A
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                                                                                                                                              461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/188,582 FILING DATE: 28-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                              LNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKP 389
                                                                                                                                          QIP-SLQVPGQANIVQIR--GPQHAQLQRTGSVQIRATTRP-----PNSVPTAN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTTSTTNHPTTTQ-IRLQTVPAAASMTNTTATSNIIVNSVASSGYANSSQPPHLTQLNAQ 243
                                                                                                                                                                                                                                      ----QCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVS----VQT 329
                                                                                                                                                                                                                                                                                     ASPQPCLIGFLKKSLPLLRQALYTKELVIEGIKPPPQHVLGLAGLSQQLPKIQAQIRPIG 405
                                                                                                                                                                                                                                                                                                                          SSPQPHLVPFLKKSVVALRQL------
                                                                                                                                                                                                                                                                                                                                                            TQQGNTKEKCRKFLANLIEL -- STREPKPVEKNVRTLIQELVNANVEPEEFCDRLERLLN 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSP 187
                                                                                                        VVSGTAVTLSLPAVTFGETSGAAICLPSVKP 420
                                                                                                                                                                                                                 PSOTTTIGQTQVRMI--TPNALGTPRPTIGHTTISKQPPN---IRLPTAPRLVNTGGIRT
                                                                                                                                                                                                                                                                                                                                                                                              TMLENVK-KCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELK 246
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                                                                       -KLTAVKVGQTQIKAI-TPSLHP 527
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N: 435
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Pred. No. 3.
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17;

US-08-188-582-16

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TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: UCLEIC ACIDS ENCODING TAFS AND METHODS OF L
NUMBER OF EXQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
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US-08-188-582-16
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                                                                  INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Dynlact, Brian D.
APPLICANT: Hoey, Timothy
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Nacko
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
MOLECULE TYPE:
                                                                                                                                     NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REBERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                NAME: Osman, Richard A
                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421
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                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release
                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/188,582 FILING DATE: 28-JAN-1994 CLASSIFICATION: 435
                                                                                                      TELEFAX: (415) 39
TELEX: 910 277299
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                                                  LENGTH:
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                                                  737 amino acids
protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IF Floppy disk
COMPUTER: POSPTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OSOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                               APPLICANT: Weinzlerl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228
                                                                                                                                                                                                                CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                               APPLICATION NUMBER: US/08/646,715 FILING DATE: 09-MAY-1996
                                                                                                                                                                                                                                                   STREET:
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APPLICATION NUMBER:
                                 CLASSIFICATION:
                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 PPKVSSG-----PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGV 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NE-PNIKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEGETSGAAICLPSVKPVVSECWDHICKPVIGTPVQIKL--AQPGPVL 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAV 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q-----ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL 118
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                                                                                                                                                                                94111-4187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Application US/08646715 5637686
                                                                                                                                                                                                                                                 E: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                    USA
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Tanese, Naoko
                                                                                                                                                                                                                                                                                                                                                                                                                                     Dynlact, Brian D.
                                                                                                                                                                                                                                                                                                                                                                   Wang, Edith
                                                                                                                                                                                                                                                                                                                                                                                                                    Hoey, Timothy
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US 08/188,582
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Pred. No. 2.2e-36;
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Title:
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Sequence:
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No.
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Maximum
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US-08-933-703-5
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US-09-579-181-2
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Copyright (c) 1993 - 2003 Compugen Ltd
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09n4s7 caenorhabdi
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076602 caenorhabdi
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Q9n5k0 caenorhabdi	Q9c105 schizosacch	. Q23587 caenorhabdi	α		Q8v015 equine herp	Q8t3k4 drosophila	Q9jk31 mus musculu	homo	_	\sim		Q92223 emericella	5	Q8v017 equine herp		Q8v016 equine herp	Q8tfg4 schizosacch	P91365 caenorhabdi	Ol4760 homo sapien		homo sap			8 arab	homo	Q9h4a3 homo sapien	homo	Q9nkc9 drosophila

ALIGNMENTS

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134 SVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNE-PNLKAENSAAVQINL 185	74 TTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTVVTTVPKPSSVQ 133 	20 PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLVSPQQTVTRAE 73 	Query Match 23.4%; Score 526; DB 11; Length 662; Best Local Similarity 35.0%; Pred. No. 3.5e-25; Indels 100; Gaps 18; Matches 155; Conservative 60; Mismatches 128; Indels 100; Gaps 18;	SEQUENCE 662 AA; 71398 MW; 91A75F38CB0D0DA4 CRC64;	MGD; MGI:2152346; Taf4a.	EXP. Cell Res. 0:0-0(2001). EMBL; AY038601; AAK94779.1;	Nervous System.";	"Cell Type Specific Expression of the TFIID Component TAFII135 in the	Metsiś M., Brunkhorst A., Neuman T.;	STRAIN-BALB/C; TISSUE-PO BRAIN;	SEQUENCE FROM N.A.	(1)		Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus		TAE4A	TATA-binding protein associated factor TAFII135 (Fragment).	$\overline{}$	(TrEMBLrel. 19,	-2001	•	Q91WW6 PRELIMINARY; PRT; 662 AA.	LT 1 W6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY069807; AAL39952.1; 665B28B9588C984C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopteryyota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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01-JUN-2002
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                                                                                             FLKKSVVALRQL---
                                                                                                                                                 CRKFLANLIEL -- STREPKPVEKNVRTLIQELVNANVEPEEFCDRLERLLNASPQPCLIG
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                                                                                                                                                                                                                                                                                                                                                                                                   TSRPAVPANPQTVKICTVPNSSS--QLIKKVAVTPVKKLAQIGTTVVTTVPKPSSVQSVA 136
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TSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVS---VQTLNPLAGPVG
                                              FLKKSLPLLRQALYTKELVIEGIKPPPQHVLGLAGLSQQLPKIQAQIRPIGPSQTTTIGQ
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AC 0766
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RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laisten N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
RA Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
T. 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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Matches 110
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Geisel C., Harmon G.;
The sequence of C. el
Submitted (JUL-1998) t
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Submitted
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[2]
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MEDLINE-94150718; PubMed-7906398;
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Rhabditidae; Peloderinae;
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TVTVPTTVPTTNPSTVVTAPSTV--VTVPTTVMTSRSTVITTPTTGGSSPSTAGTSLAST
                                                                                                                        --SGPLMLVS-PQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVK 113
                                                                                                                                                                                         TLVTKVAPVSAPPKVSSGP----RLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSN-
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                                                                                             VVTAPSTVVTVPSTVVTKPNTV--VTSSPTVATTPTTV--VTTPST-----
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3) to the
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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1008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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QDQQGPFKMCLNYEVRVLCCETPKGCPVTSTPVTA----
                                       EAEEFTRKL----YVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVI 288
                                                                                       PHGGDKETYNNIIRSGEKICRRPEEITRLQCRAESHPEVSIEHLGQVVQCSREEGLVCRN
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1349 AA;
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Last sequence update)
Last annotation update)
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Pred. No. 2.8e-05;
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Best Local :
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Gastroenterology 106:200-200(1994).
EMBL; U10281; AAC48526.1; -.
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NON_TER 528 528
SEQUENCE 528 AA; 49907 MW; OBF0F6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-YORKSHIRE/CHESTER WHITE/HAMPSHIRE CROSS; MEDLINE-95275264; PubMed-7755593; Turner B.S., Bhaskar K.R., Hadzopoulou-Cladaras
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                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-YORKSHIRE/CHESTER WHITE/HAMPSHIRE MEDLINE-94102478; PubMed-7506218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Turner B.S., Bhaskar
LaMont J.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
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LaMont J.T.;
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                       SQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPN
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                                                                LKPSSLGASSTP-----SNEPNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSG
                                                                                              SSSSVPTTSATSVRSSSSSSTPIPSTTSVQPSSSSSAPTTSATSVQPSSSSSTPIPSTTS
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                                                                                                                                                                                                                        APVSAPPKV--SSGPRLPAPQIVAVK-----APNT--TTIQFPANLQLPP--GTVLIKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V-GPT-----AATGGTTAGTGLLQTSKPLVTSV-ANTVTTVSLQPEKPVVSGTAVTLSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRTTTLYTTSTTSTPQTSTTSAPTTSTIPAST-PSTTSAPTTSTTSAPTTSTTSAPTHRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHS
                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. 308:89-96(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -AVTFGETSGAAICLPSVKPVVS
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                      Bhaskar K.R., Hadzopoulou-Cladaras
                                                                                                                                                                                                                                                                                                                                                                                                                                            N.A.
-TTSVQPSSSGSAPTTSATSVQPSSSSSPPI----SSTISVQ---
                                                                                                                                                 -SSAPTTSATSVQPSSSSSPPISSTVSVQTSSSSSVPTTSTTSVQPS
                                                                                                                                                                                                                                                              9.3%;
                                                                                                                                                                                                                                                   76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                           Score 209.5;
                                                                                                                                                                                                                                                                                                     OBF0F6879203B2EA CRC64;
                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of.
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                                                                                                                                                                                                                                                                                                                                                                               characterization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Specian
                                                                                                                                                                                                                                                                                                                                                                             cDNA clone
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                                                                                                                                                                                                                                                   137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastric
PS
                                               SS
                                                                                                                                                                                                                                                                                                                                                                                                                               MUCOSA;
                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                              Query Match
Best Local Sin
Matches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9QY35;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                    corresponding region of human xq28.";
Submilted (MAR-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF133093; AAF22156.1; .
MGD; MGI:105942; Hcfc1.
MGD; MGI:1349215; Abcd1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9QY35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosenthal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002
                       649
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  249
                                             199
                                                                  589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lost cell factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Latzer M.,
                                                                                                                                  94
                                                                                                                                                                                                                       4 VTKVAPVSAPPKVSSGPRL---PAPQIVAVKAPNTTTIQFPANL-----QLPPGTVL--
                                                              GGVTKTITLVKSPISVÞGGSALISNLGKVMSVVQTKÞVQTSAVTGQASTGÞVTQIIQTKG
                                                                                                                             CTVP----NSSSQLIKKVAV---TPVKKLAQIGTTVVTTVPKPSSVQSVAVPTSVVTVTP 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  н
PQPHLVPFLKKSVVALRQLLPNSQSFTQQCVQQTSSDMVIATCTTTVTT--
                     PLPAGTILKLVTSADGKPTTIITTQASGAGTKPTILGI--
                                           FL--AMLIKLACSGSQSP---
                                                                                     GKPLNTVTTLK-PSSL-GASSTPSNEPNL-----KAENSAAVQINLSPTMLENVKKCKN
                                                                                                            ASSPVMVSNPATRMLKTAAAQVGTSVSSAANTSTRPIITVHKSGTV-TVAQQAQVVTTVV
                                                                                                                                                        NPQMSGMAALAAAAATQKIPPSSAPTVLSVPAGTT----IVKTVAVTPGTTTLPATVKV
                                                                                                                                                                                                   VPAVLKVTGPQATTGTPLVTMRPASQ--AGKAPVTVT-SLPASVRMVVPTQSAQGTVIGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QPSSSSSPPISSTISVQPSSSSSSPTTSTTSVQPSS---SGSAPTTSATSVQPSSSSSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOTS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VQPSSSSSVPTTSAT-----SVQTSSSSSTPIPSTT-----SVQPSSSSSAPTTSATSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGG-TTAGTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSSSSPTTSTTSVQPSSSGSAPTTSATSVQPSSSSSVPTTSATSVRSSSSSSTPIPTTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQS----FIQ----
                                                                                                                                                                                                                                                                                                                                   PF00041;
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                                                                                                                                                                                                                                                                                                                SM00060;
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                                                                                                                                                                                                                                             Similarity 23.7
28; Conservative
                                                                                                                                                                                                                                                                                                                                              IPR003961; FN_III. IPR001798; Kelch.
                                                                                                                                                                                                                                                                                          1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Brenner V., Reichwald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                        fn3; 2.
Kelch;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----KPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAVTFGETSGAA
                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                              FN3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Rođentia;
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23.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                           analysis
                                                                                                                                                                             -IKSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKI 93
                                                                                                                                                                                                                                             63;
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                                                                                                                                                                                                                                                                                          W.
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Pred.
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                                           EMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSS
                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                         ABE998C5DDE688A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Χ.
                                                                                                                                                                                                                                                         205;
No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                         mouse Licam locus
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                                                                                                                                                                                                                                                       DB 11;
.00019;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Oksche
                                                                                                                                                                                                                                                                  Length 1979;
                                                                                                                                                                                                                                             Indels 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                           the
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              RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Champe M., Pfelifer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhadari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C.K., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Peccor C., Turner R., Venter B., Sun E.,
RA Palazzolo M., Pitman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pitman G.S., Pan S., Pollard J., Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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EMBL; AE003421; AAR45644 1; -
EMBL; AL031028; CAA19845 2; -
FlyBase; FBgn0025390; EG:56G7.1.
InterPro; IPR002557; Chitin_bind_PerA.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF01607; CBM_14; 2.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00494; ChtBD2; 2.
SEQUENCE 1795 AA; 194464 MW; 07F10C1
                                                                                                                                                           O61191
PRESENTED PROBLEM 101, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 21, Last annotation update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
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Cadieu E., Dreano S., Lelaur
"Sequencing the distal X chr
"Submitted (JUL-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-1999)
                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Benos
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                       TISSUE-LIVER;
Kristie T.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1018
                                                                   SEQUENCE FROM N.A.
                                                                                                             NCBI_TaxID=10090;
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l X chromosome of Drosophila melanogaster.
to the EMBL/GenBank/DDBJ databases.
  homolog
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Pred. No. 0.00026;
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                                                                                                                                  Craniata; Vertebrata; Sciurognathi; Muridae;
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  the
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  transcription
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; Murinae; Mus
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InterPro; IPR001798; Kelch.
Pfam; PF00041; fn3; 2.
Pfam; PF01344; Kelch; 5.
SMART; SM00066; FN3; 1.
SEQUENCE 2045 AA; 210537 M
                                                                                                                                                                  01-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                        Q9VGC9;
                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                            CPN protein.
CPN OR CG4795.
 MEDLINE=20196006; pubMed=10731132;
Adams M.D., Celniker S.E., Holt R.
Amanatides P.G., Scherer S.E., Li
George R.A., Lewis S.E., Richards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U53925; AAB01163.1; MGD; MGI:105942; Hcfcl.
                                                 STRAIN-BERKELEY;
                                                                                  NCBI_TaxID=7227;
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Submitted (APR-1996)
                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              877
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nes 129;
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                                                                                                                                                                                                                                                                                                                           TTGVTTLGTVTGTVST--SLAGAGAHSTSASLATPITTLGTIATLSSQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WVSNPATRMLKTAAAQVGTSVSSAANTSTRPIITVHKSGTV-TVAQQAQVVTTVVGGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLKVTGPQATTGTPLVTMRPASQ--AGKAPVTVT-SLPASVRM---VVPTQSAQGTVIGS
                                                                                                                                                                                                                                                                                                                                        -AGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVA--NTVTTVSLQPEKPVVSGTAVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTILKLVTSADGKPTTIITTQASGAGTKPTILGI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMLIKLACSGSQSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTYTTLK-PSSL-GASSTPSNEPNL-----KAENSAAVQINLSPTMLENVKKCKNFL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----NSSSQLIKKVAV---TPVKKLAQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPQQT-----VTRAETTSNI--TSRP---AVPAN-------PQTVKICTVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAPVSAPPKVSSGPRL---PAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLV
                                                                                                                                                                                                                                                                               VSAAQTTLTAAGGLTTPTITMQPV-----
                                                                                                                                                                                                                                                                                                    LSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKL-AQPGPVLSQP
                                                                                                                                                                                                                                                                                                                                                                         AVPKIATGHGQQGVTQVVLKGAPGQPGTILRTVPMGGVRLVTPVTVSAVKPAVTTLVVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                LVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTT-----SPVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTITLVKSPISVPGGSALISNLGKVMSVVQTKPVQTSAVTGQASTGPVTQIIQTKGPLPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPQMSGMAALAAAAAATQKIPPSSAPTAWSVPAGTTIVKTVAVTPGTTTLPATVKVASSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                           TTVSSSQSEKSIIVSGA----TAPRT
                                                                                                                                                                                                                                                                                                                                                                                                                         -KPGTTTIIKTIPMSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAPAKIIT
                                                                                                                                                                  0 (TrEMBLrel.
0 (TrEMBLrel.
1 (TrEMBLrel.
                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the
                                                                                                                                                                     13,
13,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -EMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ¥
                                                                                                                                                                    Last sequence up
                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 200;
Pred. No. 0.
                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B89CC2FDA35B969F CRC64;
.A., Evans C.A., Goc
P.W., Hoskins R.A.,
S., Ashburner M., H
                                                                                                                                                                                                                    842
                                                                                                                                                                                                                                                                                                                                                                                     |-----VSVQTLNPLAGPVGAK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11;
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                                                                                                                                                                                                                                                                             -SQPTQVTLITAPSGVEAQP
                                                                                                                                                                                update)
                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201;
                                                                                                        Brachycera;
            Gocayne J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
  Henderson
                                                                                                                                                                                                                                                                                                                             -VINPTAIT
                                                                                                         Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSVSPS
            ت <del>بر</del>
 S.N.,
                                                                                                                                                                                                                                                                                                    452
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RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroju L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Blusam D.A., Buther H., Cadleu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Coler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Classer K.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Coler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Classer K.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Li X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Murphy L., Murphy L., Murphy L., Murphy L., Murphy D.M., Nelson D.L.,
RA Melson D.R., Nelson K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden F.L., Shen H., Strong R., Shu E.,
RA Syliskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang S.H., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yelson X.A., Moodage T., Weinstock G.M., Weissenbach J.,
RA Lisko P., Lickor J.S., Zhan M., Strong G., Zhao Q., Zheng L.,
Weinston J., Shan M., Shoon S., Zhu X., Smith H.O.,
RA Sheng X., Hell S., Shan M., Shang G., Zhao Q., Zheng L.,
Shan M., Shan M., Shoon S., Zhu X., Smith H.O.,
Ra Glober R.A., Myers E.M., Shoon M., Venng G., Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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      326
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                                                                                                                                                                      229
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                                                                                                                                                                                                                                                                                                                                                                        KKVAVT-----PVKKLAQIGTT--VVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLK 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTLVTKV-APVSAP-----PKVSSGPRLPAP----QIVAVKAPNTTTIQFPANLQ
  EPETIAPPVVAETPEVASVAVAETTPPVVPPVAAES-----IPAPVVAT
                                            APRTVS----
                                                                                                                       RQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIV----SGAT
                                                                                                                                                                                                        KLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVAL
                                                                                                                                                                                                                                                 PVAAPVAAVPAVAPVLAPAVAPAVAPAVAPVAETPAPPPVAETPVATIPEC---VAPLI
                                                                                                                                                                                                                                                                                                                                  PPVAATPTPVAPIPVAAPVIATPPVAASAPTPAAVTPVVSP--VIATPPVVPANTTV---
                                                                                                                                                                                                                                                                                                                                                                                                               IPAPAPIAAASVAPVASVAP---PVVAAPTPP-----AASPVSTPPVAVAQIPVAVSAPVA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPPGTVLIKSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNS-SSQLI 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTIPSPVSAPVAAPVTPSAVAAPVQVVSPAAVAPAAPIAVTPVAPPPTLASVQPATVT
                                                                                                                                                                                                                                                                                       PSSLGASSTPSNEPNLKAENSAAVQINLSPTMLE------NVKKCKNFLAMLI
                                                                                 ----PVSAS-----TEPPVAAATLTTAPET-PALAPVVAESQVAANTVVATPPTPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                PEVSVVATKPLAAAEPVVVAPPATETPVVAPAAASPHVSVAPAVETAVVA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.9%;
                                      VQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 199.5;
Pred. No. 0.0
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).00015;
nes 203; Indels 153;
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369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   González M., Cuavia V., Dorsett V., Farfan D., Frise E., George González M., Guarin H., Li P., Liao G., Miranda A., Mungall C., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wai Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AV08315; AAL13544 l.; -.

FlyBase; FBgn0010218; Cpn.

SEQUENCE 864 AA; 84565 MW; E2B96CFB0CBC9802 CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001
01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BERKELEY;
Stapleton M., Brokstein P., Hong L., Agbayani A.,
Champe M., Chavez C., Dorsett V., Farfan D., Fris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CPN OR CG4795
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   366
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                                                                                                                                                                                                                                                                                                                                                                                    GTIPSPVSAPVAAPVTPSAVAAPVQVVSPAAVAPAPAAPIAVTPVAPPPTLASVQPATVT 63
                                                                                                                RQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIV----SGAT
                                                                                                                                                                                                                                                                                                KKVAVT-----PVKKLAQIGTT--VVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLK
                                                                                                                                                                                                                                                                                                                          IPAPAPIAAASVAPVASVAP---PVVAAPTPP-----AASPVSTPPVAVAQIPVAVSAPVA
   QTSKPLVTSVANTVTTVSLQPEKP--
                             EPETIAPPVVAETPEVASVAVAETTPPVVPPVAAES-----IPAPVVAT--
                                                             APRTVS----
                                                                                      ----PVSAS-----TEPPVAAATLTTAPET-PALAPVVAESQVAANTVVATPPTPAP
                                                                                                                                                                          KLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVAL
                                                                                                                                                                                                           PVAAPVAAVPAAVPVVAPVLAPAVAPAVAPVVAETPAPPPVAEIPVATIPEC---VAPLI
                                                                                                                                                                                                                                       PSSLGASSTPSNEPNLKAENSAAVQINLSPTMLE-----NVKKCKNFLAMLI
                                                                                                                                                                                                                                                                    PPVAATPTPVAPIPVAAPVIATPPVAASAPTPAAVTPVVSP--VIATPPVVPANTTV---
                                                                                                                                                                                                                                                                                                                                                       LPPGTVLIKSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNS-SSQLI 104
                                                                                                                                                -----PEVSVVATKPLAAAEPVVVAPPATETPVVAPAAASPHVSVAPAVETAVVA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQPGPVLSQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGET------SGAAICLPSVKPVVSFCWD-----HICKPVIGTP-----VQIKL 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QTSKPLVTSVANTVTTVSLQPEKP------VVSGTAVTLS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEETPETPAPASAPVTIAALDIPEVAPVIAAPSDAPAEAPSAAAPIVSTPPTTASVPETT 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -TPVPATLAVTDPDVTASAVPELPPVIAPSPVPSAVAETPVDLAPPVLPPVAAEPVPAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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(TrEMBLIE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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22.5%;
                                                       ----VQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLL
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19,
20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  70;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 199.5; DB:
Pred. No. 0.00015
0; Mismatches 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                153;
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404
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29 VGCC8
110 VGC
                                                                                                  RX MEDLINE-2019500; PubMed=10731132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Burtis K.C., Benos P.V., Berman B.P., Bhandari D., Botshakov S.,
RA Becson K.Y., Benos P.V., Berman B.P., Bhandari D., Botshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davise P.,
RA Burtis K.C., Busam D.A., Butler H., Gateu E., Center R., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davises C.,
RA Dodson K.J., Evangelista C.C., Ferriaz C., Ferritera S., Fleischmann W.,
RA Dodson K.J., Evangelista C.C., Ferriaz C., Ferritera S., Fleischmann W.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson K.A., Nixon K., Sunders R.D.C., Schelet F., Shen H.,
RA Spler E., Spradling A.C., Stapleton M., Skupski M.P., Sun E.,
RA Kenner K., Fr. Zaveri J.S., Zhan M., Venter J.C.,
RA Williams S.M., Woodage T., Worley K.C., Wan D., Yang S., Yao Q.A.,
RA Harlis R.B., Kenner S., Roll D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                         FlyBase; FBgn0010218; Cpn.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
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CPN OR CG47
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   PRICHEXTENSN.
A; 84595 MW;
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5B3635A283E5C658 CRC64;
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Best Local Similarity
Matches 124; Conser
                                                                                        SEQUENCE FROM N.A.
MEDLINB=97476275; PubMed=9334251;
Gum J.R. Jr., Ho J.J.L., Pratt W.S., Hicks
Vinall L.E., Roberton A.M., Swallow D.M.,
"MUC3 human intestinal mucin. Analysis Of
                                                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-JUN-2002 (TrEMBLrel. 21,
                                                   terminus, and a novel upstream repetitive J. Biol. Chem. 272:26678-26686(1997). EMBL; AF007190; AAC02268.1; -.
                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                              043418
 SEQUENCE
                                        PRINTS;
                                                                                                                                                               NCBI_TaxID=9606
[1]
                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                           Intestinal mucin
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                                                                                                                                                                                                                                                                                                                                                                              APPAAVPTEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PVSAS-----
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                                       PR01608; BACINVASINC
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               513
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               513
                                                                                                                                                                                       Chordata;
Primates;
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22.5%;
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D.M., Kim Y.
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  Query Match
Best Local Similarity
Matches 129; Conserv
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Best 1
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                                                                                                        EMBL;
                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                     Q9QWH2;
01-MAY-2000
                                        SEQUENCE
                                                  SMART; SM00060;
                                                                            InterPro; IPR003961; FN_III.
InterPro; IPR001798; Kelch.
                                                                                                                   Submitted (DEC-1996)
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                         Q9QWH2
                                                                                                MGD; MGI:105942; Hcfcl.
                                                                                                                                               Kristie T.M.;
                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                  HCFC
                                                                                                                             (HCF)
                                                                                                                                    cDNAs encoding the mouse homolog
                                                                                                                                                                                                                                                                                                                                         377
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 VSAPPKVSSGPRLPAPQIVAVKAPNT----TTIQFP--ANLQLP------PGTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                          transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSSSSAMSKSVIPSS-PSIQNTETSSLVSMTSATTPSLRPTITSTDSTLTSSLLTTEPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVTVTPGKPLN----TVTTLKPSSLGASSTPSNEP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MITSHTTNTTPLSTLVTTLLTTITRSTPTSETTYPTSPTSIVSDSTTEITYSTSITGTLS
                                                        PF01344; Kelch; 5.
                                                                                                                                                                                                                                                                                                                     STLTSETAYPSSPTSTVTESTTEITYPTTMTETSSTATSLPPTSSLVS
                                                                                                                                                                                                                                                                                                                                   NTYTTVSLQPEKPVVSGTAVTLSLP-AVTFGETSGAAICLPSVKPVVS 423
                                                                                                                                                                                                                                                                                                                                                         SWPTATNTLSPLTSSILSSTPVPSTEVTTSHTT-----NTNPVSTLVTTLP-ITITR
                                                                                                                                                                                                                                                                                                                                                                            SGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                   YSFSSSMSASSAGTTHTETISSLPASTNTIHTTAESALAPTTTTSFTTSPTMEPPSTTVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTAISSASPTSGTMVTSTTMTPSSL-STDTPSTTPTTTTYPSVGSTGFLTTATDLTSTFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTSPPPVSS-----SITPTNTMTSMRTTTYWPTATNTLSPLTSSILSSTPVPSTE
                                                                                                                                                                                                                                                                                                                                                                                               TTGTGQTTFPSSTATFLETTTLTPTTDFSTESLTTAMTSTPPITSSITPTDTMTSMRTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110;
                                                                                                       tted (DEC-1996) to the U80821; AAD09225.1; -.
                                                                                                                                                                                                                                 O (TrEMBLrel. 13, 0) (TrEMBLrel. 13, 0) (TrEMBLrel. 21,
                                       2045
   Conservative
                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 -NSQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSI--IV
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           8.8%;
                                       210546 MW;
  67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81; Mismatches
                                                                                                                                                                                                                                 Created)
Last sequence up
Last annotation
                                                                                                                  EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 198; DB 4; Length 513; Pred. No. 0.0001;
 Score 198; DB 11;
Pred. No. 0.00054;
7; Mismatches 202;
                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                         PRT;
                                       7AD38FCD78EABA9C
                                                                                                                                    of the
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                                                                                                                  databases
                                                                                                                                    transcription
                   Length 2045;
  Indels
                                       CRC64;
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Gaps
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Q8TE50
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Best Local S
Matches 123
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"EMSY is amplified in breast cancer and displays a BRCA2 damage response.";

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ430203; CAD22881.1; -.
EMBL; AJ430203; CAD22881.1; -.
EMBL; AJ430203; CAD22881.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C110RF30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMSY protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8TE50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8TE50
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                           149
                      109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 AMLIKLACSGSQSP-----EMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       486 VLKVTGPQATTGTPLVTMRPASQ--AGKAPVTVT-SLPASVRM---VVPTQSAQGTVIGS
                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98
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                                                                                                                                                              ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 VAPVSAPPKVSSGPRL---PAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLV
                      -VTPVK--
                                                        DEKPRK--
                                                                                                                             TTSTPTSTP--
                                                                                                                                                           TKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPAN--LQLPPG-TVLIKSNSGPLM 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSAAQTTLTAAGGLTTPTITMQPV------SQPTQVTLITAPSGVEAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGVTTLGTVTGTVST--SLAGAGAHSTSASLATPITTLGTIATLSSQ----VINPTAIT
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                                                                                      LVSPQQTVTRAETTSNITSRPAVPANPQTV----KICTVPNSS----SQLIKKVA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -AGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVA--NTVTTVSLQPEKPVVSGTAVT
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123; Conserv
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                                                      RRRTNSSSSSPVVLKEVPKAVVPVSKTITVPVSGSPKMSNIMQSIANSLPP
   -KLAQIGTT----
                                                                                                                         ----VPSGSIATVKSPRPAS---PASNVVVLPSGSTVYVKSVSCSDE
                                                                                                                                                                                                                 8.8%;
                                                                                                                                                                                                                                                                                                                                           breast cancer and displays a BRCA2
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21,
21,
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Last annotation update)
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                                                                                                                                                                                              Score 197.5; DB 4;
Pred. No. 0.00034;
8; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
-VVTTVPKPSSVQSV-----
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                AVPTSVVTV
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                                                                                                                                                       Query Match
Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 1:
01-JUN-2000 (TrEMBLrel. 15
01-JUN-2001 (TrEMBLrel. 17
Y51B11A.1 protein.
Y51B11A.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                   EMBL; AC006797; AAF60743.1; -.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           None;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-6239;
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                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cotton M.;
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SGPLMLVSPQQTVTRA--ETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKK 114
                                                   TTTAPETTSTEPPSSSTTP-----VQTTTITAPETTSTEPPSSSTTPVQTTTTTAPETTST 454
                                                                                 TKVAPVSA---PKVSSGPRLFAPQIVAVKAPNTTTIQFPANLQLPPGTVL----IKSN 56
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                                                                                                                                                                                                                                                                   1079 AA;
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EMBL/GenBank/DDBJ
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Last sequence update)
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Pred. No. 0.00038;
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TAPETTSTEPPSSSNTPVQTTTTTAPETTSTEPPSS----STSPV
                                LQP-----EKPVVSGTAV---TLSLPAVTFGETSGAAICLPSVKPV
                                                                                                      GPVGAKAGVVTLHSVGP-TAATGGTTAGTGLLQT-----SKPLVTSVANTVTTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                         EPPSSSTIPVQTTTTTAPETTS--TEPPSSSTIPVQTTTITAPETTSTEPPSSSTIPVQ- 511
                                                                     -PSSSTSPVQTTTTTAPETTSTEPPSSSTTPVQTTTITAPETTSTEPPSSSTTPVQTTTT
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Search completed: February 16, 2003, 21:59:02 Job time: 40.7465 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compu

Compugen Ltd

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Title:
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Gapop 10.0 , Gapext 0.5
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AAW25028
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Novel human diagno
Transcription fact
TATA-binding prote
Human TATA-binding
                                TATA-binding prote Human homologue of TATA-binding prote Drosophila TATA-bi
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TATA-binding prote
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Human polypeptide			2058	6.6	182	Ü,
Urosophila melanog	AAB94078	222	557	o o	183	ن ۵
S cerevisiae			881		8	אנ
Human polypeptide,	AAM93811		881	6.8	188.5	ب
Human protein			709	٠	æ	0
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Human protein			709		Ф	80
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la		22	1714		191.5	4
		15	862		193	w
	AAB41231	21	2971	7.0	194	N
Drosophila melanog		22	1658	7.0	194	ب
Human protein		22	1331		194	0
		22	1328	7.0	194	9
٠,		22	1127	7.0	194	89
FLO1 protein,		17	849	7.0	194	
Human transcriptio	AAY57452	21	2907	7.1	194.5	
trans		21	2781	7.1	194.5	
Human SRCAP.		22	3118		197	
SRCAP.		22	2972	٠	197	
_		23	2135	7.5	205.5	
Novel protein		22	1920		•	_
Human ORFX ORF2414		21	1322		206.5	0
		23	1296	7.7	211.5	9
_		23	1296	7.7	211.5	8
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Drosophila melanog		22	1795	7.8	214.5	u
pred	AAMS	22	5179		219	*
Ħ		15	2035	8.0	. 221	ω
	ABB6605	22	921	9.3	256	N
Drosophila melanog	ABB61528	22	921	9.3	256	Ц
	ABB6150	၁ ၁	921		٥	٥

ALIGNMENTS

RESULT 1 AAW31494 TATA-binding protein associated binding factor 105; human; activator; hTAFII105; transcription factor; TFIID; transcriptional activation; antibodies; diagnosis; therapy; biopharmaceutical industry. Dikstein R, 02-OCT-1996; Homo sapiens. 28-APR-1998 (first entry) AAW31494; AAW31494 standard; Protein; 801 AA. (REGC) UNIV CALIFORNIA. 02-OCT-1996; 20-JAN-1998 US5710025-A. Human hTAFII105 protein. Tjian R; 96US-0725012 96US-0725012.

DNA encoding human tata-binding protein associated factor - producing recombinant protein

for

WPI; 1998-109818/10. N-PSDB; AAV02872.

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RESULT 2
ABG09468
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Best Local
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  Human;
                         Novel human diagnostic protein #9459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA sequence represents a human tata-binding protein associated or, hTAFIII05, isolated from Daudi cell nuclear extracts. Tightly
                                                                                                                                                                              IKENVTSCFRDE 552
                                                                                                                                                                                                                                                                                VVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEK
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  chromosome
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mapping; gene mapping; gene therapy;
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Pred. No. 2.7
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                         CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC specification, but was obtained in electronic format directly from WIPO CC at fits wipo, int/pub/vibulished port sequences.
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Best Local S
Matches 552
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23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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DB; AAS73655.
                                                   VQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRK
                                                                       VQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRK
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This represents a polypeptide comprising a (modified) fragment (I) a TATA box-binding protein associated factor II 105 (TAFIIIO5). A pharmaceutical composition comprising (I) or the polynucleotide or inhibitor or antagonist of (I) is useful for treating cancers and
                                                       Polypeptide encoding TATA box binding protein associated factor useful for treating e.g. cancers and inducing apoptosis has a do negative effect on the normal biological activity of the binding protein -
                                                                                           N-PSDB;
                                                                                                                                                                                                                                               Key
Misc-difference
                                                                                                                                                                                                                                                                       Homo
                                        Claim
                                                                                                   WPI;
                                                                                                                                                              25-AUG-1999;
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                                                      protein
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                                                                                                                                                                                                                                                                                                                   Transcription
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Best Local Sim
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28-JAN-1993;
               28-JAN-1994;
                              04-AUG-1994
                                            WO9417087-A.
                                                                          diagnostic;
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bacterial infections.
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IKENVTSCFRDE
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Pred. No. 3e-191;
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156494
AAR56494 standard; Protein; 737 AA.

AAR56494;
23-MAR-1995 (first entry)
TATA-binding protein-associated factor hTAFII130.
TATA-binding protein associated factor; hTAFII130; screening; diagnostic; therapeutic; gene transcription regulation.
Homo sapiens.
WO9417087-A.
04-AUG-1994.
28-JAN-1994; 94WO-US01114.
28-JAN-1993; 93US-0013412.
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30-JUN-1993;

9308-0087119

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RESULT 5
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Best Local S
Matches 173
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Tjian R,
  AAW06084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The TATA-binding protein associated factor hTAFII130 (including specific antibodies and fusion products) are used in drug screening, diagnostics and therapeutics, are used in the development of specific blochemical assays for screening compounds that agonise or antagonise selected transcription factors involved in regulating gene expression associated with human pathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATA-binding protein associated protein factors corresponding nucleotide sequence and deriv. ant in screening, diagnostics and therapeutics
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                                                                                                                                                                                                                                                                                     SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGV
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                                                                              PGNKIL---SLQASPTQKNRIKENVTSCFRDE
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                                                                 PGTKALSAVSAQAAAAQKNKLKEPGGGSFRDD
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                                                                                                                                                                  ----PMVALRQPH-NRIMLTTPQQIQL---
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                                                                                                                                                                                                                    -TQPTQVGVGKQGQPTPLVIQ------
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.. Weinzierl ROJ;
Protein;
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Pred. No. 4.5e-31;
7; Mismatches 144;
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                                                                                                                                                                                                                                                                                            by RNA polymerase II, the RNA polymerase which transcribes messenger RNA. RNA polymerase II transcription proceeds in vitro upon addition of several nuclear fractions designated TFIIA, B, D, E, F, H, I and J to RNA polymerase II holoenzyme. Fraction TFIID has been shown to contains a TBP and other TAFS. Purification of TFIID and separation of its components reveals 7 proteins ranging in size from 30-250 kD. Serum raised against the TFIID fraction allowed cloning of the corresponens from lambda-gtll expression libraries.
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28-JAN-1993;
30-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                       This is the amino acid sequence of the human TATA-binding protein (TBP) associated factor (TAF) designated TAFIII30. The protein is a component of the TFIID fraction required for reconstituting RNA polymerase II in vitro transcription activity. The encoded protein has an estimated mol wt. of 130 kD by SDS-PAGE.
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Tjian
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                                                                                                                                                                                                                                                                    Sequence
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NE-PNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL
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DB; AAT42217.
                                                                 AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS
                                                                                               MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
                                                                                                                         LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
                                                                                                                                                   PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL
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Wang E, W
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93US-0013412.
93US-0087119.
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67; Mismatches 144
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RESULT 6
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Tjian R,
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28-JAN-1993;
30-JUN-1993;
09-MAY-1996;
                                                                                                                                                                                                                                                                                  WPI;
               AAW25018 represents TATA-binding protein associated factor (TAF) polypeptide, hTAFII100 (mol. weight 100kD). TAF peptides derived from hTAFII30 alpha, hTAFII30 beta, hTAFII40, hTAFII70, hTAFII100, hTAFII130, hTAFII250, hTAFI48 and hTAFII10 and nucleic acids encoding
                                                                                                                                                                  Nucleic acids encoding human TATA-binding (TAF) peptide(s) - for production of recommodulating transcription of TAFs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATA-binding
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DB; AAT79595.
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                                                                                                                              Column 111-116;
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Wang E,
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93US-0087119.
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Matches
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                                                                              Antifungal; MPT1; MTR2; GCD7; SKI6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 initiation. TAFS are nuclear proteins involved in RNA polymerase I, II and III transcription. The peptides act by binding to a different TAF, an activator, or TBP (TATA-binding protein) or competitively inhibiting association of a TAF domain with another compound, typical a protein like TBP or another TAF, an activator, or DNA.
                                                                                                                                                                            AAU82954;
                                                                                                                                                                                                    AAU82954
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                                            Homo sapiens.
                                                                    yeast;
                                                                                                                            Human homologue of MPT1 protein target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HI-PQOALAQMQAQAHAQDQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
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                                                                                                                                                                                                                                                                                PGNKIL--
                                                                                                                                                                                                                                                                                                                                                         TLTQT------PMVALRQPH-NRIMLTTPQQIQL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q-----ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL 118
                                                                                                                                                                                                                                                              PGTKALSAVSAQAAAAQKNKLKEPGGGSFRDD
                                                                                                                                                                                                                                                                                                                                   LFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASILKQITL
                                                                                                                                                                                                                                                                                                                                                                                 TFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPAGIPTGSSSKQ
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                                                                   fungus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -TTIIKQV---
                                                                                                                                                                                                    standard;
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                                                                               NIP1;
                                                                                        fungal
BOS1; P
                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                           -SLQASPTQKNRIKENVTSCFRDE
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                                                                                                                                                                                                                                                                                                                                                                                                         -TQPTQVGVGKQGQPTPLVIQ-----
                                                                              l gene transcription; RPC34; POL30; RSA2; SQT1; MTW1; TFF LCP5; NCE103; ECO1; ORC2; CI
                                                                                                                                                                                                    Protein;
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Pred. No. 4.5e-31;
7; Mismatches 144;
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                                                                                                                                                                                                                                                              483
                                                                                                                            for antifungal compound
                                                                              C34; POP3; TFA2; TFB1; SPC98; CNS1; YPD1;
                                                                                                                                                                                                                                                                                                                                                                                                        -QPPKP-----GALIRPPQV
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                                                                                                                                                                                                                                                                                                             NPLQPVPVVKPAVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     compound for interaction with essential proteins (EP) or for modulation of EP activity e.g fungal gene transcription. The proteins tested in the cinvention include RPC34, POP3, TRA2, NAB2, MP71, MTR2, BOS1, POL30, RSA2, SCT1, MTW1, TFB1, SPC99, BER2, RNA1, GCD7, SKI6, NIP1, LCP5, NCE103, CECO1, ORC2, CNS1, YPD1, TIM10 and SRB4 from S. cerevisiae, C. albicans and human homologues. The method involves contacting a culture with one or wast compounds and determining the effects on the growth or compounds and the centified compounds interact with one or yeast cells. Preferably the identified compounds interact with, or modulate (preferably inhibit) activity of C. albicans EP. The inhibitor compounds identified by the method are useful for preventing or inhibiting fungal, particularly C. albicans growth in culture or in a mammal. The antifungal agents interact with essential fungal elements that can be used to treat fungal infection by preventing the growth and preferentially killing the fungal infection by preventing the growth and contivity of mammalian homologues. This amino acid sequence represents a target protein used to test the antifungal compounds, described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
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Mendillo
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                     NE-PNIKAENSAAVQINISPTMIENVKKCKNFIAMLIKLACSGSQSPEMGQNVKKIVEQI
                                                                                                                                                                                                                                                                                    Q----ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL--
                                                                                                                                                RTVPGATTTSSAATE-----TMENVKKCKNFLSTLIKLASSGKQSTETAANVKELVQNL
                                                                                                                                                                                                                                       AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS 168
                                                                                                                                                                                                                                                                    MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
                                                                                                                                                                                                                                                                                                                            PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL 464
VTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAV
                                                          SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g candidate antifungal compound for interaction with essential modulation of essential protein activity, binding to essential by contacting protein with test compound and determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Z,
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                                                                                                                                                                                                                                                                                                                                                                                                      Score 521; DB 23; Pred. No. 5.5e-29;
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Sanderson K,
                                                                                                                                                                                                                                                                                                                                                                                        157;
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Haq T, Zhu S,
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1023;
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Best Local S
Matches 135
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Tjian R,
                                                                                                                                                                                           specific antibodies and fusion products) are used in drug screens diagnostics and therapeutics. They are used in the development especific biochemical assays for screening compounds that agonise antagonise selected transcription factors involved in regulating gene expression associated with human pathology.
                                                                                                                                                                                                                                                                                              TATA-binding protein associated protein factors corresponding nucleotide sequence and deriv. an in screening, diagnostics and therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JAN-1993;
30-JUN-1993;
                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                     The TATA-binding
                                                                                                                                                                                                                                                                         Disclosure; Page 56-61; 180pp; English.
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DB; AAQ70724.
         KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSP
                                                                                                 PQIVAVKAPUTTIQFPANLQLPPGTVLIKSNSGPLML-----VSPQQTVTRAETTS
                              NTTSTTNHPTTTQ-IRLQTVPAAASMTNTTATSNIIVNSVASSGYANSSQPPHLTQLNAQ 243
                                                      NITSRPAVPANPQTVKICTVPNSSSQ------LIKKVAVTPVKKLAQIGTTVVTTVP
                                                                             PQSPSITLSTLNTGQTPA------LLVKTDNGFQLLRVGTTTGPPTVTQTITNTSNNS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CKDETFLLQAPLORRILEIGKKHGITELHPDVVSYVSHATQQRLQNLVEK
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Wang E,
                                                                                                                                                                        921
                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein-associated factor dTAFII110
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86;
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Pred. No. 7.6e
86; Mismatches
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28-JAN-1993;
30-JUN-1993;
                                                                                                                                                                                                                                                                                         Comai L,
Tjian R,
                                                                                                                     Screen for cpds. that bind human TATA-binding protein associated factor - by testing ability to bind to polypeptide fragments of tl factor, useful as (ant)agonists of transcription factors involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JUL-1996
       This
                                                    Examples; Column 27-36;
                                                                                                                                                                                                                                             WPI; 1996-333245/33.
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RESULT 10 AAW25028 ID AAW25

standard;

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AAW25028 st. AAW25028; 08-OCT-1997

TATA-binding TATA-binding

associated

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(first entry)
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associated factor; TAF; nuclear protein;

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VHLPPEALRAREQMQNSLNHNSNHFDAKLVEIKAPSLHPPHMERINASLT
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                                                                                                                                                                                                                          QIP-SLQVPGQANIVQIR--GPQHAQLQRTGSVQIRATTRP-----PNSVPTAN-----
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                                SQFPPASI----LKQITLPGN-----KILSLQA---SPTQKNRIKENVT
                                                                           AAISGGPPPTPTLSVLS---
                                                                                                                                                                                     VVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVL 449
                                                                                                                                                                                                                                                                                                  PSQTTTIGQTQVRMI---TPNALGTPRPTIGHTTISKQPPN---IRLPTAPRLVNTGGIRT
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28-JAN-1993;
30-JUN-1993;
09-MAY-1996;
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Tjian
                                                                                                                                                                                                                                                                                                                                                                                                                          AAW25028 represents TATA-binding protein associated factor (TAF) polypeptide, dTAFIII10 (mol. weight 110kD). TAF peptides derived from dTAFII30 alpha, dTAFII30 beta, dTAFII40, dTAFII60, dTAFII60, dTAFII60, dTAFII10, dTAFII10, dTAFII10, and dTAFII250, their human equivalents and nucleic acids encoding them, are used to modulate transcription, including transcription initiation. TAFS are nuclear proteins involved in RNA polymerase I, II and III transcription. The peptides act by binding to a different TAF, an activator, or TBP (TATA-binding protein) or competitively inhibiting association of a TAF domain with another compound, typically a protein like TBP or another TAF, an activator,
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                    PQSPSITLSTLNTGQTPA------LLVKTDNGFQLLRVGTTTGPPTVTQTITNTSNNS
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                         PSQTTTIGQTQVRMI--TPNALGTPRPTIGHTISKQPPN---IRLPTAPRLVNTGGIRT
                                                                          ASPQPCLIGFLKKSLPLLRQALYTKELVIEGIKPPPQHVLGLAGLSQQLPKIQAQIRPIG
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Pred. No. 7.6e
86; Mismatches
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                                                   Query Match
Best Local
                                        Matches
                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from brosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLJ01840-ABLJ6175) and the encoded proteins sequences (ABLJ01840-ABLJ6175) and the encoded proteins
                                                                                                                The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                      New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-656860/75.
N-PSDB; ABL05631.
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11-JUL-2000; 2000US-0614150
                                                                                          Sequence
                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 11376; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                Venter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster.
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              25
PQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLML-----
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                                       96;
                                    Score 256; DB
Pred. No. 7.6e.
86; Mismatches
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7.6e-10;
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genes from Drosophila and
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RESULT 13 AAR57141

AAR57141 standard;

Protein;

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19-MAR-1995 (first entry)

Host cell factor protein

Herpes simplex virus; herpes virus; VP16; immediate early gene;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
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VHLPPEALRAREQMQNSLNHNSNHFDAKLVEIKAPSLHPPHMERINASLT
                                  SQFPPASI ---- LKQITLPGN-----KILSLQA---SPTQKNRIKENVT
                                                                      AAISGGPPPTPTLSVLS---
                                                                                                       SQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPT 509
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Pred. No. 7.6e-10;
6; Mismatches 193;
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Best Local
C899P predicted amino acid sequence
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                         12-OCT-2001
                                                 AAM24516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-234207/28.
N-PSDB; AAQ69229:
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                                                                                                                                   988 EQPTATVTIADSGQGDVQPGTVTLVCSNPP 1017
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                        (first entry)
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Pred. No. 7.9e-07;
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                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes colon tumour associated proteins (I) and the polynucleotides (II) that encode them. (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with happropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of TCAPs by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host cell culturing the cell to express the protein. (II) and its
                                                    3825
                                                                                                                  3765
                                                                                                                                                                                                                                                                                                     (e.g.
                                                                                                                                                                                                                                                                                                                                        complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) may also be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. Anti-(I) antibodies and antagonists may also be used to down regulate TCAP expression and activity. The anti-(I) antibodies may also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              King
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colon tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immunotherapy; diagnosis; colon cancer; colon tumour;
immunogenic; gene therapy; vaccine; colonic cancer.
                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                             as diagnostic agents for detecting the presence of TCAPs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 446-462; 472pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-DEC-2000; 2000WO-US35596.
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                    96
                                                                                   44
                                                                                                                                                    N
                                                                                                                                                                                                                                                                                                g. by enzyme linked immunosorbant assay (ELISA)). AAI28460 to AAI29512
AAM24494 to AAM24523 represent nucleotide and amino acid sequences
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                                               TQTPTTTPITTTT----VTPTPTPTGTQTPTTTPITTTTTTTPTPTPTPTGTQTPTTTPITT 3881
                                                                                                                TLVTKVAPVSAP-----PKVSSGPRLPAPQIVAVKAPNTTII------QFPAN 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-441847/47
----VPNSSSQLIKKVAVTPVKKLAQIGTTVVTTVPKPSSVQS-VAVP-TSVVTVTP----
                                                                                LQLPPGTVLIKSNSGPLMLVSPQQTVTRAETTSNITS-----
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E, Wang T,
                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                   5179
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2000US-0504629.
2000US-0519444.
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                  exemplification
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2000US-0609448
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Jiang Y;
                                                                                                                                                                                                7.98;
21.98;
                                                                                                                                                                                  63;
                                                                                                                                                                             Score 219; DB
Pred. No. 4.1e
63; Mismatches
                                                                                                                                                                                                                                                                                of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Benson
                                                                                                                                                                                 No. 4.1e-06;
smatches 227;
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                                                                                                                                                                                                              Length 5179;
                                                                                 -RPAVPANPQTVKICT
                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                              amino acid sequences
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RESULT 15
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ID ABB69
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                                                                                                                                                                            23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide
                                                                    New isolated nucleic
                                                                                           WPI; 2001-656860/75
N-PSDB; ABL13909.
                                                                                                                              Venter JC,
                                                                                                                                                                                                             23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                     27-SEP-2001
                                                                                                                                                                                                                                                            WO200171042-A2
                                                                                                                                                                                                                                                                                  Drosophila melanogaster
                                                                                                                                                                                                                                                                                                           pharmaceutical.
                                                                                                                                                                                                                                                                                                                      Drosophila;
                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                           ABB69806;
                                                                                                                                                                                                                                                                                                                                                                                                                  ABB69806 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4256 PTAPTTTSGGHTLSPPPSTT
                                              interactions
                                                                                                                                                     (PEKE ) PE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILKQITLPGNKILSLQASPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTPTGTQT-----PTTTPITT------TTTVTPT-----PTPTGTQ-TGPPTHTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPAGIPTGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----TAGTGLLQTSKPL-----VTSVANTVTTVSLQP------EKPVVSGTAVTLSL 400
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                                                       from Drosophila
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                                                                                                                                                     CORP NY.
                                                                                                                              Adams M,
                                                                                                                                                                                                                                                                                                                   developmental biology; cell signalling;
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                                                                                                                                                                            2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
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a and
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                                                                                                                             PWD,
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                                                       detection reagent for detecting for elucidating cell signalling
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                                                                                                                                                                                                                                                                                                                    insecticide;
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                                                        1000 or more and cell-cell
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The invention relates to an isolated nucleic acid detection reagent

Disclosure; SEQ ID

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36210; 21pp + Sequence Listing; English

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Best Local Similarity 20.2
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB07737-ABB72072).
                                                                                                                                                               1129 THTRTHTALTGSRNTLGGQEVPDYMDDAPSSAEAESGQATTAKAPTMSTLAAAHLLQKLF 1188
                                                                                                                                                                                                                                                                                                                                           1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 PVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQL------PPGTVLIKSNSG 58
STQKRSIPPKTLVTHNTTKEPEDSEYYDSETSEQYTDEDNEVL 1291
                                         ---QKTMPVNTII------PTSQFPPASILKQITLPGNKIL 529
                                                                                HIISTTPPSREHAPTQRPSSQPSSSQRSRGVTIAQMARHNLATSKPFIAHSLRLSIQQLA 1248
                                                                                                                          HVV-----ISHSSTLTIQKCG 497
                                                                                                                                                                                                               CWDHICKPVIGT-----
                                                                                                                                                                                                                                                    QNSTSSTDLTTVTRPPCPDPDSTSDKNTNTACTQELQQVNLLE-----LQSPQKQEQF 1128
                                                                                                                                                                                                                                                                                         VTSVANTVTTVSLQPEKP------VVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSF 424
                                                                                                                                                                                                                                                                                                                                     VSTQNPTT--TTSKTSTVTITTPNPSPSTQRPTTTTRQPTSITASTTTSIGTTRIPTTTNP 1075
                                                                                                                                                                                                                                                                                                                                                                          VQTLNPLAGPVGAKAGVVTLHSVG------PTAATGGTTA-GTGLLQTSKPL 371
                                                                                                                                                                                                                                                                                                                                                                                                                        TTS-----VTATTRITTTISESSTETTSTQKPKSTTPTSTTRTTPKVTTVI 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TQEATTSTQKVSTVTITTKKATESSPLTTLSTEEPNTTPKP-----LRTTTPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSTENPTTNSVKTSALTSSTQRA-----TSTTSEPTKTTQNITTTTPKPTTLKTS 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQ 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTSSTGKPTTTPK-PSTRTTPTTTKVTTTTQITTTPLRSSTETTSTQPPTTTTPQPTTT 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGA--TAPR--TVS 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1795 AA;
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Pred. No. 2e-06;
6; Mismatches 254;
                                                                                                                                                                                                          ----PVQIKLAQPGPVLSQPAGIPTGSSSKQLFSLF 468
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Search completed: February 16, Job time : 55.3161 secs

2003, 21:54:51

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Title:
Perfect score:
Sequence:
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Listing first 45 summaries
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TELECULARY (415) 343-4342
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 801 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-725-012-2
                                                                       Query Match
Best Local S
Matches 552
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NAME: OSMAN, RICHARD A
REGISTRATION UNMER: 36,627
REFERENCE/DOCKET NUMBER: B97-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Dikstein, Rivka
APPLICANT: Tjian, Robert
TITLE OF INVENTION: B-Cell Specific Transcription Factor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/725,012 FILING DATE: CLASSIFICATION:
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                   1 GTLYTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPL
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APPLICANT: Tjian, F
APPLICANT: Comai, I
APPLICANT: Dynlact,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16
Patent No.
          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,582
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:
ADDRESSES:
                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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Comai, Lucio
Dynlact, Brian D.
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                            A-57650-2/AJT/RAO
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er, Suite 3400
                                                                                                                                       Version
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US-08-646-715-16
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Best Local S
Matches 173
                                                                                                                                                                                                                   Sequence 16, Patent No. 5
                                                                                                                                                                                    GENERAL INFORMATION: APPLICANT: Tjian,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 737 amino acids
TYPE: amino acid
            APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPAGIPTGSSSKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NE-PNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----TTIIKQV----SQAQTTVQPSATLQRSPGVQPQLVLGGAAQTASLGTATAVQTGTPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPKVSSG------PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM 61
                                                                                                                                                                                                                                                                                                               PGTKALSAVSAQAAAAQKNKLKEPGGGSFRDD
                                                                                                                                                                                                                                                                                                                                            PGNKIL---SLQASPTQKNRIKENVTSCFRDE 552
                                                                                                                                                                                                                                                                                                                                                                                                    LESLEHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASILKQITL
                                                                                                                                                                                                                                                                                                                                                                                                                                        TLTQT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDGKIEAEDFTSRLYRELNSSPQPYLVPFLKRSLPALRQLTPDSAAFTQQSQQQPPPPTS
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173; Conserv
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5637686
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                                                                                                        Ruppert, Siegfried
Tanese, Naoko
                                                                                                                                                       Dynlact, Brian D.
                                                                                                                                         Hoey, Timothy
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                                                                                                                                                                      Comai, Lucio
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HOHBACH, TEST, ALBRITTON & HERBERT
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Pred. No. 1.4e-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                               483
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-646-715-16
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Best Local
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: OSMAI, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 737 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/188,582
FILING DATE: 28-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
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                                                                                                             404 TEGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPAGIPTGSSSKQ 463
                                                                                                                                                             377
                                                                                                                                                                                         344 VTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAV
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         438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/01 FILING DATE: 09-MAY-1996
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SYSTEM: PC-DOS/MS-DOS
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                                                                               -PMVALROPH-NRIMLTTPQQIQL--
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     -NPLQPVPVVKPAVL 451
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US-08-188-582-2
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                                                                                                                                                                                                                                                                                           9.3%;
pest Local Similarity 22.9%;
Matches 135; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION UNBER: U$/08/188,582
FILING DATE: 28-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                         188
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                                                                                                                                                 185 NTTSTTNHPTTTQ-IRLQTVPAAASMTNTTATSNIIVNSVASSGYANSSQPPHLTQLNAQ 243
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     288
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                                                                                                                                                                                       77 NITSRPAVPANPQTVKICTVPNSSSQ------LIKKVAVTPVKKLAQIGTTVVTTVP 127
                                                                                                                                                                                                                                                                   25 PQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLML-----VSPQQTVTRAETTS 76
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ZIP: 94111-4187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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                     TMLENVK-KCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELK 246
TQQGNTKEKCRKFLANLIEL--STREPKPVEKNVRTLIQELVNANVEPEEFCDRLERLLN 345
                                                                           APQLPQITQIQTIPAQQSQQQQVNNVSSAGGTATAVSSTTA
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                                                                                                             KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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Comai, Lucio
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                         Score 256; DB 1;
Pred. No. 5.5e-13;
                                                                                                                                                                                                                                                                                                       Mismatches 193;
                                                                                                                                                                                                                                                                                                                                        Length 921;
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                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Weinzierl, Robert O.J.

TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAPS AND METHODS OF USE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tent No.
                                                                                                                                                                      APPLICATION NUMBER: US 0
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-D
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                                                                            REGISTRATION NUMBER:
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Tanese, Naoko
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SYSTEM: PC-DOS/MS-DOS
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28-JAN-1994
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Best Local Similarity
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                              SQFPPASI----LKQITLPGN-----KILSLQA---SPTQKNRIKENVT
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                                                                                              SOPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPT
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                                                                  AAISGGPPPTPTLSVLS----
                                                                                                                                -----KLTAVKVGQTQIKAI-TPSLHP-----
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Pred. No. 5.5e-13;
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                                                                ----TLNSAST-----TTLPIPS-LPT
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RESULT
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Patent No. 5433362
GENERAL INFORMATION:
APPLICANT: Lamarco, Kelly
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                             APPLICANT: Wilson, Angus
APPLICANT: Herr Winship
TITLE OF INVENTION: A NOVEL EXARYOTIC TRANSCRIPTION PROTEIN:
TITLE OF INVENTION: HOST CELL FACTOR
                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH,
                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                               COUNTRY: USA
ZIP: 94111-4187
APPLICATION
                                                                                                                                                                          STATE:
                                                                                                                                                                                            CITY: San
                                                                                                                                                                                                              STREET:
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                                                                                                                                                                                                                                                                                                                                                                  Lamarco, Kelly
                                                                                                                                                                                          Francisco
NUMBER:
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FILING DATE: 12-APR-1993 CLASSIFICATION: 435

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                                                                      Sequence 5, Application US/08393703 Patent No. 5585239
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Best Local Similarity
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                                                        GENERAL INFORMATION:
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APPLICANT:
TITLE OF I
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LENGTH: 2035 amino aci
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REFERENCE/DOCKET NUMBER: ATTELECOMMUNICATION INFORMATION TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 11 MOLECULE TYPE:
                             APPLICANT:
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STRANDEDNESS: single
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                                                                                                                                                          EQPTATVTIADSGQGDVQPGTVTLVCSNPP 1017
                                                                                                                                                                                     ISHSSTLTIQKCGQKTMPVNTIIPTSQFPP
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 INVENTION:
             Lamarco, Kelly
Wilson, Angus
Herr, Winship
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Pred. No. 1.6e-09;
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US-08-393-703-5
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Best Local Similarity
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TELEX: 910 277299
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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LENGTH: 2035 amino acids
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REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
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MOLECULE TYPE:
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NUMBER OF SEQUENCES:
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ZIP: 94111-4187
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DHICKPVIGTPVQIKL-AQPGPVLSQPA-GIPTGSSSKQLFSLFHVVQQPSGGNEKQVTT 484
                                             ASLATPITTLGTIATLSSQ----VINPTAITVSAAQTTLTAAGGLTTPTITMQPV-----
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                                                                                        KPLVTSVA--NTVTTVSLQPEKPVVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCW
                                                                                                                                     LRTVPMGGVRLVTPVTVSAVKPAVTTLVVKGTTGVTTLGTVTGTVST--SLAGAGGHSTS
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Pred. No. 1.6e-09;
4; Mismatches 211
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Best Local
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GENERAL INFORMATION:
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: FP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
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CORRESPONDENCE ADDRESS:
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APPLICANT: Wilson, Angus
APPLICANT: Wilson, Angus
APPLICANT: Herr, Winship
TITLE OF INVENTION: A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN:
TITLE OF INVENTION: HOST CELL FACTOR
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FILING DATE: 03-DEC-1993
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                                      KLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ 281
                                                                          QTKPVQTSAVTGQASTGPVTQIIQTKGPLPAGTILKLVTSADGKPTTIITTTQASGAGTK
                                                                                                                                                TRPIITVHKSGTV-TVAQQAQVVTTVVGGVTKTITLVKSPISVPGGSALISNLGKVMSVV
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chrivia, John
APPLICANT: Chrivia, John
APPLICANT: Chrivia, Peter
ITITLE OF INVENTION: SNF2 Related CBP Activator Protein (SRCAP)
ITITLE OF INVENTION: SNF2 Related CBP Activator Protein (SRCAP)
ITITLE OF INVENTION: US/09/579,181
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SOFTWARE: PatentIn V
SEQ ID NO 2
LENGTH: 2972
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CURRENT FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/136,620
PRIOR FILING DATE: 1999-05-27
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-APRTV----SVQTL--NPLAGPVGAKAGVVTLHSVGPTAA--TGGT-----TAGTGLL 365
                                                                                                                               TVAPACSPVLVPASALASPF
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                                                   AP--QTAILAPSPAPPLAP-LPVLAPSPGAAPVLASSQTPVPVMAPSSTPGTSLASASPV 1389
                                                                                       QSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGAT------
                                                                                                                                                              NVKKLVEQ-LLDAKIEAEEFTRKLYVELKSSPQPH-----LVPFLKKSVVALRQLLPNS
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                                                                                                                                                                                                                                      LGASSTPSNEPNLKAENSAAVQINL--SPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQ 218
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Pred. No. 2.9e-07;
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Best Local Similarity
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LENGTH: 3118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Chrivia, John APPLICANT: Yacluk, Peter TIITLE OF INVENTION: SNF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/579,181
CURRENT FILING DATE: 2000-05-25
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FCWDHICKPVIGTPV---
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                                                                                                                                                                                                                                       QSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGAT------
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-QIKLAQPGPVLS---QPAGIPT-GSSSKQLFSLFH
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US-08-325-267A-4
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                                                                                                                                                                          Matches 120;
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                                                                                                                                                                                                                                                                                                               NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 862 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                   199 SLPPNIEGTVYMYAGYYYPMKVVYSNAVSWGTLPISVTLPDGTTVSDDFEGYVYSFDDDL
                                  259 SQSNCTVPDPSNYAVSTTTTTEPWTGTFTSTSTEMTTVTGTNGVPTD-ETVIVIRTPTT 317
100 SSQLIKKVAVTPVKKLAQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLN-TVTTLK- 157
                                                                      61 -----
                                                                                                                                    11 SAPPKVSSGPRLPAPQIVAVKAPNTTTIQF---PANLQLPPGTVLIKSNSGPL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: OBLON, NORMAN F REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 24-FE
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                                                                                                                                                                                         ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Application US/08325267A 5585271
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OGAWA, MASAHIRO
PENTTILA, MERJA
ONNELA, MAIJA-LEENA
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24-FEB-1994
                                                                 -MLVSPQQTVTRAET-----TSNITSRPAVPANPQTVKICTVPNS
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Pred. No. 1e-07;
                                                                                                                                                                        Mismatches 216;
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US-08-362-525-22
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Patent No.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                        FILING DATE: 14-DEC-1992 PRIOR APPLICATION DATA:
                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: TITLE OF INVENTION:
                                FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                          APPLICATION NUMBER: EP 9 FILING DATE: 08-JUL-1992
                                                                                                                                                                 FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                     CITY: Washington
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          REGISTRATION NUMBER:
                                                           APPLICATION NUMBER:
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20005-3918
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                                                                                                                                                                                                                                                                                                                                    1100 New York
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TOSCHKA, HOLSER Y.
VERRIPS, CORNELIS T.
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30 New York Avenue, N.W.
                                                                                                                                                                             04-JAN-1995
                                               UMBER: PCT/EP93/01763
07-JUL-1993
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Best Local S
Matches 118
                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                       APPLICANT:
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                    SOFTWARE:
        APPLICATION
      PatentIn Release #1.0, CATION DATA:
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;; Sequence 15, Application
; Patent No. 6114147
                                                                  GENERAL INFORMATION:
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LENGTH: 894 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                   INGVTTEYTTWCPISTTESRQQTTLVTVTSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTSNITSRPAVP----ANPQTVKICTVPNSSSQLIKKVAV---TPVKKLAQIGTTVVTTV 126
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                        Immobilized
                                                                                                        US/08971692
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Version #1.25 (EPO)

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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08325267A Patent No. 5585271
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE: 894 amino acid
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                              APPLICANT: TAKATA, YOSHHIRO
APPLICANT: OGAWA, MASAHIRO
APPLICANT: DENTTILA, MERJA
APPLICANT: DENTTILA, MERJA
APPLICANT: KERANEN, SIRKA
APPLICANT: KERANEN, SIRKA
TITLE OF INVENTION: YEAST AGGLUTINATION GENES
TITLE OF INVENTION: CONTAINING THEM
                                                          CORRESPONDENCE ADDRESS:
                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EYTTWCPISTTETTKQTKGTTEQTTETTKQTTVVTISSC-ESDVCSKTASPAIVSTSTAT 696
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OBLON, SPIVAK, MCCLELLAND, 55 S. JEFFERSON DAVIS HWY,
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Pred. No. 2.3e-07;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1537 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 36
FILING DATE: 26-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Rel. CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                               1256 STATUTU-----SGUTTEYTTWCPISTTETTKQTKGTTEQTTETTKQTTVVTISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1040 LVTT-TTEPWTGTFTSTSTEMSTVTGTNGLPTD-ETVIVVKT-PTTAISSSLSSSSSGQI 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                  496 CGQKTMPVNTIIPTSQFPPASILKQITLPGNKILSLQASPTQKNRIKENVTSC 548
                                                                                                                                                                                                                                                                                                                                                                            320 TAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTV 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                938 TVIVIRTPTSEGLISTTTEPWTGTFTSTSTEVTTITGTNGQPTDETVIVIRTPTSE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: OBLON, NORMAN F
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                      TPVQIKLAQPGPVLSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQK 495
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                                                                                                                                                                                                                                                                                                                  SESETSS-----AGSVSSSSFISSESSKSPTYSS------SSLPLVTSATTSQ 1215
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                                                                                                                                                                                                                                                                                                                                                                                                                                       -----SSSVISSSVTSSLFTSSPVISSSVISSSTTTSTSIFSESSKSSVIPTSSSTSGS 1173
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Search completed: February 16, 2003, 22:02:41 Job time: 29.1842 secs

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US-08-700-651-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPTOSPORTIGIUM PARVUM FILLE REFERENCE: 480.19-4(HV)

CURRENT FILLION UNMBER: US/08/700,651B

CURRENT FILLION DATE: 1997-08-14

EARLIER APPLICATION NUMBER: 08/415,751

EARLIER FILLION DATE: 1995-04-03

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PATENTIN VEY: 2.0

SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.3%; Score 174.5; Best Local Similarity 20.9%; Pred. No. 1e-(Matches 118; Conservative 65; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08700651B Patent No. 6015882
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APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUT, JIRI
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                                 ILKQITLPGNKILSLQASPTQKNRI 541
                                                                                                                                                                                      PAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIG----TPVQIKLAQPGPVLSQPAGIP 456
                                                                                                                                                                                                                                                        HSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVV-----SGTAVTLSL 400
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                                                                                                                                                                                                                              TTQKPTTTT--TTKVPG-----KP---PIATTTTL-----KPIVTTTTKATTTTTTV
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                                                                       -----KMLDKYTRMIYDYNSG----LLLDSNDEPIPGSQAGQ-----IADTSNLFPVQ 738
                                                                                                                                                    PTTT--TTTKRDEMTTTTPL------PDIGDIEITPIPIE-------
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Result
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10 US-09-801-368-104
10 US-09-804-761-34248
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10 US-09-801-368-106
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 US-10-161-510-10

US-09-905-129-2

0 US-09-905-129-10

0 US-09-905-129-13

0 US-09-991-630-2

0 US-09-991-630-13

0 US-09-991-630-13

2 US-10-124-557-14
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US-09-801-368-108
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                                                                                                                                          Sequence 1068, Ap
Sequence 1068, Ap
Sequence 1068, Ap
Sequence 1168, Ap
Sequence 114, App
Sequence 104, App
Sequence 34248, A
                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                      Sequence 14,
              Sequence
Sequence
Sequence
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110, Appl
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US-09-893-519A-14
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APPLICANT:
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  RELEVANT RESIDUES:
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MOORE, Jeffrey
BUURMAN, Ed T.
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DESILVA, Thamara
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153.5	155	155	156	156	156	156	156	156	156	157	157.5	157.5	157.5	157.5	157.5	157.5	157.5	157.5	157.5	157.5	157.5	157.5	157.5	157.5	157.5
		5.6		5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7
2828	2063	2005	2589	2587	2587	2586	2586	2586	2586	688	1404	1404	1363	1361	1354	1320	1320	1314	1313	1311	1270	1140	1049	1038	1022
10	10	10	10	10	10	10	10	10	10	10	12	12	12	12	12	12	12	12	12	12	12	12	12	12	12
N	US-09-735-367B-2	US-09-735-367B-3	US-09-991-630-24	US-09-991-630-16	US-09-905-129-16	US-09-991-630-14	US-09-991-630-11	0	US-09-905-129-11	-09-86	US-10-124-557-62	-10 - 12	٠	4		US-10-124-557-60		-10-124-557-5	•	US-10-124-557-42	4	0-124-557-1		-10-124-5	US-10-124-557-84
21	ν,	ω	24	16	16	Sequence 14, Appl	11	14	11	360	62	2	52	40	48	60	46	. 50	14		44	10,	58	74	Sequence 84, Appl

ALIGNMENTS

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; SOFTWARE: PatentIn version in No 14; SEQ ID NO 14; LENGTH: 1023; TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                     APPLICANT: DAVIDOV, Eugene
TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND
FILE REFERENCE: 0342/1G548-US2
CURRENT APPLICATION NUMBER: US/09/893,519A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,164
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: US 60/224,457
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 146
                OTHER INFORMATION: Corresponds to SEQ ID NO: 87
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Human Genbank/CAA72189
DATABASE ENTRY DATE: 1997-06-25
                                                                                                        NAME/KEY: misc_feature
                                                                                                                                                                                                                                                     PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAQ, Taring
ZHU, Shuhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SANDERSON, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MCCOY, Melissa
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KOMARNITSKY, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fan
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(1)..(1023)
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                                     APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Se
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-03-07
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
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Best Local Similarity
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SEQ ID NO 108
LENGTH: 1367
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APPLICANT:
APPLICANT:
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                            SOFTWARE:
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                            PatentIn
                                                                                                                                                                                  Sherman, Amir
Silva, Jeff
                                                                                                                                                                                                                                         Maxon, Mary
Milne, Todd
No. US20020128250Alman,
                                                                                                                                                                                                             Royer, John
Salama, Sofie
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Holtzman, Doug
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                                                                                                                                                                                                                                                                                                                                             Robert
                            version 3.0
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31.7%; Pred. No. 6.5e-27;
tive 73; Mismatches 157
                                                                                                                                                        Secondary Metabolite Production in
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:; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-025-380-1068
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1068, Application US/10025380 Publication No. US20020182191A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                      APPLICANT:
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APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C14
                                                                                                                                                                                                           APPLICANT:
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                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1010 TVPCSTSPSETASESTTTSPTTPVTTVVSTTVVTTEYSTSTKPGGEITTTFVTKNIPTTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 SNSGPLMLVSPQQT---VTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAV--
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                                                                             Clapper, Jonathan D.
Skeiky, Yasir A. W.
Fanger, Gary R.
Vedvick Thomas S.
                                                                                                                                                                                                        Stolk, John A. Wang, Tongtong Jiang, Yuqiu Smith, Carole L.
                                                                                                                                                               Wang, Aijun
                                                                                                                                                                                 King, Gordon E
                                                                                                                                                                                                                                                                                           Meagher, Madeleine
                                                                                                                                                                                                                                                                                                              Secrist, Heather
Benson, Darin R.
                                                                                                                                                                                                                                                                                                                                                     Lodes, Michael J.
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Pred. No. 8.7e-07;
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SEQ ID
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APPLICANT:
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                 SOFTWARE:
                                                PRIOR APPLICATION NUMBER: US 60/160,587 PRIOR FILING DATE: 1999-10-20
                                                                                APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR ETLING DATE: 2000-01-19
                                                                                                                                                                                                                                                                                             APPLICANT:
                                   NUMBER OF SEQ ID NOS: 440
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 NO 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGTTEQTTETTKQTTVVTISSCESDICS-----KTASPAIVSTSTATINGVTTEYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -ALRQLLPNSQSFIQQCV------QQTSSDMVIATCTTTVTTSPVVTTTVSSSQ 309
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                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
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                 PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                               Cali, Brian
                                                                                                                                                                                                       Sherman, Amir
Silva, Jeff
                                                                                                                                                                                                                                         Royer, John
Salama, Sofie
                                                                                                                                                                                                                                                                                           Maxon, Mary
Milne, Todd
                                                                                                                                                                                                                                                                                                                                           Hecht, Peter
Holtzman, Doug
                                                                                                                                                                                                                                                                                                                               Madden, Kevin
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                                                                                                                                                                                                                                                                                                                                                                                                  Robert
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; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-388-106
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US-10-161-510-10
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                                                                                  US-10-161-510-10
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/10161510 Publication No. US20020192695A1 GENERAL INFORMATION:
Query Match
Best Local Similarity
Matches 120; Conserv
                                                                                                                                                                  SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/161,510
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR FILING DATE: 2001-06-05
PRIOR PPLICATION NUMBER: US 60/328,605
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/357,253
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: PIBS AS MODIFIERS OF THE
FILE REFERENCE: EX02-074C
                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                          PRIOR FILING DATE: 2002-02-15
                                                                                                  ORGANISM: Homo
                                                                                                                          TYPE: PRT
                                                                                                                                        LENGTH: 1056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 VSPQQTVTRAETTSNITSRPAV------PANPQTVKICTVPNSSSQLIKKVAVTPV 112
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Score 159.5; DB
Pred. No. 0.0064
6; Mismatches 2
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Pred. No. 0.0011;
5; Mismatches 191;
                                     DB 9;
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56;

210;

Indels 171;

Gaps

21;

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; NAME/KEY: misc_feature
; LOCATION: (1)..(2597)
; OTHER INFORMATION: 'x'
US-09-905-129-2
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Patent No. US20020137705A1
GENERAL INFORMATION:
APPLICANT: Einat, et al
                                                                                                          SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENCTH: 2597
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THERITITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: 540579-2007.2
FILE REFERENCE: 540579-2007.2
CURRENT APPLICATION NUMBER: US/09/905,129
CURRENT FILING DATE: 2001-07-13
                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/084,944
PRIOR FILING DATE: 1998-05-11
PRIOR APPLICATION NUMBER: 60/085,673
PRIOR FILING DATE: 1998-05-15
                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/207,821
PRIOR FILING DATE: 2000-05-30
                                                                                                                                                                               NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/802,318
                                                                                       ORGANISM: rattus species
                                                                        FEATURE:
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CURRENT APPLICATION NUMBER: US/09/905,129
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 09/802,318
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/207,821
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 60/084,944
PRIOR APPLICATION NUMBER: 60/084,944
PRIOR FILING DATE: 1998-05-11
PRIOR APPLICATION NUMBER: 60/085,673
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 25
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US-09-905-129-10
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                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Einat, e
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Best Local :
                                                                                                                                                                                                                                             TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: 540579-2007.2
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Pred. No. 0.024;
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; LOCATION: (1)..(2597)
; OTHER INFORMATION: 'x' can be any amino acid
US-09-905-129-10
Sequence 13, Application US/09905129
PACENT NO. US20020137705A1
GENERAL INFORMATION:
APPLICANT: Elnat, et al
TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THERE
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 540579-2007.2
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Best Local Similarity 20.5%;
Matches 143; Conservative 8
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PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/207,821
PRIOR FILING DATE: 2000-05-30
PRIOR APPLICATION NUMBER: 60/084,944
PRIOR FILING DATE: 1998-05-11
PRIOR APPLICATION NUMBER: 60/085,673
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
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SEQ ID NO 13
LENGTH: 2597
TYPE: PRT
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CURRENT FILING DATE: 2001-07-13
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les 143; Conserv
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                                         TKGVVTDSKVTSAFQM-----TSNRVVTIYESSRHNTDLQQPSAEASPNPEIITGTTD 1516
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                                                                                                               YTQTLGNTTALETTL-----LSKSQESTTVKRASDTPPPLLSSGAPPVPTPSPPPF 1463
 -PTSQFPPASI-LKQITLPGNKILSLQASPTQKNRIK 542
                                                                                                                                                       FGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPA-GIPTGS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIQTGKD-SVETTPLPSPLSTPSIPTSTKFSKRKTP-----LHQIFVNNQKKEGMLKNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLLFKDKQNVDIEIITTTKYSGGESNHVIPTEASMTSAPTSVSLGKSPVDNSGHLSMPG 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NVSQVPATEYPGMCHTCPSAEGLTVATAALSVPSSSHSALPKTNNVGVIAEESTTVVKKP 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSLFHIPRNNNTGNFPLSRHLGRERTIWSRGRVKNPHRTPVLRRHRHRTVRPAIKGPANK 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----VLIKSNSGPLML---VSPQQTVTRAETTSN-----ITSRPAV--PANP 88
                                                                             ----SKQLFSLFHVVQQPSGGNEKQVTTISHSS--TLTIQKCGQKTMPVNTII-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----LAQIGTTVVTTVPK-------PSSVQSVAVPTSVV----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No. 0.024;
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                             -VSAVAYHSTTSLLAITELFEK 1412
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SPSNLFPSTSVPALRVDKPQNSKWKPSPWPEHKYQLK 1553

Search completed: February 16, 2003, 22:02:06 Job time: 39.8745 secs . -

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                         Result
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Maximum DB seq length: 200000000
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Perfect score:
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o
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                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                is derived by analysis of the total score distribution.
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2758
2678
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100.0
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2758
1 GTLVTKVAPVSAPPKVSSGP.....ASPTQKNRIKENVTSCFRDE 552
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compus
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/cgn2_6/ptodata/2/paa/US101_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US087_COMB.pep:*
/cgn2_6/ptodata/2/paa/US088_COMB.pep:*
/cgn2_6/ptodata/2/paa/US089_COMB.pep:*
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ptodata/2/paa/US098_COMB.pep:*
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PCT-US01-08631-39827
1 US-09-763-909-2
PCT-US02-25829-25
PCT-US02-29964-410
7 US-60-243-468-1271
PCT-US94-01114-16
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                Sequence 2, Appli
Sequence 25, Appl
Sequence 410, App
Sequence 1271, Ap
                                                                                                                                                               Description
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ALIGNMENTS

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                                                                                                                                                  ; ORGANISM: Homo sapiens PCT-US01-08631-39827
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                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
SEQ ID NO 39827
LENGTH: 801
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
                                                                                        Query Match
Best Local Similarity
                                                                           Matches
                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-08-23
                 1 GTLYTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTYLIKSNSGPL 60
GTLVTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPL 60
                                                                         100.0%;
ilarity 100.0%;
Conservative (
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                                                                       Score 2758; DB 1;
Pred. No. 2.2e-215;
Mismatches 0;
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Sequence 16, Appl

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US-09-763-909-2
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                                                                                                                                       Query Match
Best Local S
Matches 552
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GENERAL INFORMATION:
APPLICANT: Dikstein, Rivka
APPLICANT: Yamit-Hezi, Ay
                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/763,909
CURRENT FILLING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 852
TYPE: PRT
                                                                                                                                                                                                                                                                                               APPLICANT: Yamit-Hezi, Ayala
TITLE OF INVENTION: A TRANSCRIPTION FACTOR TFIID SUBUNIT,
TITLE OF INVENTION: TAPTIIO5, POLYPEPTIDES, DNA ENCODING
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
                                                                                                                                                                                                                                                                                         FILE REFERENCE: 13005/002001
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                                                                                                                                                  Local Similarity
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BOROWSKY, Mark
        WARREN,
XU, Yumi
YAO, Mon
YUE, Hen
YUE, Hui
                                                      TRAN, Uyen
WALIA, Nari
                                                                                           SPRAGUE,
TANG, Y.
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LEE,
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EMERLING, Brooke M.
FORSYTHE, Ian J.
YUE, Huibin
ZEBARJADIAN,
                                                                       THANGAVELU, Kavitha THORNTON, Michael
                                                                                                  RAMKUMAR, Jayalaxmi . SPRAGUE, William W.
                                                                                                                    LEHR-MASON, Patricia
NGUYEN, Danniel B.
                                                                                                                                                                                                       ISON, Craig H.
KHAN, Farrah A.
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HONCHELL, Cynthia
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BECHA, Shanya D.
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                                    Yuming
                                                                                                                                                           Joana X.
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Soo Yeun
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                  Henry
                           Monique
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Yeganeh
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; OTHER INFORMATION: Incyte
PCT-US02-25829-25
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Best Local Similarity
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LENGTH: 865
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SOFTWARE: PERL Program
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                       542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOR INVENTION: NUCLEIC ACID ASSOCIATED PROTEINS REFERENCE: PF-1146 PCT
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APPLICATION NUMBER: US 60/328,185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/316,751 FILING DATE: 2001-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/314,756 FILING DATE: 2001-08-24 APPLICATION NUMBER: US 60/315,105 FILING DATE: 2001-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/313,111
FILING DATE: 2001-08-17
APPLICATION NUMBER: US 60/314,682
FILING DATE: 2001-08-24
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              KNRIKENVTSCFRDE 552
                                                                    NEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASILKQITLPGNKILSLQASPTQ 537
                                                                                                                             VKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPAGIPTGSSSKQLFSLFHVVQQPSGG
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KNRIKENVTSCFRDE 616
                                                                                                             VKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPAGIPQAVQVKQL-----VVQQPSGG
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                                                       NEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASILKQITLPGNKILSLQASPTQ
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97.7%;
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Pred. No. 8.3e-209;
0; Mismatches 5;
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PCT-US02-29964-410
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                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 410
LENGTH: 843
TYPE: PRT
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Matches
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PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US00/3501
PRIOR FILING DATE: 2000-12-22
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PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
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PRIOR BEDITON NO. ....
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CURRENT FILING DATE: 2002-09-19
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                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-02-28
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les 540; Conserv
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               VQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRK
                                                        MLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGT
                                                                                                                                                                             VQINLSPIMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRK
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                                                                                                                                                                                                                                                                                                                                                                             pt_FL_genes Version 6.0
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Zhao, Qing A.
Wang, Jian-Rui
Xue, Aidong J.
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Goodrich, Ryle
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Haley-Vicente, Dana
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Ghosh, Malabika
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97.8%;
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Pred. No. 9.2e-208;
0; Mismatches 12;
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; ORGANISM: HUMAN
US-60-243-468-1271
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN DRUG TAK
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000929
CURRENT APPLICATION NUMBER: US/60/243,468
CURRENT FILING DATE: 2000-10-27
NUMBER OF SEQ ID NOS: 2121
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GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                       MLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGT 120
                                                                                                                                                                                                                                                                          GTLVTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAVTEGETSGAAICLPSVKP 420
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                       VTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTA 360
                                                          LYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPV 300
                                                                                                          VQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEETRK
                                                                                                                                   VQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRK 240
                                                                                                                                                                                                              MLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVP-----
                                                                                                                                                                                                                                                           GTLVTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPL 126
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                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                        81.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                         Windows Version
                                                                                                                                                                                                                                                                                                            Score 2235; DB 27;
Pred. No. 8.5e-173;
6; Mismatches 25;
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PCT-US94-01114-16
; Sequence 16, Applicat
; GENERAL INFORMATION:
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
FENGTH: 737 amino acids
                                                                                                                                                                    Matches 173;
                                                                                                                                                                                   Query Match
Best Local 9
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APPLICANY: Weinziell, Robert O.J.
TITLE OF INVENTION: TATA-BINDING P
TITLE OF INVENTION: NUCLEIC ACIDS
NUMBER OF SEQUENCES: 36
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NAME: Osman, Richard A
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Reli
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: FP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                   MOLECULE TYPE:
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     <u>1</u>16
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ZIP: 94
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CITY: San Francis
STATE: California
                                                                                                   83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 20 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                   13 PPKVSSG---
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                                                               LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPGK-KHDITELNSDAVNLISQATQE 562
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AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS
                                MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
                                                                                                 PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL 118
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                                                                                                                                                                                   Similarity
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Weinzieri, Robert O.J.
VENTION: TATA-BINDING PROTEIN ASSOCIATED
VENTION: TATA-BINDING PROTEIN ASSOCIATED
                                                                                                                                                                    Conservative
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Tanese, Naoko
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                                                                                                                                                                Score 547; DB 1; I
Pred. No. 6.4e-35;
7; Mismatches 144;
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                                                                                                                                                                  Indels
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PCT-US02-30474-1660
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PRIOR FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR APPLICATION NUMBER: PCT/US00/35017
                                                                                                                                                                                                                                                         APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 810CIP PCT
CURRENT APPLICATION NUMBER: PCT/USO2/30474
CURRENT FILING DATE: 2002-09-24
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                         OR APPLICATION NUMBER: PCT/US00/35017
OR FILING DATE: 2000-12-22
OR APPLICATION NUMBER: US 09/491,404
OR FILING DATE: 2000-01-25
OR APPLICATION NUMBER: PCT/US01/02623
OR FILING DATE: 2001-01-25
OR APPLICATION NUMBER: US 09/496,914
OR APPLICATION NUMBER: US 09/496,914
OR FILING DATE: 2000-02-03
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Wang, Dunrui
                                                                                                                                                                                                                                                                                                                                                    Haley-Vicente,
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Asundi, Vinod
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Xue, Aidong J.
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, Jian-Rui
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NUMBER: US 09/560,875 : 2000-04-27
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US-60-324-631-1665

Sequence 1665, Appli GENERAL INFORMATION:

Application

US/60324631

APPLICANT:
APPLICANT:
APPLICANT:

Tang, Y. Tom Zhang, Jie

Ren, Feiyan

APPLICANT: APPLICANT: APPLICANT:

Xue, Aidong J. Zhao, Qing A. Wang, Jian-Rui Wehrman, Tom

APPLICANT: APPLICANT: APPLICANT:

Zhou, Ping Ghosh, Malabika Wang, Dunrui Ma, Yunqing

APPLICANT:

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Best Local Sim
Matches 173;
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PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
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                                                                                                                      TLTQT---
                                                                                                                                                  TFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPAGIPTGSSSKQ 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
PGTKALSAVSAQAAAAQKNKLKEPGGGSFRDD
                                                                                                                                                                                                               VTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAV
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Pred. No. 1.1e-34;
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797
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US-60-324-631-1665
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Best Local Sin
Matches 173;
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SEQ ID NO 1665
LENGTH: 1051
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TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 810
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CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 09/488,725
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                                                                                                                                                                                                                                                                          PRIOR FILING DATE:
  433
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                         62 LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
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APPLICATION NUMBER: PCT/US00/35017
ETILING DATE: 2000-12-22
APPLICATION NUMBER: US 09/491,404
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                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/14827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 09/540,217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 09/574,454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 09/519,705 FILING DATE: 2000-03-07
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  MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
                                                      PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL
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                                                                                                                                                                                                                                                                                                                                             ICATION NUMBER: PCT/US01/08656
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Haley-Vicente,
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Pred. No. 1.1e-
67; Mismatches
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                                                                                                                                         Length 1051;
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APPLICATION N
FILING DATE:
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PGTKALSAVSAQAAAAQKNKLKEPGGGSFRDD 797
                                                                                                                                                                                                              TLTQT------PMVALRQPH-NRIMLTTPQQIQL
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                                                   PGNKIL---SLQASPTQKNRIKENVTSCFRDE 552
                                                                                                                                                         LESLEHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQEPPASILKQITL
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Sequence 3271, Appli GENERAL INFORMATION: APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic Acids an
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 810CIP PCT
CURRENT APPLICATION NUMBER: PCT/US02/30474
CURRENT FILING DATE: 2002-09-24 PRIOR APPLICATION NUMBER: US 60/324,631 PRIOR FILING DATE: 2001-99-24 PRIOR APPLICATION NUMBER: US 09/488,725 PRIOR FILING DATE: 2000-01-21 APPLICANT: Tang, Y. Tom APPLICATION NUMBER: US 09/552,317 FILING DATE: 2000-04-25 APPLICATION NUMBER: PCT/US00/35017 FILING DATE: 2000-12-22 APPLICATION NUMBER: US (FILING DATE: 2000-01-25 APPLICATION NUMBER: PCT/US01/02623 Xue, Aldong J. Zhao, Qing A: Wang, Jian-Rui Zhou, Ping Ghosh, Malabika Wang, Zniwe Weng, Gezhi Haley-Vicente, Asundi, Ghosh, Malab Wang, Dunrui Wehrman, Zhang, Application Yunging Indi, Vinod NUMBER: US : 2000-02-03 Felyan Zhiwei 2001-01-25 Tom PC/TUS0230474 09/496,914 09/491,404 Acids and

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Best Local Sim
Matches 168;
                                                          Sequence 14, Application PC/TUS0120592 GENERAL INFORMATION:
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APPLICANT: ANADYS PHARMACEUTICALS, INC.
APPLICANT: THOMPSON, Craig
APPLICANT: MOORE, Jeffrey
APPLICANT: BUURMAN, Ed T.
APPLICANT: BRADLEY, John
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PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: PCT/US01/03800
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-02-8
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                 VKPAVLPGTKALSAVSAQAAAAQKNKLKEPGGGSFRDD
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                                                                                                                                                                                                         GSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASI 517
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Pred. No. 1.1e-33;
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Best Local Similarity
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ORGANISM: Homo
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CURRENT APPLICATION NUMBER: PCT/US01/20592
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,164
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: US 60/224,457
PRIOR PPLICATION NUMBER: US 60/224,457
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 146
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TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND
FILE REFERENCE: 0342/16548-US1
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OTHER INFORMATION: human genbank accession #:
NAME/KEY: misc_feature
OTHER INFORMATION: Corresponds to SEQ ID NO:
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CKDETFLLQAPLQRRILEIGKKHGITELHPDVVSYVSHATQQRLQNLVEK
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                                                     SSKQLFSLFHVVQ-----QPSGGNEKQ---VTTISHSSTLTIQKCGQK 499
                                                                                                                                                                             TFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVL----SQPAGIPTGS
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KOMARNITSKY, Svetlana
MENDILLO, Marc
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SEQ ID NO 14
LENGTH: 1023
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TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND FILE REFERENCE: 0342/1G548-US1
CURRENT APPLICATION NUMBER: PCT/US01/20592A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,164
PRIOR FILING DATE: 2000-06-29
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                                                                                            VTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAV 403
                                                                                                                                 Q-----ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL--
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                                                                                                                                                                                                         LDGKIEAEDFTSRLYRELNSSPQPYLVPFLKRSLPALRQLTPDSAAFIQQSQQQPPPPPTS
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                                                                                                                                                                                                                                                                                                                                                                                          AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168;
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MOORE, Jeffrey
BUURMAN, Ed T.
BRADLEY, John
DESILVA, Thamara
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HARRIS, Sandra
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MCCOY, Melissa
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                                                      -TQPTQVGVGKQGQPTPLVIQ------QPPKP-----GALIRPPQV 756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHODS OF USE
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SOFTWARE: Patentin version 3.1
SEQ ID NO 14
LENGTH: 1023
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                                                                                                                                                                                                                                                                                                                                                                                                               Matches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 0342/1G548-US2
CURRENT APPLICATION NUMBER: US/09/893,5
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,164
PRIOR FILING DATE: 2000-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
OTHER INFORMATION: Corresponds to
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: DAVIDOV, Eugene
TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND METHODS OF USE
FILE REFERENCE: 0342/1G548-US-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/224,457 PRIOR FILING DATE: 2000-08-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATABASE ACCESSION NUMBER: Human Genbank/CAA72189
DATABASE ENTRY DATE: 1997-06-25
RELEVANT RESIDUES: (1)..(1023)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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    626
                                                                                                                                                                                                                                                                                    62 LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
                                                                                572 RTVPGATTTSSAATE-----TMENVKKCKNFLSTLIKLASSGKQSTETAANVKELVQNL
                                                                                                                                                                                                      116 AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS 168
                                                                                                                                                                                                                                            465 MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP---- 518
                                                                                                                                                                                                                                                                                                                            414 PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL 464
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                  NE-PNIKAENSAAVQINISPIMIENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL 227
LDGKIEAEDFTSRLYRELNSSPQPYLVPFLKRSLPALRQLTPDSAAFIQQSQQQPPPPTS
                                          LDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ----TS
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KOMARNITSKY, Svetlana
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BRADLEY, John
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390 VVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVL 449	B 5
330 LNPLAGPYGAKAGVYTLHSVGPTAATTGGTTAGTGLLQTSKPLYTSVANTYTTVSLQPEKP 389 : : : : : : : : : : :	Qу
277QCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQT 329 :	dg VQ
247 SSPQPHLVPFLKKSVVALRQL	Оy
188 TMLENVK-KCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEABEFTRKLYVELK 246	Qy Db
128 KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEDNLKAENSAAVQINLSP 187	QУ
77 NITSRPAVPANPOTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTVVTTVP 127	D _b
25 PQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLVSDQQTVTRAETTS 76	Оy
ry Match 9.4%; Score 258; DB 27; Length 899; It Local Similarity 22.9%; Pred. No. 3.5e-11; Indels 176; Gaps:	Query Best Match
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13 167-217-11401 ence 11401, Applicati RAL INFORMATION:	RESULT US-60- ; Sequ ; GENE
460 SSKQLFSLFHVVQOPSGGNEKQVTTISHSSTLTIQKCGQK 499 : :	Оy
404 TFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPAGIPTGS 459	Db Qy
344 VTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAV 403	ду
284 SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGV 343	Оy

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US-60-173-464-9223
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APPLICANT: Li, Peter W.D.
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CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 30269
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES
TITLE OF INVENTION: THEREOF
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565 VHLPPEALRAREQMQNSLNHNSNHFDAKLVEIKAPSLHPPHMERINASLT
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                                                                                                                                                                                                                                                                                                         330 LNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKP 389
                                                                                                                                                                                                                                                                                                                                                        406 PSQTTTIGQTQVRMI--TPNALGTPRPTIGHTTISKQPPN---IRLPTAPRLVNTGGIRT 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 APQLPQITQIQTIPAQQSQQQQVNNVSSAGGTATAVSSTTA------ATT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 NTTSTTNHPTTTQ-IRLQTVPAAASMTNTTATSNIIVNSVASSGYANSSQPPHLTQLNAQ 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        510 SQFPPASI----LKQITLPGN-----KILSLQA---SPTQKNRIKENVT 546
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                                     SQFPPASI----LKQITLPGN-----KILSLQA---SPTQKNRIKENVT 546
                                                                                                                                                                                                                                                                  QIP-SLQVPGQANIVQIR--GPQHAQLQRTGSVQIRATTRP-----PNSVPTAN----- 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TMLENVK-KCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELK 246
                                                                                                                               SQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPT 509
                                                                                                                                                                                                                                                                                                                                                                                                                                            ASPQPCLIGFLKKSLPLLRQALYTKELVIEGIKPPPQHVLGLAGLSQQLPKIQAQIRPIG 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSPQPHLVPFLKKSVVALRQL------
                                                                                                                                                                            -------KLTAVKVGQTQIKAI-TPSLHP---
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                                                                                      -----TLNSAST-----TTLPIPS-LPT 564
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RESULT 15
US-60-173-464-20611
US-60-173-464-20611, Application US/60173464
; GENERAL INFORMATION:
; APPLICANT: L1, Peter W.D.
; APPLICANT: L1, ISOLATED G-PROTEIN
Search completed: February 16, 2003, 22:18:18 Job time: 204.796 secs
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CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 30769
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 20611
LENGTH: 921
TYPE: PRT
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                                                                                VHLPPEALRAREOMONSLNHNSNHFDAKLVEIKAPSLHPPHMERINASLT 614
                                                                                                                        SQFPPASI----LKQITLPGN-----KILSLQA---SPTQKNRIKENVT 546
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/cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spl
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 63927
LENGTH: 709
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                     MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
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                                                     VTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAV
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US-10-288-798-9
US-10-196-935A-2
US-10-293-017-48
US-10-052-648A-40
US-10-028-248A-76
US-10-107-782-75
US-10-107-782-75
US-10-107-782-74
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Pred. No. 3.1e-22;
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                   QPPKP----GALIRPPQV
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Gaps

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Sequence 63927, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative sp
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT ETLING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
LENGTH: 709
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US-09-724-676A-63927
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Best Local Similarity
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               PGNKIL---SLQASPTQKNRIKENVTSCFR
                                                                                                            TFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPAGIPTGSSSKQ
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PGTKALSAVSAQAAAAQKNKLKEPGGGSFR
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                                                                                       PMVALROPH-NRIMLTTPQQIQL--
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Pred. No. 3.1e-22;
6; Mismatches 144
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US-09-724-676-63930
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RESULT 4
US-09-724-676A-63930
; Sequence 63930, Application US/09724676A
; GENERAL INFORMATION:
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TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 1.29181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SOFTWARE: 717
APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION NUMBER: US/09/724,676A CURRENT FILING DATE: 2000-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             369 MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318 PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 PPKVSSG------PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM
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RESULT 5
US-09-724-676-63921
Sequence 63921, Application
GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-63930
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Best Local Similarity
    Best Local Similarity Matches 172; Conserv
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                                   Query Match
                                                                                                                                       APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION NUMBER: US/09/724,676 CURRENT FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 97222 SOFTWARE: PatentIn version 3.2
                                                                -09-724-676-63921
                                                                           2Q ID NO 63921
LENGTH: 805
TYPE: PRT
ORGANISM: Homo sapiens
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PatentIn version
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Conservative 6
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    66;
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Pred. No. 3.2e-22;
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US-09-724-676A-63921
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LENGTH: 805
                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 63921, Appl GENERAL INFORMATION:
                                                                                                                                                                      Matches 172;
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ORGANISM: Homo
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AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS----
                                             MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
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Pred. No. 3.5e-22;
6; Mismatches 144
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Length 805; Indels 188;

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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 63924
LENGTH: 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 63924, Application US/09724676 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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                       NE-PNIKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL
                                                                                                                                                                                                         LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL
                                                                                                                                                                                                                                  PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL
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                                                                            RTVPGATTTSSAATE-----TMENVKKCKNFLSTLIKLASSGKQSTETAANVKELVQNL
                                                                                                                              ----TTIIKQV----SQAQTTVQPSATLQRSPGVQPQLVLGGAAQTASLGTATAVQTGTPQ
                                                                                                                                                        AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS 168
                                                                                                                                                                                  MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
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Sequence 63924, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative sp
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
CURRENT FILING DATE: 97222
SOFTWARE: Patentin version 3.2
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      TLTQT--
                                                        TFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPAGIPTGSSSKQ 463
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Sequence 63928, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative spl
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 63928
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                                                                                                                                                                                                                                 SVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAVTFGE 407
                                                                        GNKIL---SLQASPTQKNRIKENVTSCFRDE 552
                                                                                                                                 FSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASILKQITLP
                                                                                                                                                                                   TSGAAICLPSVKPVVSFCWDHICKPVIGTPVQI---KLAQPGPVLSQPAGIPTGSSSKQL 464
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                                                       GTKALSAVSAQAAAAQKNKLKEPGGGSFRDD
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Pred. No. 1.9e-21;
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; APPLICANT: Compugen LTD; TITLE OF INVENTION: Variants of alternative sp; FILE REFERENCE: 129181.4 Compugen; CURRENT APPLICATION NUMBER: US/09/724,676; CURRENT FILING DATE: 2000-11-28; NUMBER OF SEQ ID NOS: 97222; SOFTWARE: PatentIn version 3.2; SEQ ID NO 63931; LENGTH: 957
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SEQ ID NO 63928
LENGTH: 925
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APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative of the computer of the compu
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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641 GTKALSAVSAQAAAAQKNKLKEPGGGSFRDD
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                                                                                                                   GNKIL---SLQASPTQKNRIKENVTSCFRDE 552
                                                                                                                                                                                                                                                                                                                                                                 FSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASILKQITLP 524
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Pred. No. 1.9e-21;
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Application US/09724676

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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative sp
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 63931
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US-09-724-676-63931
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                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAVTFGE 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS
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                                                        Score 527; DB 5;
Pred. No. 2e-21;
8; Mismatches 122
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Pred. No. 2e-21;
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US-09-724-676-63922
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Best Local S
Matches 175
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SOFTWARE: PatentIn version
SEQ ID NO 63922
LENGTH: 1021
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000.11-28
                  169
                                                   487
                                                                                                                433 MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
                                                                                                                                                                               382 PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL 432
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                                                                                                                                                                                                  62 LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
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 NE-PNIKAENSAAVQINISPTMIENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQI
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                                              ----TTIIKQV----SQAQTTVQPSATLQRSPGVQPQLVLGGAAQTASLGTATAVQTGTPQ
                                                                                AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS 168
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---PKPG-----ALTQLNPLQPVPVVKPAVLP
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	69 NE-PNIKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL 227 	5 1	D Qy
	6 AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPS 168	7 116 5 487	Д
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	13 PPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM 61	ω	p Q
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,	Sequence 63922, Application US/09724676A Sequence 63922, Application US/09724676A GENERAL INFORMATION: APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen CURRENT FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 97222 SOFTWARE: Patentin version 3.2 LENGTH: 1021 TYPE: PAT ORGANISM: Homo saplens US-09-724-676A-63922	Sequence GENERAL APPLICE TITLE O FILE R CURREN NUMBER SCOTWAN SEQ ID I LENGTI TYPE: ORGAN S-09-724	US
	25 GNKILSLQASPTQKNRIKENVTSCFRDE 552	7 5	p S
	65 FSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASIIKQITLP 524	7 4	Db Qy
	18 TSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPAGIPTGSSSKQL 464	692	ф
	SVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAVTFGE 407 	7 348 5 671	д 63
-	88 IATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLH 347 	60 KJ	υ
	28 LDAKIEAEEFTRKLYVELKSSPOPHLVPFLKKSVVALROLLPNSOSFIQQCVQQTSSDMV	un N	P Q
	40 RTVPGATTTSSAATETMENVKKCKNFLSTLIKLASSGKQSTETAANVKELVQNL 593	Ui	뫄

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GRYDATCLPSVKPVVSECWDHICKPVIGTPVOIKLAOPGPVLSOPAGIPTGSSSKOL 464 GGAAICLPSVKPVVSECWDHICKPVIGTPVOIKLAOPGPVLSOPAGIPTGSSSKOL 464 GGAAICLPSVKPVVSECWDHICKPVITISHSSTLTIOKCGQKTMPVNTIIPTSOFPASILKOITLP 524
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ALIGNMENTS

A;Gene: FlyBase:Taf110
A;Cross-references: FlyBase:FBgn0010280
C;Keywords: transcription initiation transcription initiation factor IID 110K chain - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999 C;Accession: A48184 R;Kokubo, T.; Gong, D.W.; Roeder, R.G.; Horikoshi, M.; Nakatani, Y. Proc. Natl. Acad. Sci. U.S.A. 90, 5896-5900, 1993 A;Title: The Drosophila 110-kDa transcription factor TFIID subunit directly interacts A;Reference number: A48184; MUID:93317591; PMID:8327460 A; Note: sequence extracted from NCBI backbone C; Genetics:A;Status: preliminary A;Molecule type: mRNA; A;Residues: 1-921 <KOK> A;Cross-references: GB:S63550; NID:g398432; PID:g398433 A;Experimental source: embryo nuclear extract 133 PQSPSITLSTLNTGQTPA------LLVKTDNGFQLLRVGTTTGPPTVTQTITNTSNNS Local Similarity es 135; Conserv LNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKP 389 TQQGNTKEKCRKFLANLIEL--STREPKPVEKNVRTLIQELVNANVEPEEFCDRLERLLN 345 APQLPQITQIQTIPAQQSQQQQVNNVSSAGGTATAVSSTTA------ATT 287 TMLENVK-KCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELK 246 KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSP 187 NITSRPAVPANPQTVKICTVPNSSSQ------LIKKVAVTPVKKLAQIGTTVVTTVP 127 PQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLML-----VSPQQTVTRAETTS 76 NTTSTTNHPTTTQ-IRLQTVPAAASMTNTTATSNIIVNSVASSGYANSSQPPHLTQLNAQ PSQTTTIGQTQVRMI--TPNALGTPRPTIGHTTISKQPPN---IRLPTAPRLVNTGGIRT ASPOPCLIGELKKSLPLLROALYTKELVIEGIKPPPQHVLGLAGLSQQLPKIQAQIRPIG ----QCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVS----VQT Conservative protein 9.3%; ; Score 256; DB 2; 1; Pred. No. 3.8e-07; 86; Mismatches 193; (NCBIN:134863, NCBIP:134864) Length 921; Indels 176; Gaps 460 329 405 276 243 24;

QKTMPVNTIIPT 509	450 SQPAGIPTGSSSKQLESLEHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPV : : :: : :	Qy	
VQIKLAQI	390 VVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVL	Qy Db	
ANTVTTVSLQPE	330 LNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVS	Ωy	
VSGATAPRTVS : : IRLPTAPRLVNTG	277QCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVS	Db Qy	
LPNSQSFI : LPKIQAQI	247 SSPQPHLVPFLKKSVVALRQL	B 8	
EEFTRKLYVE : EEFCDRLERL	188 TMLENVK-KCKNFLAMLIKLACSGSOSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELK	ОУ	
ENSAAVQINLS : AT	128 KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEDNLKAENS	Db Db	
VKKLAQIGTTVVTTVP : YANSSQPPHLTQLNAQ	77 NITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTVVTTV	Db	
VSPQQTVTRAETT : : TTTGPPTVTQTITNTSNN	25 PQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLVSF 	ОУ	
h 921; els 176;	ery Match 9.3%; Score 256; DB 2; Length 9 t Local Similarity 22.9%; Pred. No. 3.8e-07; ches 135; Conservative 86; Mismatches 193; Indels	Quer Best Matc	
2)	Note: sequence extracted from NCBI backbone (NCBIP:123832) Genetics: Gene: FlyBase:Tafl10 Cross-references: FlyBase:FBgn0010280	A; Genet A; Genet A; Gene	
ation	not compared with conceptual transla c acid		
ophila TA	Molecular cloning and functional analysis of Drosc nce number: A45183; MUID:93145326; PMID:7678780 ton: A45183		
ht, B.D.;	ion: A45183 *sequence_revision io~NOV~1994 *cexc ion: A45183 T.; Weinzierl, R.O.; Gill, G.; Chen, J.L.; Dynlac	C; Access R; Hoey,	
}) ciated factor TFIID - fruit fly (Drosophila sp.) ss: Drosophila sp. 10-10-10-10-10-10-10-10-10-10-10-10-10-1	RESULT A45183 TBP-as C:Spec	
NVT 546 :: SLT 614	510 SQFPPASILKQITLPGNKILSLQASPTQKNRIKENV	Qy	
IQKCGQKTMPVNTIIP : : : TTLPIPS-LP	450 SQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGC : : : : :	D Qy	
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PNSVPTAN	1 QIP-SLQVPGQANIVQIRGPQHAQLQRTGSVQIRATTRP	Db	

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Biochem. Biophys. Res. Commun. 183, 821-828, 1992
A;Title: Human intestinal mucin-like protein (MLP) is homologous with rat MLP in the A;Reference number: PQ0328; MUID:92198477; PMID:1550588
A;Accession: PQ0328
A;Molecule type: mRNA
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C;Date: 10-Mar-1993 #Sequence_revision 12-Apr-1996 #text_change 05-Nov-1999
C;Accession: A49963; A45106; B45106; A43932; B33332; A61257; PQ0328; PQ0329
R;Gum Jr., J.R.; Hicks, J.W.; Torribara, N.W.; Siddiki, B.; Kim, Y.S.
J. Biol. Chem. 269, 2440-2446, 1994
A;Title: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification of t A;Reference number: A49963; MUID:94132002; PMID:8300571
A;Accession: A49963
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A:Residues: 1343-1350,'L',1352-1411,'S',1413-1448,'P',1450-1503,'T',1505-1915 <TOR>
A:Residues: 1343-1350,'L',1352-1411,'S',1413-1448,'P',1450-1503,'T',1505-1915 <TOR>
A:Cross-references: GB:M74027; NID:g188863; PIDN:ARA59875.1; PID:g188864
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:55749, NCBI:55750)
A:Roun, J.R.; Byrd, J.C.; Hicks, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.S.
J. Biol. Chem. 264, 6480-6487, 1989
A:Title: Molecular cloning of human intestinal mucin cDNAs. Sequence analysis and e.
A:Reference number: A33532; MUID:89197956; PMID:2703501
A:Accession: B33532
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R;Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Rothe, E.M.; Lagace, R.E.; Kim, Y.S. J. Biol. Chem. 267, 21375-21383, 1992
A;Title: The human MUC2 intestinal mucin has cysteine-rich subdomains located both up A;Reference number: A45106; MUID:93016075; PMID:1400449
A;Accession: A45106
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mucin 2 precursor,
N;Alternate names:
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A; Residues: 'T', 1925-1948, 'TTS', 1952-1954
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A;Title: Human bronchus and intestine express the same mucin gene.
A;Reference number: A61257; MUID:91086481; PMID:1985113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M22405; NID:g188873; PIDN:AAA36334.1; PID:g188874
A;Experimental source: intestine
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A; Residues: 1916-2193 <GU4>
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R;Toribara, N.W.; Gum Jr., J.R.; Culhane, P.J.; Lagace, R.E.; Hicks, J.W.; Petersen, J. Clin. Invest. 88, 1005-1013, 1991
A;Title: MUC-2 human small intestinal mucin gene structure. Repeated arrays and polym A;Reference number: A43932; MUID:91358717; PMID:1885763
A;Accession: A43932
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A; Residues: 2037-3020 <GU3>
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A;Note: sequence_extracted from NCBI backbone (NCBIP:116706)
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A; Residues: 626-
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mucin SMUC-41
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A; Reference number: 147141; MUID:94102478; A; Accession: 147141
                                                                               gastric mucin (clone PGM-2A) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #t
C;Accession: I47141; S55315
R;Turner, B.S.; Bhaskar, K.R.; Hadzopoulou-Cladaras,
Gastroenterology 106, 200, 1994
A;Title: Pig gastric mucin: isolation and characteriz
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147141
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A;Map position: l1p15.5-11p15.5
C;Superfamily: von Willebrand factor; von Willebrand factor type A repeat homology;
C;Keywords: glycoprotein; intestine; tandem repeat
F;2766-2834/Domain: von Willebrand factor type C repeat homology <VWC>
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A; Accession: PQ0329
A; Molecule type: protein
A; Residues: 2328-2342, 'K', 2344-2354
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A; Molecule type: mRNA
A; Residues: 1-528 < TU
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A; Cross-references:
                                A;Status: preliminary; translated
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erences: GB:M86523
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22.9%; Pred. No. 3.1
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8; Mismatches
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                                GB/EMBL/DDBJ
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                                                                  PMID: 7506218
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A;Cross-references: EMBL:U10281; NID:g915205; PIDN:AAC48526.1; PID:g915208 R;Turner, B.S.; Bhaskar, K.R.; Hadzopoulou-Cladaras, M.; Specian, R.D.; Law Blochem. J. 308, 89-96, 1995 Ricchem. J. 308 and Appearance of the control of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PISVQPSSSSS--PTTSTTSVQSSSSSSVPIPSTTSVQP-----SSSGS----APTTS 48
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--SSSVPTTSATSVQTSSSSSTPI
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                                                                                                                                                                                                                                        TSATSVQPSSSSS----PPISSTIS
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                                                       LKQITLPGNKILSLQASPTQKNRI
                                                                                                               SSGSAPTTSATSV--QPSSS----
                                                                                                                                                                       GSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASI 517
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Pred. No. 3.6e-
                                                                                                               -SSVPTTSATSVRSSSSSSTPIPT---TTSVQPSS-
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hypothetical protein H02F09.3 - Caenorl
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision
C;Accession: T33369
R;Geisel, C.; Harmon, G.
                                                                                                                                         submitted to the EMBL Data Library, July 1
A;Description: The sequence of C. elegans
A;Reference number: Z21330
                                                                                                                                                                                                                                                                                                                                           T33369
                                                                                                                     A; Reference number: A; Accession: T33369
A;Cross-references: EMBL:AF077538; PIDN:AAC64622.1; GSPDB:GN00028; A;Experimental source: strain Bristol N2; clone H02F09
                                               A; Molecule type: DNA
A; Residues: 1-1275 <
                                                                                            A; Status: preliminary; translated
                                                    <GEI>
                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
                                                                                                 from
                                                                                                                                                                                           July 1998
                                                                                                 GB/EMBL/DDBJ
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                           CESP: H02F09
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R:Wilson, A.C.; LaMarco, K.; Peterson, M.G.; Herr, W. Cell 74, 115-125, 193
A;Title: The VP16 accessory protein HCF is a family of A;Reference number: A40718; MUID:93327419; PMID:8392914
A;Accession: A40718
                                                                                                                                                                                                                                                                C)Species: Homo sapiens (man)
C;Date: 16-reb-1994 #sequence_revision 18-Nov-1994 #text_change
C;Date: A40718; g02511; A56088; I37453
C;Accession: A40718; G02511; A56088; I37453
                                                                                                                                                                                                                                                                                                                                                                        RESULT
A40718
                                                                                                     A; Molecule type: mRNA; protein
A; Residues: 1-2035 <WIL>
A; Cross-references: PIDN: AAB27583.1; PID: 9399752
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A:Introns: 42/1; 78/3; 106/3; 135/2; 161/2; 224/1
C:Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase
                                A;Experimental source: HeLa cell A;Note: sequence extracted from NCBI backbone (NCBID:135349) R;Platzer, M.; Bauer, D.; Drescher, B. submitted to the EMBL Data Library, March 1995
                                                                                                                                                                                                                                                                                                                      host cell factor C1 precursor - human
N;Alternate names: CFF; HCF; VP16 accessory protein host cell factor (VCAF)
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A; Accession: G02511
                 A; Reference number:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLAQIGTTVV----TTVPKPSSVQSVAVPTSVVT-------VTPGKPLNTV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVTAPSTVVTVPSTVVTKPNTV--VTSSPTVATTPTTV--VTTPST------VVTVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVTVPTTTVTGPTTVVTVPTTVVTTPSTVVTSPITTPSTVVTVPSTVVTVPSTAVTKPST 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLVTKVAPVSAPPKVSSGP----RLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVQIKLAQPGPVLSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STVTG-STVTEASTISGSTESSTIPGSTESTVSEASTVSGSSVSTVS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NTVTTVSLQPEKPVVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSTYIPVSSASSIYSTLSGSTGSTA-----SPGTTESSGSSTSGPSTISGSS-----A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSTATAGTSPQASTVTTVTDISTVSGSTVTSQTAESSLSTESPTSAGSSI-STVSTVSSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATQQSTKPTIGTSMSSGPTTVAPGASTESTVLQSSTPSGTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEMGQNVKKLVEQLLDA--KIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNS 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVTTETSIGSSSTP-----LPSQSTSLSMSSLSTYTPSS------STAGATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVVTVPTTVVTNPSTVVTAPSTV--VTVPTTVMTSRSTVITTPTTGGSSPSTAGTSLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SGPLMLVS-PQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GSTESTSAGASTVSGS-----
                 H01368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----LAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVA
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Pred.
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No. 3.1e-05;
                                                                                                                                                             conceptual
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               534
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A;Molecule type: DNA
A;Residues: 1-2035 <PLA>
A;Residues: 1-2035 <PLA>
A;Cross-references: EMBL:U52112; NID:g1302657; PIDN:AAC51751.1; PID:g1302663
A;Cristle, T.M.; Pomerantz, J.L.; Twomey, T.C.; Parent, S.A.; Sharp, P.A.
J. Biol. Chem. 270, 4387-4394, 1995
A;Title: The cellular C1 factor of the herpes simplex virus enhancer complex A;Reference number: A56088; MUID:95181425; PMID:7876203
A;Accession: A56088
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A;Residues: 1-664,'T',666-1637,'E',1639-1684,'A',1686-1734,'Q',1736-2035 < R;Frattini, A.; Faranda, S.; Redolfi, E.; Zucchi, I.; Villa, A.; Patrosso,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
A;Gene: GDB:HCFC1; HFC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 100-563,'R',565-603,'VS',604-1163,'P',1165-1872,'A',1874-2035 <FRA>
Ā;Cross-references: EMBL:X79198; NID:g558348; PIDN:CAA55790.1; PID:g558349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Genomic organization of the human VP16 accessory protein (HCF), a housekeep1 A;Reference number: 137453; MUID:95130085; PMID:7829076 A;Accession: 137453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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Best Local S
Matches 131
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886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLVSPQQTV 69
: : |::| | | | | | | :: | :|: | | |:| |
                                                                                                                                                                                                                                           LRTVPMGGVRLVTPVTVSAVKPAVTTLVVKGTTGVTTLGTVTGTVST--SLAGAGGHSTS
                                                                                                                                                                                                                                                                                                                            VTSSPGIKSPITIITTKVMTSGTGAPAKIITAVPKIATGHGQQGVTQVVLKGAPGQPGTI
                                                                                                                                                                                                                                                                                                                                                                      TSSDMVIATCTTTVTT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLVEQLLDAKIEAEEETRKLYVELKSSPOPHLVPFLKKSVVALROLLPNSOSFIQQCVQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---VTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLK-PSSL-GASSTPSNEPNL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTV-----
EQPTATVTIADSGQGDVQPGTVTLVCSNPP
                                      ISHSSTLTIQKCGQKTMPVNTIIPTSQFPP
                                                                                                                  DHICKPVIGTPVQIKL-AQPGPVLSQPA-GIPTGSSSKQLFSLFHVVQQPSGGNEKQVTT 484
                                                                                                                                                               ASLATPITTLGTIATLSSQ----VINPTAITVSAAQTTLTAAGGLTTPTITMQPV-----
                                                                                                                                                                                                   KPLVTSVA--NTVTTVSLQPEKPVVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCW
                                                                                                                                                                                                                                                                                                                                                                                                             PTILGI --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QTKPVQTSAVTGQASTGPVTQIIQTKGPLPAGTILKLVTSADGKPTTIITTTQASGAGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --KAENSAAVQINLSPIMLENVKKCKNFL--AMLIKLACSGSQSP-----EMGQNVK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRPIITVHKSGTV-TVAQQAQVVTTVVGGVTKTITLVKSPISVPGGSALISNLGKVMSVV 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPA--TVKVASSPVMVSNPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGSSPQMSGMAALAAAAAATQKIPPSSA---PTVLSVPAGTTIVKT----MAVTPGTTT 588
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                                                                            -SQPTQVTLITAPSGVEAQPVHDLPVS
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                                                                                                                                                                                                                                                                                    -VSVQTLNPLAGPVGAK---AGVVTLHSVGPTAATGGTTAGTGLLQTS
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23.0%; Pred
74;
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                                                                                                                                                                                                                                                                                                                                                                ---SPVVT----TTVSSSQSEKSIIVSGA----TA 321
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Pred. No. 0.00011;
4; Mismatches 211
                                                                                                                                                                                                                                                                                                                                                                                                        -SSVSPSTT---KPGTTTIKTIPMSAIITQAGATG
1017
                                        514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302/1;
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A;Map position: 9R C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase C;Superfamily: yeast glucan 1,4-alpha-glucosidase C;Keywords: glycosidase; hydrolase; polysaccharide degradation; transmembrane protein F;5-21/Domain: transmembrane #status predicted <TMl> F;1350-1366/Domain: transmembrane #status predicted <TM2>
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A; Residues: 1-1367 < ROW>
A; Cross-references: GB:Z47047; EMBL:Z38061; NID:g603997; PID:g763364; GSPDB:GN00009; R; Yamashita, I:, Nakamura, M.; Fukui, S.
J. Bacteriol. 169, 2142-2149, 1987
A; Title: Gene fusion is a possible mechanism underlying the evolution of STA1.
A; Reference number: A91831; MUID:87194600; PMID:3106330
A; Accession: A26877
A; Molecule type: DNA
A; Residues: 1-242 < YAM>
A; Residues: 1-242 < YAM>
A; Residues: 1-242 < YAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 762-1331 CYA2>
A;Residues: 762-1331 CYA2>
A;Cross-references: EMBL:M16165; NID:g172523; PIDN:AAA35015.1; PID:g172526
R;Pardo, J.M.; Ianez, E.; Zalacain, M.; Claros, M.G.; Jimenez, A.
FEBS Lett. 239, 179-184, 1988
A;Title: Similar short elements in the 5' regions of the STA2 and SGA genes from Saccha: A;Reference number: S27281; MUID:89031230; PMID:3141213
A;Accession: S27281
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glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae)
N;Alternate names: extracellular glucoamylase; mucin-like protein MUC1; protein YIR019c
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Nov-1999
C;Accession: $48478; A26877; B26877; S27281; JC6123
R;Rowley, K.
submitted to the EMBL Data Library, October 1994
A;Reference number: $48478
A;Accession: $48478
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A;Residues: 1-1367 <LAM>
A;Cross-references: GB:U30626; NID:g1304386; PIDN:AAC49609.1; PID:g1304387
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A;Cross-references: MIPS:YIR019c; SGD:S0001458
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A; Residues: 1-31 < PAR>
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A;Accession: B26877
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202 MLIKLACSGSQS------PEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLV 254 :: | :: | |: | ||
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                                                                                               SSSTTESSVAPVPTPSSSSNITSSAPSSTPFSSSTESSSVPV---PTPSSSTTESSS--- 851
                                                                                                                                                     SSSAPVTSSTTESSSAPVTSSTTESSSAPVPTPSSSTTESSSAPVPTPSSSTTESSSAPV 737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 8.0%; Score 220; DB 1;
Similarity 22.5%; Pred. No. 7.5e-05;
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Qy 255 PELKKSVVALROLLPNSOSFIQCYQOTSSDNYLATCTTVTTSPVTTTVSS- Qy 255 PELKKSVVALROLLPNSOSFIQCYQOTSSDNYLATCTTVTTSPVTTTVSS- Db 905				1.0															
KKSVVALROLLPNSOSFI LUTSVALROLLPNSOSFI IVSGATAPRIVSVOTI IVSGATAPRIVSVOTI I	258	Qy 220 Db 997	Qy 174 Db 947	146 887	86 853	26 801	Query Ma Best Loc Matches	A; Experime A; Experime C; Genetics A; Gene: CE A; Map posi A; Introns:	A; Status: A; Molecule A; Residues	R;Geisel, submitted A;Descript A;Referenc	RESULT 8 T34434 hypothetic C; Species: C; Date: 29 C: Accessio	1102	160	415	368 1010	950			Db 852
י אי פי ש	SP-VESSTSGATSSSGSPGTTLTSISPSPSPSSTIGSSQGSTSPVVSTISQGSTETPGS	VKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHL	KAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQN 219	GKPLNTYTTLKPSEPNL 	VKICTVPNSSSQLIKKVAVTPVKKLAQIGTTVVTTVPKPSSVQSVAVPTSVVTVT :::	PANLQLPPGTVLIKSNSGPLMLVSPQQTVTRAETTSNITSRPAVP 8PSTVSGSTSSGSTVTVGSTEASTSGSSVASSSPAPSTS 8	7.7%; Score 212.5; DB 2; Length 2232; Similarity 21.9%; Pred. No. 0.00039; B; Conservative 73; Mismatches 247; Indels 173; Ga	Telence: Employed; Fiber, RKC/050.1; GSPUB; GN00026; CESF; tall Source; Strain Bristol N2; clone K06A9; SP:K06A9.1a Lion: X 38/1; 75/3; 103/3; 132/2; 158/2; 222/1; 1088/1; 1367/1; 203	type: DNA type: DNA type: DNA type: DNA type: DNA type: DNA	Gattung, S. the EMBL Data Library, December 1996 The sequence of C. elegans cosmid KO umber: Z21525	protein K06A9.la - Caenorhabditis elegans enorhabditis elegans t-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2	113	CINOCALLATOROGO CANONINA TIPO CIO	WDHICKPVIGTPVQIKLAQPGPVLSQPAGIPTGSSSKQLFSLF 4	KPLYTSVANTVTTVSLQPEKPVVSGTAVTLSLPAVTFGETSGAAIC	: :	GSQT ETSVSSTTETTIVPTKTTTSVTTPSTTTTTTVCSTGTN	VVTTTVSSSQSE	APVSSSTTESSVAPVPTPSSSSNITSSAPSSIPFSSTTESFSTGTTVTPSSSK 904

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calphotin - fruit fly (Drosophila melanogaster)
C;Specias: Drosophila melanogaster
C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_cr
C;Accession: A47283
R;Ballinger, D.G.; Xue, N.; Harshman, K.D.
Proc. Natl. Acad. Sci. U.S. A. 90, 1536-1540, 1993
A;Title: A Drosophila photoreceptor cell-specific protein,
A;Reference number: A47283; MUID:93165730; PMID:8434015
A;Contents: photoreceptor cells
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A;Molecule type: nucleic acid
A;Molecule: 1-873 <BAL>
A;Cross-references: GB:L05080; NID:g157071; PIDN:AAA28420.1; PID:g157072
A;Note: sequence extracted from NCBI backbone (NCBIN:124958, NCBIP:124959)
A;Note: sequence extracted from NCBI backbone (NCBIN:124958, NCBIP:124958, NCBIP:124958)
A;Note: sequence extracted from NCBI backbone (NCBIN:124958, NCBIP:124958, NCBIP:12495
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     AVTFGETSGAAICLPSVKPVVS
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21.5%; Pred. No. 0.00016;
Live 82; Mismatches 239
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hypothetical protein T19D12.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #te: C;Accession: T34369 
R;Favello, A.  
Symmitted to the EMBL Data Library, November 1995 
N;Description: The sequence of C. elegans cosmid T19D1: A;Reference number: Z21513 
A;Accession: T34369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 2
A; Introns: 36/1; 134/2; 180/1; 622/3; 691/2; 754/1; 1111/2; 1174/1; 1271/3; 1322/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U41263; PIDN:AAC24428.1; GSPDB:GN00020; CESP:T19D12 A;Experimental source: strain Bristol N2; clone T19D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-1777 <FAV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              675 --NITR-KGYQGFVILVA------NSDESVQASVDSATNLKAQGF-NVITVAFKS
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KLAQPGPVLSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCG---
                                                                                                                                                                                                                                                   TTQGSSSQAPSSTVTVPTTGTTSGAASTTGSITSTQQATSTSSVITTGSTSAPQSSTAVS
                                                                                                                                                                                                                                                                                   CVQQTSSDMVIATCT--TTVTTSPVVTTT--VSSQ---SEKSIIVSGAT-APRT---VS
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                                                  LTSSSAQSTASTGVSTVASSTTIPQGSSS----
                                                                                                                                                        STTTSP-----
                                                                                                                                                                                                VQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQ-
                                                                                                                                                                                                                                                                                                                                                                                                              S-----PQPH----LVPFLKKSVVA-----
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                                                                                                ----PEKPVVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQI
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Pred. No. 0.00
87; Mismatches
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RESULT 11
A47282
A47282
calcium-binding protein calphotin - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-
C;Accession: A47282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Martin, J.H.; Benzer, S.; Rudnicka, M.; Miller, C.A.
Proc. Natl. Acad. Sci. U.S.A. 90, 1531-1535, 1993
A;Title: Calphotin: a Drosophila photoreceptor cell calcium-binding
A;Reference number: A47282; MUID:93165729; PMID:8094559
A;Accession: A47282
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C;Superfamily: collagen alpha 1(I) chai
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A;Gene: FlyBase:Cpn
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A; Residues: 1-865 <MAR>
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PVQIKLAQPGPVLSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKC
                                                     VVATTPVPATL-AVTDPDVTASAV--PELPPVIAPSPVPSAVAETPVDLAPPVLPPVAAE
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                                                                                          VVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVS-----
                                                                                                                                                               LNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKP
                                                                                                                                                                                                       VSAS-----TEPPVAAATLTTAPET-PALAPVVAESQVAANTVVATPPTP-APEPET
                                                                                                                                                                                                                                        NSQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQT
                                                                                                                                                                                                                                                                              ----PEVSVVATKPLAAAEPVVVAPPATETPVVAPAAASPHVSVAPAVETAVVA----P
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Pred. No. 0.00025;
2; Mismatches 242;
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R;Geisel, C.; Gattung, S.
submitted to the EMBL Data Library, Decemb
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A;Residues: 1-1032 <
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;Species: Caenorhabditis elegans
;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #te
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                                                                                                                                                                                                                              VVTLHSVGPT-----AATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVV
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LGTQSTNSSPSSSSSPST-SGMSTLTSEPSPSSTQSSGAQSTLTT
                   I---PTSQFPPASILKQITLPGNKILSLQASP--TQKNRIKENVTS
                                                                                                                                                                        SGTAVTLSLPAVTFGETSGAAICLP-SVKPVVSFCWDHICKPVIG--TPVQIKLAQPGPV 448
                                                                                                                                                                                                                                                                                                                                                    PVSSSTFG-----SSTP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGTTVVTTVPKPSS------VQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AASSSSYATVSTIAGSTGSTIT----PVPGSSSTIGSSTPSASSSSSGTMSTIS-----GS
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                                                                    MNPSSSTPTGSSQSTITPEGSTASSPTG
                                                                                                   LSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTI--QKCGQKTMPVNTI 506
                                                                                                                                                                                                           VVPGSSTSPAPSSSPNPSSSPASTGSTITISG---SSSIIVSTVSGS---
                                                                                                                                                                                                                                                                                                              CTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNP-----LAGPVGAKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDA 230
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                                                                                                                                      SGSTGTSQSTLASSTATPGSSSTVPSSSSPQPS---SQSPAPNTGSTTPSQTSSQSPSPS
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Pred. No. 0.00038;
4; Mismatches 227
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DNA-binding protein R kappa B - human C; Species: Homo sapiens (man) C; Date: 08-May-1995 #sequence_revision 21 C; Accession: S52863; A45580 R; Nieters, A.; Bouwmeester, T.; Scheidere submitted to the EMBL Data Library, Augus A; Reference number: S52863 A; Accession: S52663 A; Status: preliminary
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New Biol. 3, 1063-1073, 1991

A;Title: Cloning of R kappa B, a novel DNA-binding protein A; Reference number: A45580; MUID:92135142; PMID:1777480

A; Accession: A45580

A; Molecule type: mRNA

A; Residues: 313-1292, 'ISNREQLLAPP', 1304, 'QSPLLL' <ADA>
A; Rosi references: GB:008191; GB:S79520; NID:9476273; PIDN

A; Note: sequence extracted from NCBI backbone (NCBIN:79520)
C; Keywords: DNA binding; transcription factor
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A; Molecule type: mRNĀ
A; Residues: 1-1324 <NIE>
A; Cross references: EMBL; X80878; NID: 9695578; PID: 9695579
A; Cross references: K,Y,; Hanley, E.W.; Nabel, G.J.
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---PASHLQQGTASGSSKAVSTVVVTTAPSPKQ 1319
                                                                                                                                                                                                                                                                     GVVTLHSVGPTAATGGTTAGTGLLQTSKP-LVTSVANTVTTVSLQPEKP--VVSGTAVTL 398
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                                                                                                                                                                                           SLPAVTFGETSGAAICLPSVKPVVSFCWDHICKP--VIGTPVQIKLAQPGPVLSQPAGIP
                                                                                                                                                                                                                                  TVATHAKQGASVASGSGTVHTSAV--SLPSMNAAVSKTVAVASGAASTPISISTGAPTVR
                                                                                                                                                                                                                                                                                                                PDLKPTEASSSAFRLMPALGVSVADQKGKSTVASSEAKPAATIRIVQGLGVMPPKAGQTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPAQTLPQMPAGPQIRVPATATQTKVVPQ----TVMATVP-----VKAQTTAATVQRPG
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                                                                         LSGLGRNII----LTTMPAGTKLIAGN-KPVSFLTAQQLQQLQQQQQQATQVRIQTV----
                                                                                                                                                                                                                                                                                                                                                           PVVTTTVSSS----
                                                                                                                                                                                                                                                                                                                                                                                              LTQDLFGTGG----NTTGKGISATLHVTSNPVHAADSPAKASSASAPSSTPTGTTVVKVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKPQTGNSIPLTATNFRIQGKDVLRLPPSSITTDAKGQTVLRITPDMMATLAKSQVTTVK 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGQTGLTVTSLPATASPVSKPATSSPGT--SAPSASTAAVIQNVTGQNIIKQVAITGQLG
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                                                                                                              TGSSSKQLFSLFHVVQQPSG-----GNEKQVTTISHSSTLTIQKCGQKT-MPVNTIIPTS
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22.0%; Pred. No. 0.00056;
1ve 91; Mismatches 252;
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Library, August 1994
                                    ILSLQASPTQ
                                                                                                                                                                                                                                                                                                                                                     -QSEKSIIVSGATAPRTV--SVQTLNPLAGPVGAKA 341
                                                                                                                                                       ---RITVPLSVISQPMKGKSVVTAPIIKGNLGAN
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A;Note: differential splicing converts alphaNAC into a tissue-specific DNA-binding
C;Keywords: alternative splicing; DNA binding; transcription factor
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A;Title: Differential splicing-in of a proline-rich
A;Reference number: Z20889; MUID:96312450; PMID:8698
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A;Gene: Naca
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A; Residues: 1-2187 <
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R;Yotov, W.V.; St-Arnaud,
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                                    514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 TLVTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTT-IQFPANLQLPPGTVLIKSNSGPL
PAPSAKQPVLKNNK
                                    PASILKQITLPGNK
                                                                        KLPVPAEEDELPPLI-PPEAVSGEPFQPILVN-----
                                                                                                         GIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFP
                                                                                                                                                SVAPKPAPAASLTLAPSPVAPLPPKQPLLE-
                                                                                                                                                                                 TAVTLSLPAVTEGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPA 453
                                                                                                                                                                                                                                                                                                                             TSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTV------SVQTLNPL 333
                                                                                                                                                                                                                      VSPA---KGSDCLHS--PKGPVGS-----QVATPLA----AFTSDKVPPE--AVSA
                                                                                                                                                                                                                                                           AGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSG
                                                                                                                                                                                                                                                                                                                                                                                                           KLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASSTPSNE-PNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSCKKAAATETPIETSTAPSLEGAPKETSETSV---SKYLMSSPPKKAS-----SKR 1725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPVKKLAQIGTTVVTT-----VPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LQKAPSTTIPKENLAAPAVLPVSSKSPAAPARASASLSPATAAPQTAPKEAT-----TI 1675
                                                                                                                                                                                                                                                                                                                                                                        ------LPSKKGPTAFT-----EMLAAPAP-----ESALAITAPIQKSPG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                ASTLPATTLPSLK---EASV---LSPTATSSGK--DSHISPVSDACSTGTTTPQASEK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL: U48363; NID: g1666688; PID: g1666689; PIDN: AAB18732.
1995
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Pred. No. 0.0012;
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                                                                      MPAPK--PAGTPA 1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      converts alphaNAC
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RESULT 15 F96615

probable Myb-family transcription factor F16M22.4
C; Species: Arabidopsis thaliana (mouse-ear cress) [imported] -Arabidopsis thaliana

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RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonsó, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

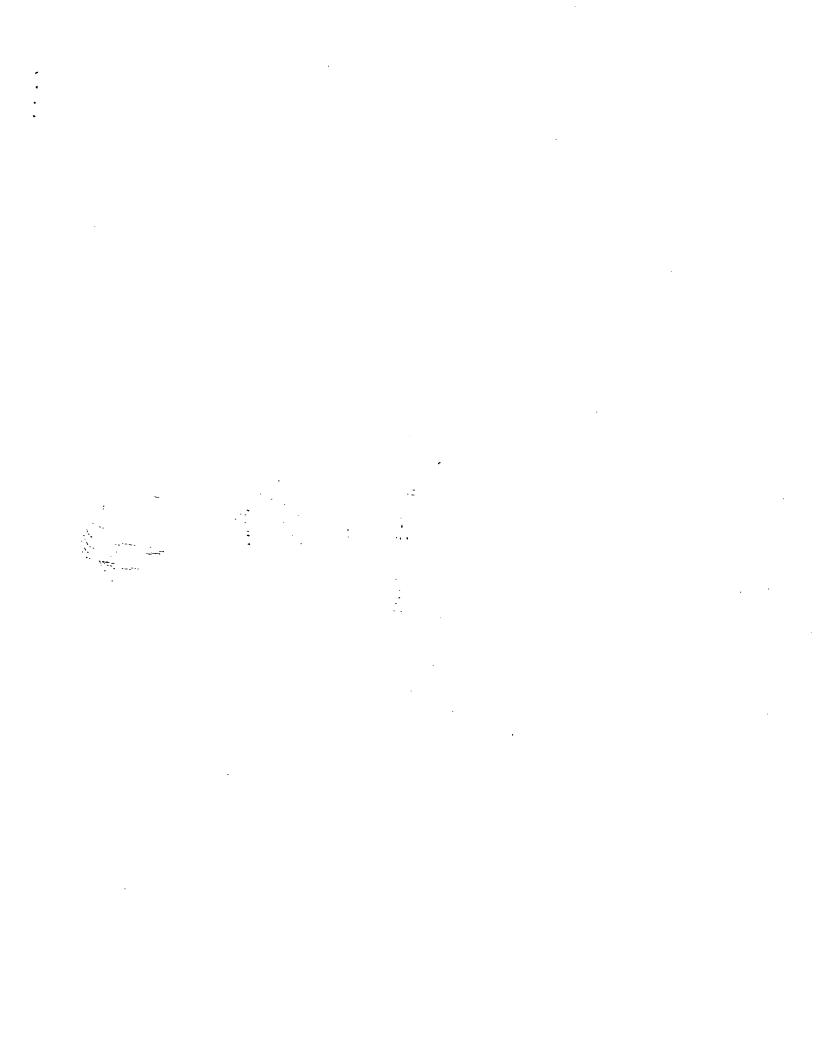
A.; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, S.X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A.; Rosquence and analysis of chromosome 1 of the plant Arabidopsis.

A.; Reference number: A86141; MUID:21016719; PMID:11130712
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C;Accession: F96615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: F16M22.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA A; Residues: 1-873 <STO>
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                                                511 ---- OFPPASILKQITLPGNKILSLQASPTQKNRIKENVTS 547
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                                                                                                                                                                                                                                                                                                                                                                                                                                     682 ------SRLVPTQRAPAATVVTPQ--KPSVVAAAT------VVTPQK 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    633 VGPLNLRHAVNGSPNHTIPSSPFTKPL------HMAPLSKGSTIQSNSVPPSFAS- 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             579 ASLPCTSGIISSPK-----AELVKSAASAASFPRPSSMLSAPKADPVKIVPAAATNTKS 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 VTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S-----PRPSGMISAPKVESVKT-----TASMPRPSGIISAPKAE--LVKSAASA 578
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                                                                                                                                                                                                                                                                                                                                                                                 GPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGT 394
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AAKVETPPSLMPKKNEVVGS---CTDKSSLDKPPEKESTTT 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLA 334
                                                                                                         -----QKEQTQGNRASPLVTATLPPNKTIPANSVIGTAKAV 808
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Search completed: February 16, 2003, 22:00:30 Job time: 32.6758 secs



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Minimum
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2758
1 GTLVTKVAPVSAPPKVSSGP....
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YAG3_YEAST
ZAU_HUMAN
VG50_HSVI1
VGLX_HSVEB
YJH8_YEAST
MUC1_XENLA
N1121_RT
FIG2_YEAST
AGA1_YEAST
AGA1_YEAST
AGA1_YEAST
AGA1_YEAST
ALS1_CANAL
FLO5_YEAST
ALS1_CANAL
FLO5_YEAST
PIK2_DICDLI
PIK2_YEAST
PIK2_DICDLI
PIK3_TEAST
PIK3_DICDLI
PIK3_TEAST
P
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T2D3_DROME
HFC1_HUMAN
HFC1_MESAU
AMYH_YEAST
MUC2_HUMAN
CPN_DROME
ZAN_MOUSE
MSB2_YEAST
YM96_YEAST
OCT1_HUMAN
HRX_MOUSE
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SEQUENCE FROM N.A., MEDLINE-97011146; Pu

Dikstein R., Zhou

hTAFII130."

87:137-146(1996)

"Human TAFII 105 is a cell type-specific TFIID subunit related

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., AND PARTIAL SEQUENCE.
PubMed=8858156;
S., Tjian R.;

15- 15- 15- 17- TAF TAF HOM MAM NCB	ULT 1 T_HUMAN T2DT_		4 4 5	43	4 1	40	ນ ພ 8	37	36	35	34	
15-JUL-1998 (Rel. 36, Created 15-JUL-1998 (Rel. 36, Last se 15-JUL-1998 (Rel. 41, Last an Transcription initiation fact (TAFIIIO5) (Fragment). TAP4B OR TAF2C2 OR TAFIIIO5. HOMO Sapiens (Human). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID-9606;	T 1 HUMAN T2DT_HUMAN		153 152	157.5	160.5	161	162	163	164.5	165	166	
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36, Created) 36, Last seq 41, Last ann iation facto nt). tarinio. tarillos. ni). chordata; primates;	STANDARD;		739 604	907	630	1509	3969	860	1365	606	3726	
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yuence update) notation update) or TFIID 105 kDa subuni or TGIID 105 kDa subuni or TGIID 105 kDa subuni	PRT; 801 AA.	ALIGNMENTS	OCT1_CHICK MTG8_HUMAN	VGP3_EBV	MUC1_MOUSE	GSR1_HUMAN	HRX_HUMAN	CHI2_COCIM	SUZ2_DROME	SP2_HUMAN	TRX_DROME	
lt (TAFII-105) Euteleostomi;			P15143 Q06455	P03200	Q02496	Q9nzm4	Q03164	P54197	P25172	002086	P20659	
·105)			gallus gall homo sapien	mesocricetu epstein-bar	mus musculu	homo sapien	homo sapien	coccidioide	drosophila	homo sapien	drosophila	

Query Match Best Local S Matches 552 EMBL; Y09321; CAA70499.1; -. Genew; HGNC:11538; TAF4B. MIM; 601689; -. modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way Transcription regulation; Nuclear protein. 1InterPro; IPR003894; TAF_hom.
SMART; SM00549; TAFH; 1. SEQUENCE SIMILARITY: BELONGS TO THE TAF2C FAMILY. al Similarity 552; Conser 801 AA; 85658 MW; D12B4932FE4A9CD2 CRC64; Score 2758; DB 1; Pred. No. 8.3e-147; ; Mismatches 0; There are no restrictions ong as its content is in Length

-1- FUNCTION: CÊLL TYPE-SPECIFIC SUBUNIT OF TFIID THAT MAY FUNCTION AS A GENE-SELECTIVE COACTIVATOR IN CERTAIN CELLS. TFIID IS A MULTIMERIC PROTEIN COMPLEX THAT PLAYS A CENTRAL ROLE IN MEDIATING PROMOTER RESPONSES TO VARIOUS ACTIVATORS AND REPRESSORS.
-1- SUBUNIT: TFIID IS COMPOSED OF TATA BINDING PROTEIN (TBP) AND A NUMBER OF TBP-ASSOCIATED FACTORS (TAFS). TAFIIIOS MAY FORM HETERODIMERS WITH TAFIII30.
-1- SUBCELLULAR LOCATION: Nuclear.

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1 GTLYTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPL 60

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SEQUENCE FROM N.A.

MEDLINE=97336072; PubMed=9192867;

Mengus G., May M., Carre L., Chambon P., Davidson I.;

"Human TAF(II)135 potentiates transcriptional activation by the of the retinoic acid, vitamin D3, and thyroid hormone receptors mammalian cells.";
Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Claek D., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clay V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
                                                                                                                                                                                                                                                                                                                                                                                                        T2D3_HUMAN STANDARD; PRT; 1083 AA.
000268; Q99721; Q9Bx42; Q9Bx40;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transcription initiation factor TFIID 135 kDa
(TAFII135) (TAFII-130) (TAFII130).
TAF4 OR TAF4A OR TAF2C1 OR TAF2C OR TAF1I135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
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Mammalia; Eutheria:
                                                                                                                                                         MEDLINE=21638749;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAA
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                                                                                                                                                                                                          11:1381-1395(1997).
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                                                                                                                                                         PubMed=11780052;
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                                                                                                                                                                                                                                                                                                                                                              Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                              OR.
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RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Al Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Al Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Al Kay M.P., Kimberley A.M., King A., Knights A., Lalrd G.K., Lawlor S., A. Lehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., A. Lehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., A. Mille S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., A. Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Pilliams S.A., Mistry D., Soott C.E., Sehra H.K., Shwnkeen R., Sims S., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shwnkeen R., Sims S., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tacey A., Tromans A.C., Vaudin M., Walli M., Walliams L., Williams S.A., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Walling L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.:
                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBI. the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 105-1083 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rogers J.; "The DNA sequence and comparative analysis of human chromosome Nature 414:865-871(2001).
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G -> GPG (IN REF. 2).
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Query Match Best Local S Matches 173

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Conservative

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Score 547; DB 1; Pred. No. 2.4e-23; 7; Mismatches 144

Length 1083;

Indels

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Gaps

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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transcription initiation factor TFIID 110 kDa
(TAFII-110) (110 kDa TBP-associated factor).
TAFI10 OR CG5444.
  Kokubo T., Gong D.-W., Roeder R.G., Ho
"The Drosophila 110-kDa transcription
interacts with the N-terminal region c
Proc. Natl. Acad. Sci. U.S.A. 90:5896-
                                                                                                                                                                                                                                                                                                                                                                                                                           Muscomorpha; Ephydroidea;
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata;

Insecta; Pterygota; Neoptera; Endopterygota;

Muscomorpha; Ephydroidea; Drosophilidae; Dros
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                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.,
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                                                                                               MEDLINE-93317591;
                                                                                                                                                                                                                                                                                                                              MEDLINE-93145326;
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l R.O.J., Gill G
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Diptera; Brachycera;
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                                                                     Nakatani Y.;
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RA Dorkova D., Botchen A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gentles B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Correll J.H., Gu Z., Gunn P., Harris M.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Hernandez J.R., Houck J.,
RA Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkllov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkllov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Marin M., Ralum R., Sunders R., D.C., Scheeler F., Shen H.,
RA Marin M., Ralum R., Sunders R., D.C., Scheeler F., Shen H.,
RA Sylraka R., Pecileb J.M.,
RA Shue B.C., Stapleton M., Zhang G., Jhao Q., Zhen
                                                                                         DOMAIN
                                                                                                                    SMART; SM0054
Transcription
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MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                           FlyBase; FBgn0010280;
                                                                                                                                                                                                                                                                                              EMBL; L06861; -; NOT_ANNOTATED_CDS EMBL; S63550; AAB27433.1; -.
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SEQUENCE FROM
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SMART; SM00549; TAFH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF TBP-ASSOCIATED FACTORS (TAFS) SUBCELLULAR LOCATION: Nuclear. SIMILARITY: BELONGS TO THE TAF2C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: TFIID IS A MULTIMERIC PROTEIN COMPLEX THAT PLAYS A CENTRAL ROLE IN MEDIATING PROMOTER RESPONSES TO VARIOUS ACTION AS A COACTIVATOR BY SERVING AS OF PROTEIN PROTEIN CONTACT BETWEEN ACTIVATORS LIKE SP1 (OR EVEN ACTIVATORS AS A COACTIVATOR BY SERVING BY SE
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SUBUNIT: TFIID IS COMPOSED OF TATA BINDING
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Query Match Best Local

Local Similarity

9.3%;

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HFC1_HUMAN
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P51610;
01-OCT-1996
01-OCT-1996
15-JUN-2002
                                                                                                                                                                              MEDLINE=93327419; pubMed=8392914; Wilson A.C., Lamarco K., Peterson M.G., "The VP16 accessory protein HCF is a fairom a large precursor protein."; Cell 74:115-125(1993).
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
Frattini A., Faranda S.; Redolfi E., Zucchi I., Villa Patrosso M.C., Strina D., Susani L., Vezzoni P.; "Genomic organization of the human VP16 accessory pro
                                                                                                        TISSUE-Fetal
                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCFC1 OR HCF1
                                                                             rissue=Fetal brain;
medLine=95130107;    pubMed=7829097;
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                                                                                                                                   OF 65-2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
actor C1 (HCF) (VP16 accessory pro
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                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                 (LONG
                                                                                                                                   FROM
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                                                                                                                                   N.A.
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                                                                                                                                                                                                                                                                                                            SHORT ISOFORMS), AND
                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                   (LONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     accessory protein) (HFC1) (VCAF)
                                                                                                                                   AND
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family c
accessory protein,
                                                                                                                                   SHORT
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                                                                                                                                ISOFORMS)
                                                                                                                                                                                                                                   polypeptides
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Query Match Best Local

Similarity

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Score Pred.

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140 194 265 313 1439 1035 1097

KELCH 8 X 26 HCF RI

26 AA APPROXIMATE

REPEATS

KELCH KELCH KELCH KELCH

REPEAT REPEAT SMART; Pfam;

SM00060;

FN3; Repeat;

68

Alternative splicing;

Glycoprotein.

PF00041; fn3; 1 PF01344; Kelch;

Kelch. <u>ب</u>

Nuclear

REPEAT DOMAIN

REPEAT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wilson A.C., Peterson M.G., Herr W.;
"The HCF repeat is an unusual proteolytic cleavage signal.";
                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003961;
InterPro; IPR001798;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96033796; PubMed-7590226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             housekeeping gene (HCFC1) mapping Genomics 23:30-35(1994).
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TRANSACTIVATOR PROTEIN VP16 ASSOCIATES WITH HCF. BINDING TO HCF
ACTIVATES VP16 FOR ASSOCIATION WITH THE OCTAMER MOTIF-BINDING
PROTEIN OCT-1. TO FORM A MULTIPROTEIN-DNA COMPLEX RESPONSIBLE FOR
ACTIVATING TRANSCRIPTION OF THE HSV IMMEDIATE EARLY GENES.
SUBUNIT: COMPOSED PREDOMINANTLY OF SIX POLYPEPTIDES RANGING FROM
110 TO 150 KDB AND-A MINOR 300 KDB POLYPEPTIDE. THE MAJORITY OF N-
AND C-TERMINAL CLEAVAGE PRODUCTS REMAIN TIGHTLY, ALBEIT
NONCOVALENTLY, ASSOCIATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASSOCIATE.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL TISSUES AND ADULT KIDNEY. PRESENT IN ALL TISSUES TESTED.
POPMATH: THE HCF REPEAT IS A HIGHLY SPECIFIC PROTEOLYTIC CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Nuclear.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND SHORTER FORM; MAY BE PRODUCED BY ALTERNATIVE SPLICING. IN THE SHORTER FORM THE N- AND THE C-TERMINAL FRAGMENTS FAIL TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 5 KELCH REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: EXISTS AS A FAMILY OF POLYPEPTIDES THAT ARISE THROUGH
CLEAVAGE AT ONE OR MORE CENTRALLY LOCATED SITES. CLEAVAGE
AT A DEFINED SITE, PPCE/THET, WITHIN THE HCF REPEAT.
PTM: GLYCOSYLATED; CONTAINS O-LINKED N-ACETYLGLUCOSAMINE F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                         w; HGNC:4839; HCFC1.
300019; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    L20010; -; NOT_ANNOTATED_CDS
X79198; CAA55790.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epeat is an unusua
9:2445-2458(1995)
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16-OCT-2001 (Rel.
Host cell factor
                                                                                                                                                                                                                                                                                             HFC1_MESAU
P51611;
01-OCT-1996
SEQUENCE FROM N.A.

GOTO H., NIShItahi H., Umene K.I., Nakabepu Y., Nishimoto T.;

GOTO H., NIShItahi H., Umene K.I., Nakabepu Y., Nishimoto T.;

Submitted (FEB-1995) to the EMBL/Genbank/DDBJ databases.

-I- FUNCTION: UPON LYTIC INFECTION OF PERMISSIVE CELLS, THE HSV

TRANSACTIVATOR PROTEIN VP16 ASSOCIATES WITH HCF. BINDING TO HC

ACTIVATES VP16 FOR ASSOCIATION WITH THE OCTAMER MOTIF-BINDING

PROTEIN OCT-1, TO FORM A MULTIPROTEIN-DNA COMPLEX RESPONSIBLE

ACTIVATING TRANSCRIPTION OF THE HSV IMMEDIATE EARLY GENES (BY

SIMILARITY).

-I- SUBUNIT: COMPOSED PREDOMINANTLY OF SIX POLYPEPTIDES RANGING FR
                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                             Mesocricetus auracua
Enkaryota; Metazoa;
                                                                                                                                                                                                                             HCFC1
                                                                                                                                                                                                                                                                                                                                          MESAU
                                                                                                                                                       NCBI_TaxID=10036;
                                                                                                                                                                     Mesocricetus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLKGAPGQPGTILRTVPMGGVRLVTPVTVSAVKPAVTTLVVKGTTGVTTLGTVTGTVST-
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                                                                                                                                                                                                                                                                 (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 40, Last annotation updat
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                                                                                                                                                                                 Chordata;
Rodentia;
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                                                                                                                                                                             hamster).
; Craniata; Vertebrata; I
; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                    accessory protein) (HFC1) (VCAF)
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                                                                                                                                                                                                                                                                                                                       IGSNPQMSGMAALAAAAAATQKIPPSSA---PTVLSVPAGTTIVKT----VAVTPGTTT
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           IATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLH
                                                     AKIEAEEFTRKL-YVELKSSP-QPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMV
                                                                                                                                                                                                                                                                                          TRAETTSNITSRPAVPANPQT------VKICTVPNSSSQ---LIKKVAVTPVKKL 115
                                     PKIATGHGQQGVTQVVLKGAPGQPG-----
                                                                                             TIIKTIPMSAIITQAGATGVTSTPGIKSPITIITTKVMTSGTGAP----
                                                                                                                                                  TQIIQTKGPLPAGTILKLVTSADGKPTTIITTTQASGAGSKPTILGISSVSPSTTKPGTT
                                                                                                                                                                                                        AQVVTTVVGGVTKTITLVKSPISVPGGSALISNLGKVMSVVQTKPVQTSAVTGQASTGPV 706
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--VVTVTPGKPLNTVTTL-----KPSSLGASST----

766 170 SSVQSVAVPTS-----

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Gaps

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-AILRTVP-

----MSGVR

855

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modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                       Pfam; PF00041; fn3; 2.
Pfam; PF01344; Kelch; !
SMART; SM00060; FN3; 2
                                                                                                                                                                                                                                                                                             InterPro; IPR001798;
                                                                                                                                                                                                                                                                                                      InterPro; IPR003961; FN_III.
                                                                                                                                                                                                                                                                                                                      EMBL; D45419; BAA08258.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NONCOVALENTLY, ASSOCIATED (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR.
DOMAIN: THE HCE REPEAT IS A HIGHLY SPECIFIC PROTEOLYTIC CLEAVAGE AT A BELLY SIMILARITY).
SIGNAL (BY SIMILARITY).
PTM: EXISTS AS A FAMILY OF POLYPEPTIDES THAT ARISE THROUGH EXISTS AT ONE OR MORE CENTRALLY LOCATED SITES. CLEAVAGE AT A DEFINED SITE, PPCE/THET, WITHIN THE HCF REPEAT (BY
                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
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SIMILARITY: CONTAINS 5 KELCH REPEATS
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AND
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een the Swiss Institute
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8 x 26 AA APPROXIMATE REPEATS.
HCF REPEAT 1.
HCF REPEAT 2.
HCF REPEAT 3.
HCF REPEAT 4 (DEGENERATE).
HCF REPEAT 5.
HCF REPEAT 6.
HCF REPEAT 6.
HCF REPEAT 8.
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X
Score 223; DB 1;
Pred. No. 6.2e-05;
5; Mismatches 190
                                                                                                                                                                                                     KELCH 2.
KELCH 3.
                                                  E495E8B1F2385E17 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-S288c / AB972;
Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser
Centles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

NCBI_TaxID=4932;
                                                                                                                                              or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-31
STRAIN-SPX101-1C;
MEDLINE-89031230;
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Yamashita I., Naki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          981
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                                                                                                                                                                                                                                                                                                                                    glucose residues successively from non-rewith release of beta-D-glucose.
SIMILARITY: TO S. POMBE SPEC215.13.
SIMILARITY: SOME, TO S. POMBE SPCC285.13C.
                                                                                                                                                                                                                                                                                                                                                                                                                                   m Saccharomyces cerevisiae.";
S Lett. 239:179-184(1988).
CATALYTIC ACTIVITY: Hydrolysis
                                                                                                                                                                                                                                          European Bioinformatics Institute.
                        ; Z38061; CAA86176.1;
; M16164; AAA35014.1;
; M16165; AAA35015.1;
; X13857; CAA32069.1;
                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                           requires a license agreement (Some email to license@isb-sib.ch).
                                                                                                                                                                            non-profit institutions as iony and this statement is not removed.
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Nakamura M., Fukui
is a possible mechan
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from non-reducing ends of the ch
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PIR; S48478; S48478.
SGD; S0001458; MUC1.
Hydrolase; Glycosidase; Pol'
Signal; Multigene family.
I SIGNAL 1 21
T CHAIN 21 1367
TD DOMAIN 210 1367
TARBOHYD 817 817
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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  SEQUENCE FROM N.A TISSUE-Intestine;
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MIM; 158370; ...
InterPro; IPR000359; Cys_knot.
InterPro; IPR000561; EGF-like.
InterPro; IPR002400; GF_cysknot.
InterPro; IPR002919; TIL_Cysrich.
InterPro; IPR001007; WF_D.
InterPro; IPR001846; VWF_D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and polymorphism.;
J. Clin. Invest. 88:1005-1013(1991).
I. Clin. Invest. 88:1005-1013(1991).
I. FUNCTION: COATS THE EPITHELIA OF THE INTESTINES, AIRWAYS, AND OTHER MUCUS MEMBRANE-CONTAINING ORGANS. THOUGHT TO PROVIDE A PROTECTIVE, LUBRICATING BARRIER AGAINST PARTICLES AND INFECTIOUS AGENTS AT MUCOSAL SURFACES.
I. SUBUNIT: MULTIMERIC.
I. SUBCELULAR LOCATION: Secreted.
I. TISSUE SPECIFICITY: COLON, SMALL INTESTINE, COLONIC TUMORS, BRONCHUS, CERVIX AND GALL BLADDER.
INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).
INTERCHAIN DISULFIDE BONDS (BY SIMILARITY).
I. POLYMORPHISM: THE NUMBER OF REPEATS IS HIGHLY POLYMORPHIC AND VARIES AMONG DIFFERENT ALLELES.
II SIMILARITY: THE N-TERMINAL DOMAIN SHOWS SOME SIMILARITY TO THAT OF SILKRORM HEMOCYTIN.
I. SIMILARITY: CONTAINS 2 VWFC DOMAINS.
II SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE (CTCK) DOMAIN.
    Pfam; PF01826;
PRINTS; PR0041
SMART; SM00214
SMART; SM00216
PROSITE; PS0010
PROSITE; PS011
PROSITE; PS011
PROSITE; PS011
CHYCOPTOTE11;
CHYCOPTOTE11;
SIGNAL
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SEQUENCE OF 6:
TISSUE=Colon;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wum J.K. Jr., Hicks J.W., Toribara N.W., Siddiki B., Kim Y.S.;
"Molecular cloning of human intestinal mucin (MUC2) cDNA.
Identification of the amino terminus and overall sequence similarity to prepro-von Willebrand factor.";
J. Biol. Chem. 269:2440-2446(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Toribara N.W., Gum J.R. Jr., Culhane P.J., Lagace R.E., Hicks J.W., Petersen G.M., Kim Y.S.;
Petersen G.M., Kim Y.S.;
"MUC-2 human small intestinal mucin gene structure. Repeated arrays
                                                                                                                                                                                                                                                                                                       Genew;
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Gum J.R. Jr., Hicks J.W., Toribara
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Gum J.R. Jr., Hicks
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158370; -.
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                                                                                                                                                                                                                                                                                                                  L21998; AAB95295.1; -. M74027; AAA59875.1; -. M94131; AAA59163.1; -. M94132; AAA59164.1; -.
                                                                                           SM00214; VWC; 2
SM00216; VWD; 4
                                                                                                                         PR00438;
                                  PS00022; EGF_1; UNKNOWN_1.
PS01185; CTCK_1; 1.
PS01225; CTCK_2; 1.
PS01208; VWFC; 2.
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ks J.W., Toribar
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Eusecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Musccmorpha; Ephydroidea; Drosophilidae; Drosophila.
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Ballinger D.G., Xue N., Harshman K.D.;
"A Drosophila photoreceptor cell-specific protein, calcium and contains a leucine zipper.";
Proc. Natl. Acad. Sci. U.S.A. 90:1536-1540(1993).
                                            SEQUENCE FROM N.A.
STRAIN-Canton-S;
MEDLINE-93165730; PubMed-8434015;
                                                                                         Martin J.H., Benzer S., Rudnicka M., Miller C.A.; "Calphotin: a Drosophila photoreceptor cell calcium-binding Proc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).
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GTIPSPVSAPVAAPVTPSAVAAPVQVVSPAAVAPAAPIAVTPVAPPPTLASVQPATVT

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KKVAVTPVKKL-AQIGTTVVTTVPKPSSVQSVAVPTSVVT-VTPGKPLNTVTTLKPSSLG

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PVVAETPEVASVAVAETTPPVVPPVA-----

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zonadhesin gene (ZAN).";
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                                                                                                                                                                                                                                                                                                                               DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS. DOMAIN: THE VWFD DOMAIN 2 MAY MEDIATE COVALENT OLIGOMERIZATION (BY SIMILARTTY TO HUMAN INTESTINAL MUCIN MUC2).
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European Bioinformatics Institute.
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APICAL REGION OF THE SPERM HEAD
TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPI
DOMAIN: THE MAM DOMAINS PROBABLY MEDIATES SPERM
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
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an email to license@isb-sib.ch).
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CELL WALL PROTEIN DANA.

REMOVED IN MATURE FORM (POTENTIAL).

GPI-ANCHOR (POTENTIAL).

MW; 7954C15D69F0CA58 CRC64;
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P39712;
01-FEB-1995
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                                                                                                        CHAIN
                                                                                                                                         EMBL, U12980; AAC04971.1; -. SGD; S000059; YAL063C. InterPro, IPR001389; Flocculin. Pfam; PF00624; Flocculin; 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, 0
01-FEB-1996 (Rel. 33, I
01-FEB-1996 (Rel. 33, I
Hypothetical 138.1 kDa
                                                                                                                                                                                                                                                                                                                                                   STRAIN-S288c / AB972;
MEDLINE-95249563; PubMed-7731988;
Bussey H., Kaback D.B., Zhong W., Vo
                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Saccharor
                                                                                                                                                                                                                                                                                                                   cerevisiae.
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Storms R.K.;
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Last annotation update)
a protein in FLO9-GDH3 i
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Barton
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A.B., Su Y.,
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Best Local Similarity
Matches 118; Conser
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                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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SEQUENCE OF 1-2379 FROM N.A. MEDLINE-99018118; PubMed-9799793; Glockner G., Scherer S., Schattev
                                                                                                                                                                                                                                           1060
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                                        NCBI_TaxID=9606;
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                                                                       Homo sapiens
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                                                                                                                                                                                               AGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKC---
                                                                                                                                                                                                                                                                                 TSSLPPVTTTKTSEQTTLV----TVTSCESHVCTESISSAIVSTATVTVSGATTEYTTW
                                                                                                                                                                                                                                                                                                    TLSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPV----QIKLAQPGPVLSQP
                                                                                                                                                                                                                                                                                                                                             AKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVA--NTVTTVSLQPEKPVVSGTAV
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                                                                                                                                                                                                                                        CPISTTEITKQ----TTETTKQTKGTTEQTTETTKQTTVVTISSCESDVCSKTASPAIVST
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(Rel. 40, Last ann
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Primates;
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 Schattevoy
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annotation update)
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                                                  Craniata; Vertebrata; Catarrhini; Hominidae;
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R.,
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Homo.
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"Large-scale sequencing of analysis of 650 kb of reveals 17 genor
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Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        zonadhesin gene (ZAN).";
Genomics 41:119-122(1997).
-!- FUNCTION: BINDS IN A SPECIES-SPECIFIC
OF THE EGG. MAY BE INVOLVED IN GAMETE
                                                                                                                     DOMAIN
                                                                                                                                                                       Glycoprotein;
                                                                                                                                                                                                                              SMART;
                                                                                                                                                                                                                                                                      Pfam; PF00094; vwd;
                                                                                                                                                                                                                                                                                                                                      MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gao Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Testis; MEDLINE-97271566; PubMed-9126492;
                                                                                                                                 DOMAIN
                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                           interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNALING.
SUBGUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
SUBGELLULAR LOCATION: TYPE I MEMBRANE PROTEIN,
APICAL REGION OF THE SPERM HEAD (BY SIMILARITY)
TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAP
TOWN THE WAND FORMATINE DEFINABLY MEDIATE SPERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE T SPERMATOZOA OR PROMOTING ADHESION TO THE OUTDUCTAL DOMAIN: THE VWED DOMAINS 2 AND 3 MAY MEDIATE COVALE OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL SIMILARITY: CONTAINS 3.5 MAM DOMAINS.
SIMILARITY: CONTAINS 4.5 WWFD DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION ZONA PELLUCIDA.

DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE
                                                                                                                                                                                                                           PF00629; MAM; 4.; PF01826; TIL; 5.; PF02345; TILa; 4.; PF02345; VWD; 1.
                                                                                                                                                                                                                                                                                                                                     602372
                                                                                                                                                                                                                                                                                                                                                        AF053356; AAC78790.1; -. U83191; AAC51208.1: -
                                                                                                                                                                                                                                                                                                                                              HGNC:12857; ZAN.
                                                                                                                                                                                           ; PS01186; EGF_2;
; PS00740; MAM_1;
; PS50060; MAM_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harum1
                                                                                                                                                                                                                                                                             ; IPR000561; EGF-11ke.

; IPR00998; MAM_domain.

; IPR002919; TIL_Cysrich.

; IPR00338; TILa_Cysrich.

; IPR001846; VWF_D.
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. 8:1060-1073(1998).
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                                                   MAM 3.

MAM 4.

66 x HEPTAPEPTIDE REPI
(MUCIN-LIKE DOMAIN).

VWED 1 (PARTIAL).

VWED 2.

VWED 3.

VWED 4.

VWED 5.
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N-LINKED
N-LINKED
                                                                                                                                                                                  Cell
                                                                                                                   X HEPTAPEPTIDE REPEATS (APPROXIMATE)
                                                                                                                                                                                 adhesion;
                                                                                                                                                  (PARTIAL)
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(GLCNAC.
(GLCNAC.
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Viruses; dsDNA viruses, Ictalurid Herpes-like v NCBI_TaxID=10401; [1]

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PIR; F36791; F36791.
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Virology 186:9-14(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92087490; PubMed=1727613;
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STRAIN-Auburn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e by non-profit institutions as long as its content is in no way dified and this statement is not removed. Usage by and for commercial titles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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LKS-----SPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSP
                               TTPAMPTGANDTAN-ITTATPAGANDTANVTMPAGATDTVVTTTPAMPAGANDTANVTKP
                                                  LSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVE
                                                                       AGANDTANGTA-VTTTPAMPAGANDTANITTATPT--GANDTANVTMPAGATDTV---VT
                                                                                           SSVQSVAVPTSVVTVTPGKPLN----TVTTLKPSSLGASSTPSNEPNLKAENSAAVQIN 184
                                                                                                                NDTANITTATPAGANDTAVTTTSATPAGANDTAVTTTPATPAGANDTANDTVVTTTPAMP
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                                                                                                                                                                                                                                                                                                                                                         "The DNA sequence of equine herpesvirus-1."; Virology 189:304-316(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses;
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01-DEC-1992 (Rel.
01-DEC-1992 (Rel.
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                                                                                                                                                                                                                                                                                           use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92295566; PubMed=1318606; Telford E.A.R., Watson M.S., McBr
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Viruses; dsDNA viruses, no RNA stage; Herpesviri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTAATGGTTAGTG-----LLQTSKPLVTSVANTVTTVSLQP-----
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---SSSTAATSSSAPSTASSTTSIPTSTSTETTTTPTASTTTPTTTTAAPTTAAT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTAK-PTGANG----TVTTTTAKPAGANGTVTTTTAKPAGANGTVTTTTAKPAGANGTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTVTT----TTAKPTGANGTVTTTTAKPT--
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                                                                                                al Similarity
118; Conserv
                                                                                                                                                                                                                                                                   s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                            766
590
797
                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - VYTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVG
                                                                                                                                                                                                                     Transmembrane;
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24, Last
24, Last
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465
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                                                                                                                                                80342 MW;
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                                                                                                65;
                                                                                                                                                                                                                                                                              agreement
                                                                                                                                                                                                         Signal.
POTENTIAL.
                                                                                              Score 189.5; DB Pred. No. 0.0014; Mismatches 26
                                                                                                                                             POTENTIAL.

N-LINKED (GLCNAC. . .) (P
50C9ED9211F5E5B2 CRC64;
                                                                                                                                                                                 GLYCOPROTEIN
SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Herpesviridae;
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                                                                                                                    DB 1;
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                                                                                                                                                                                                                                                                                            Usage
                                                                                                                                                                                                                                                                                                                                                                                          A.J.;
                                                                                                                     Length
                                                                                              Indels 173;
                                                                                                                                                          (POTENTIAL)
                                                                                                                      797;
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RESULT 15
YJH8_Y
AC P47033
DT 01-FEB
DT 01-FEB
DT 01-FEB
DT 01-FEB
OS Saccha
OC Eukary
OC Saccha
OC SACCHA
ON HOLOT
RN [1]
RP SEQUEN
RC STRAIN
RX MEDLIN
RA MIOSIZ
RA BOLES
RA Zimmes
RT Sacch
RT Gacch
R
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01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 89.2 kDa protein in SCP160-SMC3
YJJ078C OR J1027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YJH8_YEAST
P47033;
O1-FEB-1996
                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence analysis of a 33.1 kb fragment from the left arm of Saccharomyces cerevisiae chromosome X, including putative proteins with leucine zippers, a fungal Zn(II)2-Cys6 binuclear cluster doma and a putative alpha 2-SCB-alpha 2 binding site."; Yeast 11:681-689(1995).
                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restitute the company of the comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miosga T., Schaaff-Gers
Boles E., Fournier C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-S288c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zimmermann F.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-96093911; PubMed-7483841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PDRPIIELGVATLRKNFMEASCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schaaff-Gerstenschlaeger I., Chalwatzis N.,
Fournier C., Schmitt S., Velten C., Wilhelm N
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SMART; SM00198; SCP; 1.
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X83502; CAA58492.1;
X88851; CAA61314.1;
P04284; ICFE.
 TNTVVPASSFP
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Search completed: February Job time: 25.6381 secs

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1: sp_archea:*
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Match
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1 GTLYTKVAPVSAPPKVSSGP......ASPTQKNRIKENVTSCFRDE 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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CKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVP
                                                                                                                                         I-----VNSVASSGYANSSQPPHLTQLNAQAP--QLPQI--TQIQTIPAQQSQQ---
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with a novel tandem repeat.";
Gastroenterology 106:200-200(1994).
EMBL: U10281; AAC48526.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
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LaMont J.T.;
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                                                                                                                                                     Score 233.5; DB 6
Pred. No. 1.4e-06;
                                                                                                                                                                                                                     OBF0F6879203B2EA CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update
Hypothetical 122.9 kDa protein.
H02F09.3.
Caenorhabditis elegans.
Chromadorea: Rhabdi
                                                                                                                                                                                                                                                              Wilson R., Alnscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Coulson
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston I
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkee
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of
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MEDLINE=94150718; PubMed=7906398;
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NCBI_TaxID=6239;
     SEQUENCE
                                                                                                                                     STRAIN-BRISTOL N2;
                                                                                                                                                                 SEQUENCE FROM N.A.
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sequence of C. elegans
itted (JUL-1998) to the
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EMBL/GenBank/DDBJ databases
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Matches
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Waterston R.;
Submitted (OCT-1998) to the E
EMBL; AF077538; AAC64622.1; -
HypothetLcal protein.
SEQUENCE 1275 AA; 122924 M
                                                                                                                                                                         MUCSAC.
HOMO sapiens (Human).
Homo sapiens (Human).
'harvota; Metazoa; Chordata;
'harvota; Primates;
                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                         Q8WWQ4;
                    SEQUENCE FROM N.A.
MEDLINE-21426417; PubMed-11535137;
MEDLINE-21426417; PubMed-11535137;
MEscande F., Aubert J.P., Porchet N., Butter Broad Brochem MUCSAC: organization repetitive region.";
Biochem. J. 358:763-772(2001).
                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GOKTMPVNTIIPTSQFPPASILKQITLPGNKILSLQAS
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  AJ298318;
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358:763-772(2001).
318; CAC83675.1; -.
                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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22.3%;
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Last annotation update)
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Pred. No. 1.
                                                                                                                                                                                             Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                                                     Buisine M.
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Best Local Sin
Matches 143;
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NON_TER
SEQUENCE
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                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caer
                                                                                                                                                                  Q9N4S7;
01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                       Q9N4S7
                                                                                                                                                                                                                                                                                                                                                                                         1182
                                      SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
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                                                                                                                                           Y51B11A.1
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  investigating biology.
                                                                                         NCBI_TaxID=6239;
                                                                                                                                                       Y51B11A.1 protein.
Genome sequence of the nematode C. elegans: a platform investigating biology. The C. elegans Sequencing Consort
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             V-GPT----AATGGTTAGTGLLQTSKPLVTSV-ANTVTTVSLQPEKPVVSGTAVTLSLP
                                                                                                                                                                                                                                                                                                            KTMPVNTIIPTSQFPPASILKQITLPGN----KILSLQASPT
                                                                                                                                                                                                                                                                                                                                                                                      QTSKTSAATSSTTSGSG-TTPSPVPTTS-TTSASTTSTTSAPTTSTTSGPG---TTPSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                        TSGPTTSTTLAPTTSTTSAPTTSTNSAPTTSTISASTTSTISAPTTSTISSPTSSTTSTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QDQQGPFKMCLNYEVRVLCCETPKGCPVTSTPVTA----PSTPSGRATSPTQSTSSWQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAEEFTRKL----YVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHGGDKETYNNIIRSGEKICRRPEEITRLQCRAESHPEVSIEHLGQVVQCSREEGLVCRN 1007
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                                                                                                                                                                                                                                                                                                                                    PSTSITSAATTSTTSAPTTRTTSAPTSSM---TSGPGTTPSPVPTTSTTSAPTTSTTSGP
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1349
1349
                                                                                                                                                                                                                                                                                                                                                                                                              -AVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPAGI 455
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                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                             -TGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQ
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15,
17,
                                                                                                      oda; Chromadorea;
Caenorhabditis.
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                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                                                 Q9QY35
Q9QY35;
                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Host cell factor C1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science [2]
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InterPro; IPR002595; P_Tich_extensn. PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 1079 AA; 110532 MW; 8DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The sequence of C. Submitted (MAR-1999)
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Best Local S
Matches 140
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MGD; MGI:1349215; Abcd1.
Interpro; IPR003961; FN III.
Interpro; IPR001798; Kelch.
Pfam; PF00041; fn3; 2.
Pfam; PF001344; KRlch; 4.
SMART; SM00060; FN3; 1.
Q8TE50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Comparative sequence analysis of the mouse L1cam locus corresponding region of human Xq28."; submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF133093; AAF22156.1; .
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NCBI_TaxID=10090;
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                                                                                                                                                                                  TAVTLSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKL-AQPGPVLSQP 452
                                                                                                                                                                                                          VVKGTTGYTTLGTVTGTVST--SLAGAGAHSTSASLATPITTLGTIATLSSQ----VINP
                                                                                                                                                                                                                             GAK--AGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVA--NTVTTVSLQPEKPVVSG
                                                                                           FPP 514
                                                                                                                  VHDLPVS-
                                                                                                                                      A-GIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQ
                                                                                                                                                              TAITVSAAQTTLTAAGGLTTPTITMQPV
                                                                                                                                                                                                                                                        KIITAVPKIATGHGQQGVTQVVLKGAPGQPGTILRTVPMGGVRLVTPVTVSAVKPAVTTL
                                                                                                                                                                                                                                                                               PVVT----TTVSSSQSEKSIIVSGA-----TAPRT------VSVQTLNPLAGPV
                                                                                                                                                                                                                                                                                                      VSPSTT----KPGTTTIIKTIPMSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAPA
                                                                                                                                                                                                                                                                                                                            PQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTT-----S 298
                                                                                                                                                                                                                                                                                                                                                                          FL--AMLIKLACSGSQSP-----EMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ASSPVMVSNPATRMLKTAAAQVGTSVSSAANTSTRPIITVHKSGTV-TVAQQAQVVTTVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VPAVLKVTGPQATTGTPLVTMRPASQ--AGKAPVTVT-SLPASVRMVVPTQSAQGTVIGS
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            PRELIMINARY;
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Pred. No. 3.5e-05;
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          PRT;
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RESULT 9
Q61191
ID Q611
AC Q611
DT 01-N
DT 01-N

Q61191; Q61191; 01-NOV-1996 01-NOV-1996

PRELIMINARY; (TrEMBLrel. (TrEMBLrel.

01,

Created)

2045

Last sequence update)

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hughes-Davies L.;
"EMSY is amplified in breast cancer and displays a BRCA2 damage response.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ430203; CAD22881.1;
SEQUENCE 1322 AA; 141467 MW; 7F8C95E8BA0FC9F0 CRC64,
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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                                                                                                                                                                                                                          SISPIMVVSSIGAIMTTKLYTTPTGTQATYTRPTVSPSIGRMAATPGAATYVKTTSGSII
                                                                                                             TTLLNAGGEKTIQTVP-----TGAKPAILTATRPITKMI---VTQPKGIGSTVQPAAKI
                                                                                                                                          S----S
                                                                                                                                                                                                                                                    TTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVT-----
                                                                                                                                                                                                                                                                                PSPVSHQQQPQQSPLPPGIKPTIQIKQ-----ESGVKIITQQVQPSKILPKPVTATLPTS
                                                                                                                                                                                                                                                                                                            KLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTT----TV
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EGKEEPQNYTDSSSSSTESSQSSQDSQPVVHVI
                                                     IPTKIVYGQQGKTQVLIKPKPVTFQATVV--SEQTRQLVT--ETLQQASRVAEAGNSSIQ
                                                                                                                                                                                               -----LHSVG-----PTAATGGTTAGTGLLQTSKPLVTSVANTV---TTVSLQPEKPVV
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                         -GGNEKQVTTISHSSTLTIQKCGQKTMPVNTII
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                                                                                                                                         -GTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPV-IGTPVQIK---
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                                                                               ---LAQPGPVLSQPAGIPTGSSSKQLFSLFHVVQQPS--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in breast cancer and displays a BRCA2 dependent DNA
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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RESULT 10
Q9QWH2
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AC Q9QWH
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Best Local (
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   Q9QWH2;
Q9QWH2;
01-MAY-2000
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Pfam; PF00041; En3; 2.
Pfam; PF01344; Kelch; 5.
SMART; SM00060; FN3; 1.
SEQUENCE 2045 AA; 210537 MW;
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Kristle T.M., Dashner R.;
"CDNAs encoding the mouse
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:105942; Hcfc1.
InterPro; IPR003961; FN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                   PVS-----ILASP-----TTEQPTATVTIADSGQGDVQPGTVTLVCSNPP
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Query Match
Best Local
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InterPro; IPR003961; FN_III.
InterPro; IPR001798; Kelch.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pfam; PF01344; Kelch; 5.
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    PVS---
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                                        PTGSSSKQLESLEHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPP 514
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CE 2045 AA; 210546 MW;
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Pred. No. 9.8e-05;
-TTEOPTATVTIADSGQGDVQPGTVTLVCSNPP
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US-10-025-380-1068
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CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1068
LENGTH: 5179
                                                                                                                                               GENERAL
                                              APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                              APPLICANT: Xu, Jiangchun APPLICANT: Lodes, Michae
                                APPLICANT:
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Local Similarity 21.9%;
ses 136; Conservative 6
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                                                                                                                                               INFORMATION:
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                         Meagher, Madeleine
Stolk, John A.
Wang, Tongtong
                                                                            Secrist, Heather
Benson, Darin R.
             Jiang,
                                                                                                              Lodes, Michael J.
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             Yuqiu
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                                                               Joy
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RESULT 5 US-09-833-263-1068

US/09833263

Sequence 1068, Application Patent No. US20020110547A1 GENERAL INFORMATION:

APPLICANT: Wang, Aijun APPLICANT: Clapper, J.

Clapper, Jon Stolk, John

Jonathan

APPLICANT:

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APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1068
LENGTH: 5179
TYPE: PRT
ORGANISM: Homo sapiens
US-09-922-217-1068
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Best Local Similarity
Matches 136; Conserv
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APPLICANT:
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                                                                                TAPIAEL -- TTSNPPPESSTPQTSRSTSSPLT--
                                                                                                                    SKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIP----TSQFPPAS
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Wang, Aijun
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21.9%;
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Pred. No. 5.8e-06;
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US-09-801-368-114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1068 LENGTH: 5179
                                                                                                         Sequence 114, Application US/09801368 Patent No. US20020128250A1
                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity Matches 136; Conserv
                APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Dou
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CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
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TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
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Madden, Kevin
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SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 114
LENGTH: 1322
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Best Local Similarity
Matches 118; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
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APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving
FILE REFERENCE: 109272.147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                663 LPTDETIIVIRTPTTATTAMTTTQPWNDTFTSTSTEITTVTGTNGLPTDETIIVIRTPTT 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 LPAPQ-IVAVKAPNTTTIQF----PANLQLPPGTVLIKSNSG------PLMLVSPQQT 68
                                                                                                                                                                                   TLSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPV----QIKLAQPGPVLSQP 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLAQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLN-TVTTLK-PSSLGASSTPSNEP 171
STATINGVTTEYTTWCPISTTESKQQTTLVTVTSCGSGVCSETTSP 1162
                                        KTMPVNTI - - - -
                                                                              CPISTTEITKQ----TTETTKQTKGTTEQTTETTKQTTVVTISSCESDVCSKTASPAIVST 1116
                                                                                                             AGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKC------GQ
                                                                                                                                                          TSSLPPVTTTKTSEQTTLV-----TVTSCESHVCTESISSAIVSTATVTVSGATTEYTTW 1059
                                                                                                                                                                                                                                          SKSSVIPTSS--STSGSSESETGSASSASSSSSISSESPKSTYSSSSLPPVTSATTSQEI
                                                                                                                                                                                                                                                                                                                                                                                                                                            LVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTAMTTTQPWNDTFTSTSTEMTTVTGTNGVPTD-ETVIVIRTPTSE-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTRAETT------SNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVK 113
                                                                                                                                                                                                                                                                                  AKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVA--NTVTTVSLQPEKPVVSGTAV
                                                                                                                                                                                                                                                                                                                          SDTSSLVISSSVTSSLVTSSPVISSSFISSP-----VISSTTTSASILSES------
                                                                                                                                                                                                                                                                                                                                                              S--SDMVIATCTTT--VTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WTGTFTSTSTEMTTITGTNGQPT-----DETVIIVKTPTTAISSSLSSSSGQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----NLKAENSAAVQINLSPTMLENVKKCKNFLAMLIK---LACSGSQSPEMGQNVKK 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GLISTTTEPWTGTFTSTSTEMTTVTGTNGQPTDETVIVIRTPTSEGLVTT-TTEP
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Milne, Todd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.1%; Score 195; DB 10;
20.1%; Pred. No. 3.8e-05;
ative 91; Mismatches 219;
                                   ---IPTSQFPPASILKQITLPGNKILSLQASP
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RESULT 7 US-09-801-368-104 ; Sequence 104, Application US/09801368 ; Patent No. US20020128250A1

INFORMATION:

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US-09-801-368-104
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LENGTH: 1537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/160,587 PRIOR FILING DATE: 1999-10-20 NUMBER OF SEQ ID NOS: 440
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CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
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ITLE OF INVENTION: Methods for Improving
ILE REFERENCE: 109272.147
                                                                                                                                                                                                                                              1174
1306 C-ESDVCSKTASPAIVSTSTATINGVTTEYTTWCPISTTESRQQTTLVTVTSC
                                                                                                                                                                                                                                                                                                                   1120 -----SSSVISSSVTSSLFTSSPVISSSVISSSTTTSTSIFSESSKSSVIPTSSSTSGS 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1040 LVTT-TTEPWTGTFTSTSTEMSTVTGTNGLPTD-ETVIVVKT-PTTAISSSLSSSSSGQI
                                                                                 1256 STATUTY-
                                                                                                                                                                1216 ETAS-----
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                                         496
                                                                                                                436 TPVQIKLAQPGPVLSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQK 495
                                                                                                                                                                                                                                                                               320 TAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTV 379
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                                                                                                                                                                                                380 TTVSLQPEKPVVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCWDHIC----KPVIG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 KKVAVTPVKKLAQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLN-TVTTLK-PSSLG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          938 TVIVIRTPTSEGLISTTTEPWTGTFTSTSTEVTTITGTNGQPTDETVIVIRTPTSE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                            QCVQQTSSDMVIATCTTTV-TTSPVVTTTVSS-----SQSEKSIIV-----SGA 319 `
                                   CGQKTMPVNTIIPTSQFPPASILKQITLPGNKILSLQASPTQKNRIKENVTSC 548
                                                                                                                                                                                                                                                                                                                                                                                                                                          GONVKKLYEQLLDAKIEAEEFTRKLYVELKSSPOPHLVPFLKKSVVALRQLLPNSQSFIQ 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GLISTTTEPWTGTFTSTSTEMTTVTGTNGQPTDETVIVIRTPTSEG 1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 6.5%; Score 179.5; DB 10; Length 1537;
Similarity 20.5%; Pred. No. 0.00049;
09; Conservative 82; Mismatches 195; Indels 147;
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Hecht, Peter
Holtzman, Doug
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Silva, Jeff
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No. US20020128250Alman,
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                                                                                                                                                                                                                                       -----AGSVSSSFISSESSKSPTYSS------SSLPLVTSATTSQ 1215
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                                                                                                                                                          -----SLPPATTTKTSEQTTLV-----TVTSCESHVCTESISPAIV 1255
                                                                                                                                                                                                                                                                                                                                                                                                  ------TSSRPIITPFYPS-----NGTSVI- 1119
                                                                           SGVTTEYTTWCPISTTETTKQTKGTTEQTTETTKQTTVVTISS
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RESULT 8 US-09-864-761-34248

Matches 123;

Similarity 22.4 23; Conservative

69;

Indels 155;

Gaps

26;

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SEQ ID NO 34248
LENGTH: 2665
                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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CURRENT FILING DATE: 2001-05-23
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Annomax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/774,203
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PRIOR FILING DATE: 2001-01-30
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OTHER
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                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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Hanzel, David K.
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                                                                                                                                                                                                                            EXPRESSED
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                                                                                                                                                                                                       D IN BONE MARROW, SIGNAL = 1.
D IN FETAL LIVER, SIGNAL = 8.
D IN ADULT LIVER, SIGNAL = 4.
D IN PLACENTA, SIGNAL = 1.
D IN HEART, SIGNAL = 7.2
D IN HEART, SIGNAL = 9.5
D IN BRAIN, SIGNAL = 9.5
                                                                                         IN HBL100, SIGNAL = 7.7
IN BT474, SIGNAL = 12.
HIT: AU117052.1. EVALUE 0.00e+00
HIT: P08640, EVALUE 3.00e-10
                                                                                                                                                                     IN HELA, SIGNAL = 7.
IN LUNG, SIGNAL = 9.
Score 177.5; DB
Pred. No. 0.0014;
9; Mismatches 20
                                     DB 10;
                                     Length 2665;
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US-09-862-027-40
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                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 40

LENGTH: 1501

TYPE: PRT

ORGANISM: C. elegans

US-09-862-027-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 40, Application US/09862027 Patent No. US20020142428A1 GENERAL INFORMATION:
                                                                                                                                                                Query Match
Best Local
                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                          APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: NO. US20020142428A1el Kinases
FILE REFERENCE: 35800/234862
CURRENT APPLICATION NUMBER: US/09/862,027
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-66-30
NUMBER OF SEQ ID NOS: 82
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                                                                                                                                                              Local Similarity
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NIPAMSPTSAQPQPVLS--PTSAAVPVPTTMIHVPKPSEIPVQNVATT----AA;VAANN 613
                                                                       TPIPPTPATPH-SSAQQQPIPPPLSTQ----TSAEIQQSAQQP
                                                                                                        TKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLVS 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NRIK-ENVTS 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KOVTTISHSSTLTIOKCGOKTM-PVNTIIPTSQFPPASILKQITLPGNKILSLQASPTOK 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTV----TMAGAVIAPSTK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLVS--PQ
                                 --PQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLA()IGTTV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQVKPDSVTA 2246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IAPKITSVISR-----MPVSIDLENSQKITLAKPAPQTLTGLVSA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVTPP----SDPSIPIPTLPSVTA-----AKLSPPVASGGIPHQSPPTKVTEWITR
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                                                                                                                                               Conservative
                                                                                                                                            6.4%; Score 176.5; DB 1
20.6%; Pred. No. 0.00082;
Live 93; Mismatches 244
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                                                                                                                                                                               DB 10;
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                                                                                ; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-110
                                                                                                                                                                                                         APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Se
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT APPLICATION NUMBER: US 09/487,558
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
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US-09-801-368-110
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  Query Match
Best Local Similarity
Matches 139; Conserv
                                                                                                                                                       NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version
SEQ ID NO 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                      TYPE: PRT
                                                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 APRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTG------LLQTSKPL 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVIGTPVQIKLAQPGPV---LSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHS 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATPISSSISTATV --- IPIVAATPTNI ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NVRKVSQESNAESVQSIPRPGGIIVM---SPTNQTDSAPPPTGAAAKPSRFQVTKSADPI 903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QLL-PNSQS--FIQQCVQQTSSDMVIATCTTTVTTSPVVTT--TVSSSQSEKSIIVSGAT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -TPSNEPNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQ-----SPEMGQN 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STLTIQKCGQKTMPVNTIIPTSQFPPASILKQITLP----
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                                                                                                                                         1075
                                                                                                                                                                                                                                                                                                                                                                                                                                 Royer, John
Salama, Sofie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. US20020128250Alman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maxon, Mary
Milne, Todd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Holtzman, Doug
Madden, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hecht, Peter
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Robert
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                      6.3%;
    80;
Score 174; DB 10;
Pred. No. 0.00072;
0; Mismatches 244;
                                                                                                                                                                                                                                                                                                                                                      Secondary Metabolite Production in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -TSEPVIVQPITAQVIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNKILSLQASPTQ 537
                                        Length 1075;
  Indels 174;
Gaps
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RA Beeson K.T. Benos P.V. Berman B.P. Bhandari D. Bolshakov S.RA Borkova D., Betchan M.R. Bouck J. Brokstein P., Brottier P., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Chandra I., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Glods R., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA McInculov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Palazzolo M., Pitman G.S., Pan S., Pollard J., Purl V., Reese M.G., RA Nelson D.R., Strong R., Sun E., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA 
  Query Match
Best Local S
Matches 130
                                                                                    EMBL; AE003421; AAF45644.1; -...
EMBL; AL03102B; CAA19845.2; -..
FlyBase; FBgn0025390; Eg:5667.1.
InterPro; IPR002557; Chitin_bind_PerA.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF01607; CBM_14; 2.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00494; ChtBD2; 2.
SEQUENCE 1795 AA; 194464 MW; 07F10C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Basenca P V Rarman R.D. Rhandari D. Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                 Cadieu E., Dreano S., Lelaure V., Mottier S., Galibert F.; "Sequencing the distal X chromosome of Drosophila melanogaster."; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                               Submitted (APR-1999)
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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EG:56G7.1 OR CG14796
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01-JUN-2002 (TrEMBLrel.
    al Similarity
130; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
    Conservative
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                       20.2%;
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V., Berman B.P., Bhandari D., Bolshakov S.,
                                            7.8%;
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Last
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                                            Score 214.5;
  Pred. No. 9e-
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                                                                                        07F10C129BD9557B
                       9e-05;
                                          DB 5;
    254;
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                                                                                      CRC64;
                                            Length 1795;
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., Baldwin D.,
  173;
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Gaps
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                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=21845432; PubMed=11855812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21,
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                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8TDH7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8TDH7
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                                                                                                                                                                                   .R. Jr., Crawley S.C., Hicks 7, a novel membrane-tethered em. Biophys. Res. Commun. 291
                              Similarity
                                                                                                          1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                          Ä
                                                                                                                                                            AAL89737.1;
                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
                           21.9%;
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    Last sequence update)
    Last annotation updat
    MUC17 (Fragment).

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                         Score 214; DB 4;
Pred. No. 4.9e-05
                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                cks J.W., Szymkows
red mucin.";
291:466-475(2002)
                                                                                                       5E1AD19E4BF948E3 CRC64;
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                                                  Length 1029;
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Query Match
Best Local Sin
Matches 135;
  Conservative
  76;
  Mismatches
  Indels
 146;
 Gaps
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P913612
P91361
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P91365;
01-MAY-1997
01-MAY-1999
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Submilted (JAN-1997) to the EMBI
-I- ALTERNATIVE SPLICING OF THE
ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                       K06A9.1.
                              VARSPLIC
                                                                                                         EMBL; U80846; AAC70889.1; EMBL; U80846; AAC70890.1;
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                        Alternative
                                                                                                                                                                                                                                                         STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-6239;
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                                                                      VARSPLIC
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                              870
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                                                                                                                                                                                                                                                                                                                                        Nematoda; Chromadorea; rinae; Caenorhabditis.
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                                                                                                                                                                       EMBL/GenBank/DDBJ databases.
WO FORMS (A AND B) MAY BE PRODUCED
THE SAME GENE. THE SEQUENCE SHOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                     VASSSPAPSTSQNPNPSTSSGSSMI -> LATTSAPKPSVT
CLEMYD (IN ISOFORM B).
PYPSQSTSPVESSTTPSPGSPGTTLTSTSPSPSQSTTIGST
      QGSTSPGISTTSEEMTSQGSTQTPGSTGSTVTQPSTVSDST
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata;
Pterygota; Neoptera; Endopterygota; Diptera
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                           01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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                                                                                                         CPN protein.
CPN OR CG4795.
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                                                                                                                                                                                                                                                                                                                                                                                                                    TTTGEMTSHGSTQTPSTIGSTVTQPSTVSGSNSSGSTVTIGSSEASTSGSSFKTSPSSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTLTSISPSPSQSSTIGSSQGSTSPVVSTTSGDMTSQGSTQIP-----GSTGSTVTQPST
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                                                                                                                                                                                                                                                                                                                                      PVPTSSPIPSTTFASST-SGSTISDVSSVST
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                                                                                                                                                                                                                                   PRELIMINARY;
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13,
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Last sequence
Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 212.5;
Pred. No. 0.
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SSQSTSPVESSTSGATSSGSSGFTTLTSISPSPSPSSTIGS
SQGSTSPVESTISQSSTE -> KEIDQTAINTKTYFNAL
LVASKLINGSILTGYIDNFGYSAGLNDHQYPPTDDYNGIKS
VPFPIDGTDDDIDLDLKDVDKSLATADWTPPVADQTCMIFI
SAAPEDEYGGTTIKSTYTYFFTVVGVLVGGAKSIPGLSIDK
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                                        cheata; Hexapoda; Insecta;
Diptera; Brachycera; Musc
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                                          Muscomorpha;
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RA Doubin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Goog F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mcrkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mchason D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Woodage T., Worles K.G., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R., F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,
RA Zhense, Fennollonzia, Cor,
RT The genome sequence of Drosophila melanogaster.";
DR EMBL, AE003694; AAP54755.1; ..
DR EMBL, AE003697; AAP54755.1; ..
DR EMBL, AE003697; AAP54755.1; ..
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Best Local
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InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Asburnar M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
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SEQUENCE FROM N.A.
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RQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRT
                                                                                                                                  PVAAPVAAVPAAVPVVAPVLAPAVAPAVAPVVAETPAPPPVAEIPVATIPEC---VAPLI
                                                                                                                                                                               PSSLGASSTPSNEPNLKAENSAAVQINLSPTMLE-----
                                                                                                                                                                                                                            PPVAATPTPVAPIPVAAPVIATPPVAASAPTPAAVTPVVSP--VIATPPVVPANTTV---
                                                                                                                                                                                                                                                                       KKVAVT-----PVKKLAQIGTT--VVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLK 157
                                                                                                                                                                                                                                                                                                                    IPAPAPIAAASVAPVASVAP---PVVAAPTPP-----AASPVSTPPVAVAQIPVAVSAPVA 116
                                                                                                                                                                                                                                                                                                                                                            LPPGTVLIKSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNS-SSQLI 104
                                                                                                                                                                                                                                                                                                                                                                                                            GTTPSPVSAPVAAPVTPSAVAAPVQVVSPAAVAPAPAAPTAVTPVAPPPTLASVQPATVT
                                                                                     KLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVAL
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                                             -PEVSVVATKPLAAAEPVVVAPPATETPVVAPAAASPHVSVAPAVETAVVA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82242 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.7%; Score 212; DB 5; 22.1%; Pred. No. 5.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81; Mismatches
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  324
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                                          278
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RESULT 15
Q95U45
ID Q95U44
AC Q95U4
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AC Q95U4
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Best Local S
Matches 125
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Q95U45;
01-DEC-2001 (TTEMBLTel. 1
01-DEC-2001 (TTEMBLTel. 1
01-MAR-2002 (TTEMBLTEL. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J. Champe M., Chavez C., Dorsett V., Farfan D., Frise E., Georg Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AV058315; AAL13544.1; -. FlyBase; FBgn0010218; Cpn. EMBL, CEBGCEBOCBC9802 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=7227;
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        265
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Search completed: February 16, 2003, 21:58:53 Job time: 50.77 secs

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      The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity -
quantitating a
                                                                                                                                                        Claim
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                                                                                                                                                                                     biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 supplement;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome mapping; gene mapping; gene therapy; forensic; upplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                              RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                     SEQ ID No 39827; 103pp; English.
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polypeptide
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Best Local
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N-PSDB;
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                Polypeptide encoding TATA box binding protein associated factor II 105 useful for treating e.g. cancers and inducing apoptosis has a dominant negative effect on the normal biological activity of the binding
                                                                                                                                                                            Dikstein
                                                                                                                                                                                                                            27-AUG-1998;
                                                                                                                                                                                                                                                                              09-MAR-2000.
                                                                                                                                                                                                                                                                                                                                                      Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcription factor; apoptosis; cytostatic; immunosuppressive; antiinflammatory; virucide; antibacterial.
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                                                                                                                                      2000-256640/22.
DB; AAZ90465.
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This represents a polypeptide comprising a (modified) fragment (I) a TATA box-binding protein associated factor II 105 (TAFII105). A pharmaceutical composition comprising (I) or the polynucleotide or

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02-JUN-2000;
07-JUL-2000;
                     pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as attached the content of the co
                                                                                                                                                                                                                                                                                                                                                     polypeptides. The proteins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions caused by p. acnes. The disorders include SAPHO syndrome (synovitis, acne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes vaccinating against and
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for treating autoimmune
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   determining
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, Jen S, Carter
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joint; central nervous system; ELISA;
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irter D;
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presence,
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example,
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are used in
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RESULT 5
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Best Local
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15-SEP-2000;
06-NOV-2000;
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Note: The sequence data for this patent did no specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                  sequence is a polypeptide encoded by a cDNA an expressed sequence tag (EST) found to be foetal tissue cDNA libraries.
                                                The invention relates to novel foetal polypeptides encoded by polynucleotides comprising one of 477 sequences fully defined in the specification. The foetal polypectides and polypeptides are useful in the treatment and diagnosis of diseases such as cancers, immune disorders, growth disorders (e.g. osteoporosis), thrombolytic disorders, nervous system disorders and inflammation. The present
                                                                                                                                                         Novel fetal proteins useful for the treatment and diagno associated with dysfunction of the protein e.g. cancers, disorders, growth disorders, thrombolytic disorders, ner
                                                                                                                                                                                                                                 Yeung Liu C,
                                                                                                                          Claim 10; Page 258; 715pp; English.
                                                                                                                                                                                                    N-PSDB;
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growth disorder;
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                                                                                                                                                  disorders
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                                                                                                                                                                                                                                                                                                                                                                                                               nervous system
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Asundi V,
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2000US-0663870.
2000US-0707351.
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Zhou P, W
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80
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                                                                                                                                                                                                                                                                                                                                                                                                                inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombolytic; osteopathic; an apy; cancer; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71
                                                                                                                                                                                                                                   Werhman
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Pred. No. 5
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directly from
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                                                                                                                                                                                                                                            YT;
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Query Match

Sequence

71

8

Best Local Similarity

70

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Score Pred.

No.

DB 4.3;

22;

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The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a modern as the control of consideration of sites expressing (II). (I) and (II) are useful for treating CC imaging of sites expressing (II). (I) and (II) are useful for treating CC diagnostics, forensics, gene mapping, identification of mutations in CC diagnostics, forensics, gene mapping, identification of mutations considered the produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed considered in the format directly from WIPO at the content of the format directly from WIPO at the content of the format directly from WIPO at the content of the format directly from WIPO at the content of the format directly from WIPO at the content of 
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                       Query Match
Best Local S
Matches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID No 44366; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-639362/73.
N-PSDB; AAS78194.
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23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
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                       Similarity
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                     0;
                     Score 42; DB Pred. No. 30; 0; Mismatches
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05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
11-MAY-1999;
14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
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05-MAR-1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
29-MAR-1999
01-APR-1999
06-APR-1999
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16-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein identification; signal transduction pathway; metabolic pathway; hubridiaation assay; genetic mapping; gene expression control; promoter;
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9908-0130510
9908-0131449
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99US-0128234.
99US-0128714.
99US-0129845.
99US-0130077.
99US-0130449.
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20-AUG-1999
20-AUG-1999
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AAU00449 standard;

Protein;

362

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19-JUN-2001 AAU00449;

(first entry)

Arabidopsis 17-OCT-2000

thaliana protein fragment SEQ

Ħ NO: (first entry)

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RESULT 9
AAG29892
                                                                                                                                                                                 Query Match
Best Local
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    AAG29892;
                                                                                                                                                                                                                                                                 disease resistance protein in a plant. The polynucleotides encoding the disease resistance proteins are useful for increasing resistance in a plant to disease, controlling cell death, and conferring resistance to herbicides. They are useful as probes or amplification primers in the detection, quantification, or isolation of gene transcripts. They can be used for recombinant expression of their encoded polypeptides, as immunogens in the preparation and/or screening of antibodies, and in sense or antisense suppression of the polynucleotide in a host cell,
                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                     resistance polynucleotide operably linked to a promoter, or by culturing the plant cell under plant growing conditions to produce a regenerated plant, or by inducing expression of the polynucleotide to modulate the
                                                                                                                                                                                                                                                                                                                                                                                                                                and transgenic plants including maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley or millet. The level of disease resistance protein is increased by transforming a plant cell with a recombinant expression cassette which comprises the disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated maize disease resistance polynucleotide useful for increasing resistance in a plant to disease, controlling cell death, and conferring resistance to herbicides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize; plant disease resistance; crop; soybean; sunflower; sorghum; canola; wheat; alfalfa; cotton; rice; barley; millet; plant cell death; herbicide resistance; ZmPtil-1; Ptil; Ptol.
                                 AAG29892 standard; Protein; 365 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a Zea mays gene homologue to the plant disease resistance genes Ptil and Ptol in tomato. These novel maize disease resistance polynucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence representing maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 89-90;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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                            Arabidopsis thaliana protein fragment SEQ ID NO: 35640.
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14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
21-0CT-1999;
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21-0CT-1999;
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21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
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25-OCT-1999;
25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
            6-Transmembrane protein; SDR2; cancer; inflammation; autoimmunity; allergy; asthma; rheumatoid arthritis; CNS inflammation; cerebellar degeneration; Alzheimer's disease; Parkinson's disease; multiple sclerosis; amylotrophic lateral sclerosis; head injury damage; neurological abnormality; septic shock; sepsis; stroke; osteoporosis; osteoarthritis; ischaemia reperfusion injury; cardiovascular disease; kidney disease; liver disease; ischaemic injury; myocardial infarction; hypotension; hypotension
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13-OCT-1999
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13-0CT-1
                                                                                                                                                                             A 6-Transmembrane
                                                                                                                                                                                                                12-MAY-1999
                                                                                                                                                                                                                                                   AAW97359;
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14-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                              (first entry)
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99US-0161404.
99US-0161405.
99US-0161406.
99US-0161359.
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99US-0159331.
99US-0159637.
99US-0159638.
99US-0159584.
99US-0160741.
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99US-0161993.
99US-0162142.
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99US-0160768.
99US-0160770.
99US-0160814.
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990S-0161361
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99US-0157865
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                                                                                                                                                                           protein designated SDR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.48;
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 aplastic
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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50;
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   male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 397;
pattern
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                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Matches

Conservative

2;

Mismatches

0;

Indels

0,

Gaps

0

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Query Match
Best Local
                                                                                                   determining SDR2 polypeptide expression levels. SDR2 polypeptides can be used to screen for agonists and antagonists and to produce antibodies. Diseases diagnosed, prevented and treated include: cancer, inflammation, autoimmunity, allergy, asthma, rheumatoid arthritis, CNS inflammation, cerebellar degeneration, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amylotrophic lateral sclerosis, head injury damage, and other neurological abnormalities, septic shock, sepsis, stroke, osteoporosis, osteoarthritis, ischaemia reperfusion injury, cardiovascular disease, kidney disease, liver disease, ischaemic injury, myocardial infarction, hypotension, hypertension, AIDS, myelodysplastic syndromes and other hematological abnormalities, aplastic anaemia, male
                                                                                                                                                                                                                                                                                                                                                                                       New 6-Transmembrane protein (SDR2) polypeptide and polynucleotide useful as diagnostic reagents and for prevention and treatment of cancer, AIDS and microbial infections
                                                                                          syndromes and other pattern baldness,
                                                                                                                                                                                                                                                                           diagnosing susceptibility to diseases by detecti
gene, and can diagnose diseases associated with
                                                                                                                                                                                                                                                                                                           The present designated s
                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Albone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-DEC-1997;
12-AUG-1997;
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Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                        Page
                                                                                                                                                                                                                                                                                      t sequence represents a 6-Trans
SDR2, SDR2 polypeptides and po
susceptibility to diseases by
                                                              592 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kikly KK;
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97US-0055375.
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                                                                                                                                                                                                                                                                                                                                                     19pp;
                                                                                          and bacterial,
                77
75
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                 .08;
                              .48;
                Score 41;
Pred. No.
                                                                                        fungal,
                                                                                                                                                                                                                                                         6-Transmembrane protein polypeptide s and polynucleotides are useful for asses by detecting mutations in the SDR2 ssociated with SDR2 protein imbalance by ession levels. SDR2 polypeptides can be
              DB
74;
                                                                                          protozoan
                              20;
                              Length 592;
                                                                                          infections
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ABP11105
ID ABP1
AC ABP1
AC ABP1
AX 24-J
DY 24-J
XX XX
XX Huma
AXX
KW Huma
KW hype
KW hype
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                                                                                                                                                                                                                                                                       RESULT 12
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                                                                    Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
               myasthenia
                             autoimmune
                                                                                                                                                 Human
                                                                                                                                                                                                            ABP11105;
                                                                                                                                                                                                                                         ABP11105
                                           hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease;
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                                                                                                                                                 ORFX protein
                                                                                                                                                                                                                                         standard;
               gravis
                             disorder;
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                                                                                                                                                                                                                                                                                                                   165
                                                                                                                                                                                                                                                                                                                                               10
                                                                                                                                                 sequence SEQ ID NO:22192.
                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                              entry)
                                          disorder;
                                                                                                                                                                                                                                         63
                            thyroiditis;
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Homo sapiens

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RESULT 13
ABB03730
ID ABB03
XX
AC ABB03
XX
DT 08-JA
XX
KW Cytos
KW antis
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                                                                                                                                                                                                                                                                                                              Best
                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (referred to as open reading frame, ORFX, where X is 1-1191 (see Table in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer
                                                                                                                                                                                                                                                                                                                                                                            lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune thoroders as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. OREX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The
                                         Human musculoskeletal system related polypeptide SEQ ID NO 1677.
                                                                         08-JAN-2002
                                                                                                    ABB03730
                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                 N.B. The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
                                                                                                                              ABB03730 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID 22192; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shimkets RA,
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                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention
                                                                                                                                                                                                                            AQPGPVLSQP 10
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DB; ABN26857.
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                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                       Conservative
                                                                      (first entry)
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                                                                                                                              Protein; 113
                                                                                                                                                                                                                                                                   75.5%;
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                                                                                                                              A
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                                                                                                                                                                                                                                                                                                                                                 or form part of the printed format directly from WIPO
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                                                                                                                                                                                                                                                                                Length 63
                                                                                                                                                                                                                                                      Indels
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1-11491
    antiulcer;
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 14-AUG-2000;

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14-AUG-2000;
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26-JUL-2000;
14-AUG-2000;
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cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
neurological disease; infection; human; secreted protein;
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17-MAR-2000;
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                        2000US-0229509

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2000US-0230437

2000US-0231243

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2000US-0231414

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2000US-0227009.
2000US-0228924.
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2000US-0225270.
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2000US-0217487.
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2000US-0215135.
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2000US-0209467
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Sequence Listing;

English.

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21-SEP-2000

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2000US-0249264
2000US-0249265
2000US-0249299
2000US-0249299
2000US-0259160
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2000US-02517198
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2000US-0234274.
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2000US-0239937.
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ABG20476
ID ABG20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel genes (AAL34669-AAL37666) and proteins C (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, c antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and cother cancers of the adrenal gland, bone, bone marrow, breast, c discretise autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; c multiple sclerosis diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 7
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11-DEC-2000;
05-JAN-2001;
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 parasitic infections.

Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis -
               31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis
                                                                              30-MAR-2001; 2001WO-US08631.
                                                                                                                           11-OCT-2001
                                                                                                                                                                    WO200175067-A2
                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                         Human; chromosome mapping;
                                                                                                                                                                                                                                                                                                                      Novel
                                                                                                                                                                                                                                                                                                                                                                                                           ABG20476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG20476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11;
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                                                                                                                                                                                                                                                  food supplement;
                                                                                                                                                                                                                                                                                                                                                                18-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 OPGPTLROP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 QPGPVLSQP 10
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DB; AAL35312.
                                                                                                                                                                                                                                                                                                                   human diagnostic protein #20467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 AA;
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; 2000US-0254097.
; 2001US-0259678.
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               2000US-0540217
2000US-0649167
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                                                                                                                                                                                                                                                       medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
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77.8%;
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                                                                                                                                                                                                                                                       imaging;
                                                                                                                                                                                                                                                  gene mapping; gene therapy; forensic;
maging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome cc and gene mapping, and in recombinant production of (II). The cc and gene mapping, and in recombinant production of (II). The cc and gene mapping, and in recombinant production of (II). The cc and gene mapping, and in recombinant production of (II). The cc are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (II) is useful for generating antibodies against it, detecting or committating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating cc imaging of sites expressing (II). (I) and (II) are useful for treating cc disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in classometics, forensics, gene mapping, identification of mutations composition for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cc amino acid sequences. ABG00010-ABG30377 represent novel human cc diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO cat fits wipe, introubplished pot sequences.
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                                                                                                                                         Human; leucine-rich repeat; LRR; AZAD; neurodegenerative disorder; CNS disorder; central nervous system disorder; prostatite disorder; prostatitis; benign prostatite typerplasia; adenocarcinoma; prostatite cancer; genitourinary system carcinoma; testicular tumour; hlzheimer's disease; dementia; parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis; epilepsy; psychiatric disorder; mania; depression; schizophrenia; anxiety; phobic disorder; learning disorder; memory disorder; ammesia; migraine; protein interaction;
                                                                                                                                                                                                                                                                                                                                                                  07-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE03611 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                            Human
                                                                                                                                                                                                                                                                                                                                                                                                        AAE03611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biodiversity
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                                                                       Homo sapiens
                                                                                                             forensic identification;
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)B; AAS84663.
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8; Conserv
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                                                                                                                                 activity; neoplastic
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                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                             gene therapy
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38;
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CC Parking of disease, multiple sclerosis, amytrophic lateral sclerosis, epilepsy, psychiatric disorders e.g. depression, schizophrenic cdisorders, mania, anxiety or phobic disorders, learning or memory cdisorders e.g. amnesia or age-related memory loss, and neurological disorders e.g. migraine. AZAD molecules are useful as markers of cdisorders e.g. migraine. AZAD molecules are useful as markers of cdisorders or disease states, as markers for precursors of disease state or as markers for precursors of disease state, companies of disease state or as markers of drug activity or cplanucleotide are capable of modulating protein protein interaction, cc e.g. by interacting with an extracellular component, thereby modulating cellular activities, including attachment, adhesion, migration, cc patterning, growth and/or differentiation of a cell. AZAD proteins crequiate embryonic development and differentiation, tissue maintenance and function, pathological conditions, e.g. neuronal degeneration, cc neoplastic transformation and tumour progression. AZAD proteins are useful to screen for drugs or compounds which modulate its activity. AZAD proteins are useful as immunogens to raise anti-AZAD antibodies which are useful to screen for drugs or compounds which modulate AZAD substrates and useful as primers or hybridisation compounds which modulate AZAD activity. AZAD capable of the AZAD protein are useful in gene therapy. AZAD sequences are also cuseful to map their respective genes on a chromosome, for tissue typing and in forensic identification of a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human AZAD protein which is a multiple leucine-rich repeat-containing secreted protein. AZAD polypeptide is useful for identifying a compound which modulates its activity and binds to it. AZAD proteins and nucleic acid molecules are useful for treating and diagnosing AZAD-mediated or related disorders, which includes a neural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorder (e.g. neurodegenerative disorders, including CNS disorders) and a prostate disorder, e.g. prostatitis, benign prostatic hyperplasia and cancer (e.g. adenocarcinoma, prostate cancer, genitourinary system carcinomas and testicular tumour). The neurodegenerative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New leucine-rich repeat-containing protein and nucleic acid molecules for diagnosing, treating neural disorders, such as neurodegenerative disorders, such as Alzheimer's disease, dementia, epilepsy and prosta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-DEC-2000; 2000WO-US33140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a leucine-rich repeat of human AZAD protein which is a multiple leucine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  include Alzheimer's disease, dementias related to Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۲,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
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Result
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Perfect
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,
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3: /cgn2_6/ptodata/2,
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5: //gn2_6/ptodata/2,
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1 AQPGPVLSQP 10
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Gapop 10.0 , Gapext 0.5
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Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 60/055,375
PTILING DATE: 12-AUG-1997
COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                  APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Patterson, Chandra
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: GROWTH-ASSOCIATED TRYPSIN-TYPE
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REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                    158 PGPIISQP 165
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STRANDEDNESS: sir
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SOFTWARE: FastSEQ for Windows Version 2.0
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SEQUENCE CHARACTERISTICS:
LENGTH: 942 amino acids
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                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: WORD Perfect 6.1/MS-DOS 6.2
CURRENT APPLICATION DATA:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0505 US
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US,
FILING DATE: HEREWITH
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                                                 ATTORNEY/AGENT INFORMATION: NAME: Cerrone, Michael C
                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
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CITY: Palo Alto
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ZIP: 94304
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REGISTRATION NUMBER: 39,
REFERENCE/DOCKET NUMBER:
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Guegler, Karl J
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                                                                                             09/074,579
                                                                                                                                                          US/09/388,774
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Score 37;

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Length 349;

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RESULT 6
US-09-161-241-8
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                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                         Sequence 8, Application US/09161241 Patent No. 6344541
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
SEQ ID NO 72
                                    SOFTWARE: PatentIn
SEQ ID NO 8
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                                                                                                APPLICANT: Bass, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
APPLICANT: Wang, Daguang
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-548
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Compositions affecting TITLE OF INVENTION: death and their use in
                                                                         CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
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              LENGTH:
TYPE: PR
                                                            NUMBER OF SEQ ID NOS:
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TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pinus radiata
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6; Conserv
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650-845-4166
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Pred. No.
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Pred. No.
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Best Local :
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US-08-887-518-4
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US-08-791-115B-6
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                                                                                                                                Sequence 4, Application US/08887518 Patent No. 5843721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION MADER: US/08/791,115B FILING DATE: 30-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Ihnen, Jeffrey L.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: 5CIENCE & TECHNOLOGY LAW
ADDRESSEE: SCIENCE & TECHNOLOGY LAW
STREET: 268 BUSH STREET, SUITE 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 202-683-6040
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APPLICANT:
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APPLICANT:
                                                                                  APPLICANT: Rothe, Mike APPLICANT: Wu, Lin
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: A TUMOR SUPPRESSOR DESIGNATED TS10Q23.3
                                                               TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
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                                                                                                                                                                                                                                  126 PGPVLSLP 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 38,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09023321 Patent No. 5844073
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION UMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICANT:
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                                                                                                                                              PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wu, Lin
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide
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                                      T97-008
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                                          US-09-032-475-4
                                                          RESULT 11
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US-08-890-853-2
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                                                                                                                                                                                                                           US-08-890-853-2
          Sequence 4, Application US/09032475 Patent No. 5854003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 2, Application US/08890853
Patent No. 5851812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local :
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Goeddel, David V. APPLICANT: Woronicz, John TITLE OF INVENTION: IKK- Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                      682 SQPGQLMSQP 691
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                                                                                                                                                                                                                                                                   STRANDEDNESS:
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STRANDEDNESS: sir
                                                                                                                                  1 AQPGPVLSQP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                    amino acid
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Pred. No. 1.2e+02;
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Pred. No. 1.2e+02;
                                                                                                                                                                Mismatches
                                                                                                                                                                                          Length 756;
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                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09099125A Patent No. 5916760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                           CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                         ITLE OF INVENTION: IKK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                               STREET: 268 BUSH STREET, CITY: SAN FRANCISCO
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CLASSIFICATION:
                                                                                                                                               COUNTRY:
                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AQPGPVLSQP 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INVENTION: NIK Proteins, Nucleic Acids and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OSMAN,
                                                                                                                                                                 CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                       Goeddel, David V.
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                                                       PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
                                                                                                                                                                                              SCIENCE & TECHNOLOGY LAW GROUP
8 BUSH STREET, SUITE 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                         US/09/099,125A
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                                                                                                                                                                                                                                                      Proteins, Nucleic Acids and Methods
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Pred. No.
                                                         Version #1.30
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; MOLECULE TYPE: US-09-099-124A-2
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INFORMATION FOR SEQ ID NO:
                                                                                                   TELEFAX: (415) 343-43 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                             REFERENCE/DOCKET NUMBER: T9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      682 SQPGQLMSQP 691
                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                          STRANDEDNESS
                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                        ENGTH:
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T: 268 BUSH STREET, SUITE 3200
SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 60.06; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     94104
                                                          amino acid
                                                                                                                                                                                        OSMAN, RICHARD
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                                                                      756 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                (415)
             peptide
                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
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Pred. No.
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Query Match

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Score 37;

DB

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Length 756;

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US-08-890-854-2
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US-09-032-476-2
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Best Local Similarity 60.0
                                                                                                         Sequence 2, Application US/08890854 Patent No. 6235512
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Matches 6; Conserv
                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cao, Zhaodan
APPLICANT: R gnier, Catherine
TITLE OF INVENTION: IKK-\ Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: Sir
TOPOLOGY: linear
MOLECULE TYPE: pepi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: T9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
                        APPLICANT: Cao, Zhaodan
APPLICANT: R gnier, Catherine
TITLE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods
                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO
                                                                                                                                                                                                                          1 AQPGPVLSQP 10 :||| ::|||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                  756 amino acids
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Pred. No. 1.2e+02;
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3; Mismatches 1;
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                                                                                                                                                                                                                                                                                                   Length 756
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//Search completed: February 16, 2003, 22:02:59 
/ Job time : 2.25696 secs
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                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-08-890-854-2
                                                                                                       Query Match
Best Local Similarity bull
Conservative
                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 343-4342 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 756 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                682 SQPGQLMSQP 691
                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: T9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                               1 AQPGPVLSQP 10
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                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CALIFORNIA
                                                                                                                                                                                                                                  linear
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                                                                                                                                Score 37; DB 4;
Pred. No. 1.2e+02;
3; Mismatches 1
                                                                                                                                                               DB 4; Length 756;
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /cgn2_6/ptodata/2/pubpaa/U
2: /cgn2_6/ptodata/2/pubpaa/U
3: /cgn2_6/ptodata/2/pubpaa/U
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13: /cgn2_6/ptodata/2/pubpaa/U
14: /cgn2_6/ptodata/2/pubpaa/U
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length: 2000000000
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53
1 AQPGPVLSQP 10
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0 US-09-764-877-1677

0 US-09-789-404-14

0 US-09-789-404-2

1 US-09-944-403-55

1 US-09-944-896-55

9 US-09-944-907-55

9 US-09-944-907-55

9 US-09-944-907-55

9 US-09-944-907-55

9 US-09-944-907-55

9 US-10-176-58-60

9 US-10-175-737-60

9 US-10-175-738-60

9 US-10-175-738-60

9 US-10-175-738-60

9 US-10-176-482-60

9 US-10-176-913-60

9 US-10-176-913-60

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9 US-10-176-913-60
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                                                                    Sequence 1677, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 55, Appl
Sequence 60, Appl
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Sequence
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
38	38	38	38	38	38	38	38	38	38	38	38	3 8	38	38	38	38	38	38	38	38	38	38	38	38	38
71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7	71.7
694	694	694	694	694	694	694	694	694	694	694	694	694	694	694	694	694	694	694	694	694	694	694	694	694	694
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-09-944-396	-945-019	-945-587	944-862	944-457	944-	6-028		6-993-	6-992-	US-10-176-991-60	6-987-	US-10-176-985-60	6-750-	6-747-	5-492-	US-10-176-488-60	-10-175-743-	-10-175-740-	US-10-175-739-60		82-	79-	US-10-174-572-60	9	US-10-180-557-60
55,	55,	55,	Sequence 55, Appl			e 55,	_	60,	60,	60,	60,	Sequence 60, Appl	60,	60,	Sequence 60, Appl	60,	,09		60,	60,	•	60,	60,	Sequence 60, Appl	•

ALIGNMENTS

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RESULT 2
US-09-789-404-14
; Sequence 14, Application US/09789404
; Patent No. US20020025554A1
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; APPLICANT: Khodadoust, Mehran
                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (67)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (73)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-877-1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
US-09-764-877-1677
US-09-764-877-1677; Sequence 1677, Application US/09764877; Patent No. US20020147140A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prior application data removed - refer to PALM NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1677
LENGTH: 113
TYPE: PRT
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                              102 QPGPTLRQP 110
                                                                                                                                                                                                                                     2 QPGPVLSQP 10
                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                   75.5%;
77.8%;
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                                                                                                                                                                                                                                                                             Mismatches
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RESULT 3
US-09-789-404-2
; Sequence 2, Application US/09789404
; Patent No. US20020025554A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens US-09-789-404-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-789-404-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2
LENGTH: 794
TYPE: PRT
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Best Local S
Matches 8
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Patent No. USLC.
INFORMATION:
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APPLICANT: Khodadoust, Mehran
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                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                          APPLICANT: Baker, APPLICANT: Botst
                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US
CURRENT FILING DATE: 2001-02-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 10448/008001
CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2001-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ
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NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2001-02-20 PRIOR APPLICATION NUMBER: 09/456,592 PRIOR FILING DATE: 1999-12-08
                                                                        APPLICANT:
                                                                                                                                                                          APPLICANT:
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TYPE: PRT
                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                           55, Application US/09944413
5. US20020156004A1
 INVENTION:
                                                                                                     Gurney, Austin
Hillan, Kenneth
                                                                                                                                      Godowski, Paul
Grimaldi, Christopher
                                 Roy, Margaret
Tumas, Daniel
                                                                     Napier, Mary
                                                                                      Kljavin, Ivar
                                                                                                                                                                          Goddard, Audrey
                                                                                                                                                                                        Gerritsen, Mary
                                                                                                                                                                                                          Filvaroff, Ellen
                                                                                                                                                                                                                          Ferrara, Napoleone
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                                                                                                                                                                                                                                                           Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
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CURRENT FILING DATE: 2001-09-26
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APPLICATION NUMBER: 60/069,278
APPLICATION NUMBER: 11, 1997
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APPLICATION NUMBER: PCT/US99/20407
ETITING DATE: No. US20020156004Alember 30, 1999
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APPLICATION NUMBER: 60/069,696
FILING DATE: December 16, 1997
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APPLICATION NUMBER: 60/074,086
FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/074,092
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NUMBER: PCT/US00/05841
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US-09-944-413-55
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NUMBER OF SEQ ID NOS: 120
SEQ ID NO 55
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PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
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PRIOR APPLICATION NUMBER: PCT/US01/06520
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CURRENT FILING DATE: 2001-09-26
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TYPE: PRT
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APPLICATION NUMBER: 60/069,278
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FILING DATE: December 12, 1997
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US-09-944-896-55
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Sequence 55, Application US/09944896
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GENERAL INFORMATION:
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NIMBER: PCT/US99/12252
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Pred. No.
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Botstein,David

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PRIOR FILING DATE: December 11, 199
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PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
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FILING DATE: February 0
                               APPLICATION NUMBER: PCT/US99/21090 FILING DATE: September 15, 1999
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FILING DATE: MATCH 3, 1999
APPLICATION NUMBER: PCT/US99/12252
FILING DATE: June 22, 1999
                                                                                                                                                                                                                                                               FILING DATE: December APPLICATION NUMBER: 60 FILING DATE: July 28, APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                    FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/146,222
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APPLICATION NUMBER: 50/075,945
APPLICATION February 25, 1998
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APPLICATION NUMBER: 60/074,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: December 17, 1997
APPLICATION NUMBER: 60/068,017
FILING DATE: December 18, 1997
APPLICATION NUMBER: 60/070,440
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Tumas, Daniel
Wood, William
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Godowski, Paul
Grimaldi, Christopher
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Filvaroff, Ellen
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NUMBER: 60/112,850
NUMBER: 16, 1998
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; ORGANISM: Homo
US-09-944-896-55
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Best Local :
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SEQ ID NO 55
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CURRENT APPLICATION NUMBER: US/09/944,9
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/886,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
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APPLICATION NUMBER: 60/069335
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FILING DATE: March 30,
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FILING DATE: NO. US20020168715Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
FILING DATE: December1, 1999
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Tumas, Daniel
Wood, William
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Grimaldi, Christopher
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Pred. No.
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; ORGANISM: Homo Sapien US-09-944-944-55
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ENGTH: 694
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DR APPLICATION NUMBER: 60/U

R FILING DATE: February

R APPLICATION
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R APPLICATION N
FILING DATE:
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APPLICATION NUMBER: 09/254,311
FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
FILING DATE: June 22, 1999
APPLICATION NUMBER: PCT/US99/21090
                                                                                        APPLICATION NUMBER: PCT/US01/06520 FILING DATE: February 28, 2001 R OF SEQ ID NOS: 120
                                                                                                                                                                                    APPLICATION NUMBER: 22, 2000 FILING DATE: May 22, 2000 PCT/US00/20710
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APPLICATION NUMBER: 60/112,850
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FILING DATE: March 2,
                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US00/04414
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US00/03565
                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: December 16,
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US99/30095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US99/28301
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                                                                                                                                                                                                                                                                                                                               ILING DATE: February
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1 NUMBER: 60/146,222
28, 1999
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NUMBER: 60/074,
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NUMBER OF SEQ ID NOS: 120
SEQ ID NO 55
LENGTH: 694
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-907-55
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Best Local S
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Best Local :
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CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
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6; Conser
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Wood, William
                                                               Godowski, Paul
Grimaldi, Christopher
                                                                                                      Gerritsen, Mary
                                                                                                                 Filvaroff, Ellen
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Hillan, Kenneth
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         Kljavin, Ivar
Napier, Mary
                                   Hillan, Kenneth
                                                                                         Goddard, Audrey
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                                                 Gurney, Austin
                                                                                                                                               Eaton,Dan
                                                                                                                                                       Botstein, David
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Pred. No.
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RESULT 11
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US-10-174-590-60
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US-10-174-590-60
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LENGTH: 694
TYPE: PRT
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Gurney, Austin L
                                                                             Sequence 60, Application US/10176758 Publication No. US20030008353A1 GENERAL INFORMATION:
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Best Local :
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SEQ ID NO 55
LENGTH: 694
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Best Local :
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                           APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
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CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
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Goddard, Audrey
Godowski, Paul J
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66.78;
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                                                                                                                                                                                                                                                          Score 38; DB Pred. No. 75; Mismatches
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Pred. No.
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Query Match
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Best Local Similarity
Thes 6; Conserve
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US-10-173-706-60
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; ORGANISM: Homo
US-10-176-758-60
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Sequence 60, Application US/10173706
Publication No. US20030022293A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                        Prior Application removed
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 60
LENGTH: 694
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LENGTH: 69
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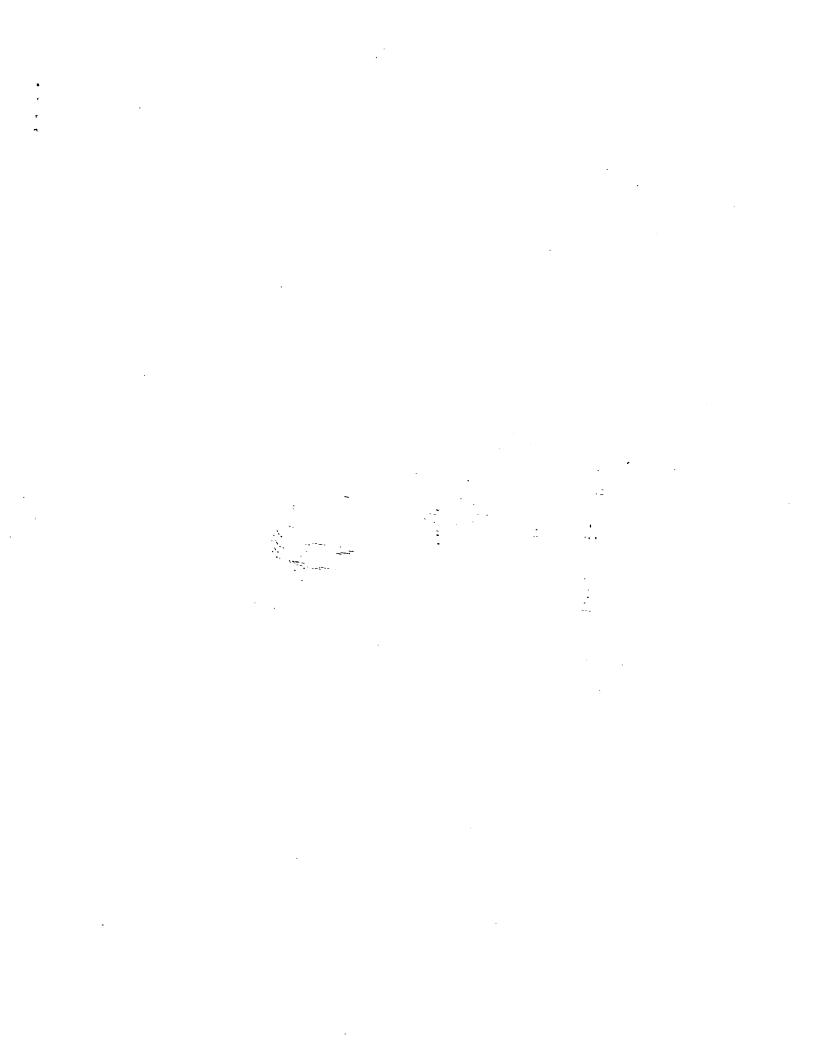
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C104
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CURRENT FILING DATE: 2002-06-19
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CURRENT FILING DATE: 2002-06-21
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                                                                                                                                      2 QPGPVLSQP 10
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658 QPGPLLKKP 666
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Gurney, Austin L.
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Godowski, Paul
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Pred. No.
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Pred. No. 75;
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RESULT 15
US-10-175-752-60
; Sequence 60, Application US/10175752
; Publication No. US20030022295A1
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CURRENT FILING DATE: 2002-06-17
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 60
LENGTH: 694
TYPE: PRT
ORGANISM: Homo Sapien
US-10-173-706-60
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US-10-175-738-60
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US-10-175-738-60
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Matches
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 60
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Publication No.
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2002-06-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C7
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APPLICANT:
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                                                                                                658 OPGPLLKKP 666
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                                                                                                                                                                         Local Similarity
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Goddard, Audrey
Godowski, Paul J
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Godowski, Paul J.
Gurney, Austin L.
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Gurney, Austin L.
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                                                                                                                                                          Conservative
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66.7%;
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66.7%;

    See File Wrapper or Palm

                                                                                                                                                                         Score 38; DB
Pred. No. 75;
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Pred. No. 75;
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; SEQ ID NO 60
; LENGTH: 694
; TYPE: PAT
; ORGANISM: HOMO S
US-10-175-752-60
Search completed: February 16, Job time: 2.197 secs
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APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
                                                                                                                               Matches
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                                                                                                                                                                                                                                                                         Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
                                                                                                                                                                                                                                                                                                      FILE REFERENCE: P3430R1C60
CURRENT APPLICATION NUMBER: US/10/175,752
CURRENT FILING DATE: 2002-06-19
                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                              658 QPGPLLKKP 666
                                                                                              2 QPGPVLSQP 10
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Goddard, Audrey
                                                                                                                               Conservative
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   February 16, 2003, 22:01:05; Search time 3.52891 Seconds (without alignments) 1827.005 Million cell updates/sec
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53
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                                                                                                                         /cgn2_6/ptodata/2/paa/US088_COMB.pep:*
/cgn2_6/ptodata/2/paa/US089_COMB.pep:*
/cgn2_6/ptodata/2/paa/US090_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US06_COMB.pep:*
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/paa/US087_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB ID	DB	ID	Description
	53	100.0	685	27	US-60-243-468-1271	Sequence 1271, Ap
N	53	100.0	801	ᆫ	PCT-US01-08631-39827	Sequence 39827, A
ω	53	100.0	843	_	PCT-US02-29964-410	Sequence 410, App
4	53	100.0	852	21	US-09-763-909-2	Sequence 2, Appli
տ	53	100.0	865	سر	PCT-US02-25829-25	Sequence 25, Appl
6	43	81.1	71	\vdash	PCT-US01-02723-214	Sequence 214, App

RESULT 2

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-10-242-515-16 -US01-08631-50 -09-417-507-28	-543-091-2 01-01338-167 -764-877-167	-10-219-999-	09-708-427-171 US02-27143-71	09-513-996A-3564	S-09-602-472-6	-09-791-	-573-655B-	-09-573-655A-	-09-513-996A-	-10-219-999-3 -60-324-109-1	-09-708-427-5	-09-655-073-1	-10-219-999-51795	S-09-791-537-1144	-513-996A	-09-478-081-504	-09-708-427-54	S-60-324-109-25	S-10-219-999-38	5-10-219-999-49	09-708-427-54°	S-60-324-631-2	-US02-30474-29	-US01-08631-44	S-60-365-384-25	-60-365-384-5	09-707-351-2
5083 287	e 2, App 1677, A 1677,	e 44:	71, 1	Sequence 35640, A	equence 60, A	equence	equence 1205,	equence 1205,	equence 35641,	e 33627, e 18893.	e 54706,	14, App	51795,	Sequence 1/1/, Ap	1717	Sequence 504, App	54707,	25624,	equence 38659	equence 4984	o 5470	0	2979,	equence 44366	equence 254	e 578,	equence 21

ALIGNMENTS

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; TYPE: PRT
; ORGANISM: HUMAN
US-60-243-468-1271
                                                                                                                                                                                                                                                                                                                                                                              US-60-243-468-1271
; Sequence 1271, Application US/60243468
                                                                                                                                                                             SOFTWARE: Fas
SEQ ID NO 1271
LENGTH: 685
                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                 Matches
                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                               APPLICANT: Beasley, Ellen TITLE OF INVENTION: USCLATITILE OF INVENTION: AUGLESTILE REFERENCE: CL000929
                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/60/243,468
CURRENT FILING DATE: 2000-10-27
                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
473 AQPGPVLSQP 482
                                                               Local Similarity
nes 10; Conserv
                              1 AQPGPVLSQP 10
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                                                            100.0%;
illarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                               ISOLATED HUMAN DRUG TARGET PROTEINS,
NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
AND USES THEREOF
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                                                               Score 53; DB Pred. No. 12; O; Mismatches
                                                                                              27; Length 685;
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                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/323,739
PRIOR FILING DATE: 2001-09-19
PRIOR PELICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
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LENGTH: 801
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CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: PCT/US02/29964 CURRENT FILING DATE: 2002-09-19
                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/US01/02623 PRIOR FILING DATE: 2001-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 809ACIP PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 60736 SOFTWARE: Custom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/649,167 PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/540,217 PRIOR FILING DATE: 2000-03-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEPLICANT: Drmanac, Radoje T
ITLE OF INVENTION: Novel Nucleic Acids and
ITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT:
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                      FILING DATE: 2000-04-2/
SAPPLICATION NUMBER: PCT/US01/03800
STITUS DATE: 2001-02-05
                                                                                                                FILING DATE: 2001-01-25
APPLICATION NUMBER: US 09/496,914
FILING DATE: 2000-02-03
                                                                           APPLICATION NUMBER: US 09/560,875 FILING DATE: 2000-04-27
                                                                                                                                                                                                APPLICATION NUMBER: US 09/491,404 FILING DATE: 2000-01-25
APPLICATION NUMBER: US 09/515,126 FILING DATE: 2000-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQPGPVLSQP 452
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10; Conserv
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Haley-Vicente, Dana
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Goodrich, Ryle W.
Weng, Gezhi
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Wang, Jian-Rui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ghosh, Malabika
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens PCT-US02-29964-410
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GENERAL INFORMATION:
APPLICANT: Dikstein, Rivka
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SEQ ID NO 2
LENGTH: 852
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Best Local (
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NUMBER OF
SOFTWARE:
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TITLE OF INVENTION: A TRANSCRIPTION FACTOR TEIID SUBUNIT,
TITLE OF INVENTION: TAFILIOS, POLYPEPTIDES, DNA ENCODING THEREFOR
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS
FILE REFERENCE: 13005/002001
                                                                                                                                                                                                                                                                                                     APPLICANT:
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10; Conserv
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10; Conserv
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                                                                                                                                  ELLIOTT, Vicki S.
EMERLING, Brooke M.
FORSYTHE, Ian J.
GIETZEN, Kimberly J.
GORVAD, Ann E.
                                                                                                                                                                                                                                                                                                                INCYTE GENOMICS, INC
                                                                                        HONCHELL,
                                                                                                      HAFALIA, April
                                                                                                                                                                                                           BOROWSKY, Mark L.
BURFORD, Neil
DUGGAN, Brendan M.
                                                                                                                                                                                                                                                        BLAKE, Julie J.
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Sally
Soo Yeun
                                              Preeti G
                                                           Farrah A.
                               Ernestine A.
                                                                                                                                                                                                                                                                     , Shanya D.
                                                                                                                                                                                                                                                                                      Mariah R.
                                                                                                                      Jennifer A.
                                                                                          Cynthia D.
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2001-02-26
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Pred. No.
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Pred. No.
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PPLICANT:

EHR-MASON, Patricia M.

Joana X. Dyung Aina M.

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CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: US 60/313,111
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 60/314,682
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/314,756
PRIOR APPLICATION NUMBER: US 60/315,105
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/315,105
PRIOR APPLICATION NUMBER: US 60/316,751
PRIOR APPLICATION NUMBER: US 60/316,751
PRIOR APPLICATION NUMBER: US 60/316,751
PRIOR FILING DATE: 2001-08-31
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Best Local Similarity
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SOFTWARE: PERL Program
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APPLICANT:
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TITLE OF INVENTION: NUCLEIC ACID ASSOCIATED PROTEINS
FILE REFERENCE: PF-1146 PCT
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OTHER INFORMATION: Incyte
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ORGANISM: Homo sapiens
FEATURE:
                 TTLE OF
                                  PPLICANT:
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                                                                                                                                                                                                                                                                                                               512 AQPGPVLSQP 521
                                                                                                                                                                                                                                                                                                                                  1 AQPGPVLSQP 10
   REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/316,856
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                 T: Wehrman, Thomas INVENTION: NOVEL
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                                              Tang, Y. Tom
Liu, Chenghua
Asundi, Vinod
Zhou, Ping
                                                                                                Drmanac, Radoje T.
Tang, Y. Tom
                                                                                                                               Arterburn, Matthew C.
                                                                                                                                                               Yeung, George
Ford, John E.
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SPRAGUE, William W.
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                                                                                                                                              Boyle, Bryan J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WARREN,
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                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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HOVEL FETAL NUCLEIC ACIDS AND POLYPEPTIDES 21272-020
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Pred. No. 15;
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US-60-365-384-578
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                                                                Sequence 578, Application US/60365384 GENERAL INFORMATION:
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Best Local (
                                                                                                                                                                                                                                                                                                      SOFTWARE: |
SEQ ID NO 214
                                                                                                                                                                                                 Matches
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Best Local
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SEQ ID NO 214
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                                         APPLICANT:
                                                 APPLICANT: Tang, Y.
                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/707,351
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Wang, Jian-rui
Wang, Zhiwei
Zhang, Jie
Zhou, Ping
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Liu, Chenghua
Asundi, Vinod
Zhou, Ping
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Pred. No.
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US-60-365-384-254
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US-60-365-384-578
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CURRENT FILING DATE: 2002-03-14
NUMBER OF SEQ ID NOS: 666
SOFTWARE: Pt_ft_genes Version 6.0
SEQ ID NO 578
LENGTH: 71
TYPE: PRT
                                                                                                                             SOFTWARE: pt_FL_genes Version 6.0 SEQ ID NO 254 LENGTH: 91
                                                         Query Match
Best Local
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Best Local S
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CURRENT FILING DATE: 2002-03-14
                                                                                                                                                                 NUMBER OF SEQ ID NOS:
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40 SRPGPVLSEP 49
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SRPGPVLSEP 49
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7; Conservative
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Wang, Dunrui
Weng, Gezhi
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Asundi, Vinod
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Wang, Jian-Rui
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Wang, Zhiwei
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Pred. No. 41;
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Sequence 44366, Application PC/TUS0108631
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
ITITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POI
FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
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Thes 8; Conserve
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LOCATION: (1)...(348);
OTHER INFORMATION: Xaa = X or * as defined in Table
PCT-US01-08631-44366
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PCT-US01-08631-44366
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SEQ ID NO 44366
LENGTH: 348
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PRIOR FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
                                                                                                                                                                                                                                                APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 810CIP PCT
CURRENT APPLICATION NUMBER: PCT/US02/30474
CURRENT FILING DATE: 2002-09-24
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ORGANISM: Homo sapiens
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                                                                   APPLICATION NUMBER: US 09/491,404 FILING DATE: 2000-01-25
                                                  APPLICATION NUMBER: PCT/US01/02623
                                   FILING DATE:
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Asundi, Vinod
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Wang, Jian-Rui
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TUMBER: US 09/496,914
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Pred. No. 3.3e+02;
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Best Local Similarity
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FERTURE:
NAME/KEY: misc_feature
LOCATION: (1)...(348)
OTHER INFORMATION: Xaa = a
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CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                            APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: NOVEL Nucleic
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 810
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APPLICANT:
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OR APPLICATION NUMBER: US 09/552,317
OR FILING DATE: 2000-04-25
OR APPLICATION NUMBER: PCT/US00/35017
OR FILING DATE: 2000-12-22
OR APPLICATION NUMBER: US 09/491,404
OR FILING DATE: 2000-01-25
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                                      APPLICATION NUMBER: US 09/560,875 FILING DATE: 2000-04-27 APPLICATION NUMBER: PCT/US01/03800 FILING DATE: 2001-02-05
                                                                                                    APPLICATION NUMBER: US 09/496,914 FILING DATE: 2000-02-03
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FILING DATE: 2000-04-27
APPLICATION NUMBER: PCT/US01/03800
FILING DATE: 2001-02-05
APPLICATION NUMBER: US 09/515,126
FILING DATE: 2000-02-28
FILING DATE: 2000-02-28
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APPLICATION |
                           APPLICATION NUMBER: US 09/515,126
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Jian-Rui
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NUMBER: US 09/577,409
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Pred. No.
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; ORGANISM: Zea mays
US-10-219-999-44244
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                                                                                                        SEQ ID NO 44244
LENGTH: 235
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 44244,
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                                                                                                                                                                                                           APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
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LOCATION: (1)...(348)
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                                                                               ORGANISM:
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FILING DATE: 2000-04-18
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8; Conserv
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Hinkle, Gregory J.
Kovalic, David K.
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              77.4%; Score 41; 100.0%; Pred. No.
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Pred. No. 3.3e+02;
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PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-08-15
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 63520
SEQ ID NO 49842
LENGTH: 255
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..250
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..250
; OTHER INFORMATION: Ceres Seq. ID 1933788
US-09-708-427-54708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-219-999-49842 : Sequence 49842, Application US/10219999 ; GENERAL INFORMATION:
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US-10-219-999-49842
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US-09-708-427-54708
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Matches 8
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TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243P

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: Patentin version 3.1

SEQ ID NO 54708

LENGTH: 250

TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                           Query Match
Best Local Similarity
Matches 8; Conserv
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APPLICANT:
                                                                                                                                                                                                                                                                                                        APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cao, Yongwei
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AQPGPVLS 63
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Kovalic, David K.
Liu, Jingdong
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                                                                Conservative
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                                                            77.4%; Score 41; 100.0%; Pred. No. tive 0; Mismatch
                                                                  Mismatches
                                                                DB 26; I
. 3.4e+02;
ches 0;
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1 AQPGPYLSQP 10
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US-09-602-472A-60
PCT-US02-10366-58
US-10-155-923A-60
US-10-125-923A-60
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US-10-1174-575-60
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US-10-1187-755-60
US-10-1197-755-60
US-10-1197-755-60
US-10-1197-749-60
US-10-1199-672-60
US-10-129-672-60
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213, Appl
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6510, Ap
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Sequence 236, App	Sequence 236, App	Sequence 3, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 23821, A	Sequence 23821, A	Sequence 11392, A	Sequence 2, Appli	Sequence 525, App	Sequence 8, Appli	Sequence 2090, Ap	Sequence 7, Appli	Sequence 13166, A	Sequence 2472, Ap	Sequence 1535, Ap	Sequence 1513, Ap	Sequence 1766, Ap	

ALIGNMENTS

PCT-US02-32727-6510

Sequence 6510, Application PC/TUS0232727 GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer

RESULT 1

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RESULT 2
US-10-057-498-6510
Sequence 6510, Application US/10057498
; GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
APPLICANT: Skeiky, Yasir
APPLICANT: Persing, David
TITLE OF INVENTION: Compositions and Methods fo:
FILE REFERENCE: 210121.514
CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
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LENGTH: 136
TYPE: PRT
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Best Local
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER: OF SEQ ID NOS: 30992
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61 ARPGPVLPQP 70
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Barth, Brenda
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Bhatia, Ajay
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Jones, Robert
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Lodes, Michael
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Persing, David
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Pred. No.
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Sequence 60, Application US/09602472A

GENERAL INFORMATION:

APPLICANT: Bidney, Dennis L.

APPLICANT: Hu, Xu

APPLICANT: Hu, Xu

APPLICANT: Li, Guihua

FILE REFERENCE: 35718/200630

CURRENT APPLICATION NUMBER: US/09/602,472A

CURRENT FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: 06/140,876

PRIOR APPLICATION NUMBER: 06/140,876

PRIOR FILING DATE: 1999-06-24

NUMBER OF SEQ ID NOS: 64

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 60

LENGTH: 370
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US-10-057-498-6510
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                                                                                                                                                                                                                                                                                                                                 PCT-US02-10366-58
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SEQ ID NO 6510
LENGTH: 136
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8; Conservative
                                   Vernet, Corine
Spytek, Kimberly
Malyankar, Uriel
Patturajan, Meera
Miller, Charles
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Kekuda, Ramesh
Rastelli, Luca
                                                                                                                                                                                                      Smithson, Glennda
Guo, Xiaojia
                                                                                                                                                                                                                                                                                                                   Application PC/TUS0210366
                                                                                                           Tchernev, Veli:
Gangolli, Esha
                                                                                                                                                                              Gerlach, Valer
Casman, Stacie
                                                                                                                                                                                                                                    Mezes, Peter
           Heyes, Melvyn
                           Taupier, Raymond J.
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b; Pred. No. 48;
0; Mismatches
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Pred. No.
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Query Match
Best Local Similarity
Whiches 8; Conserve
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; ORGANISM: Homo sapiens
PCT-US02-10366-58
                                                                                                                     PRIOR APPLICATION NUMBER: 09/489,847
PRIOR FILING DATE: 2000-01-24
PRIOR PPLICATION NUMBER: PCT/US99/17130
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: 60/094,657
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: 60/095,486
PRIOR FILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-05
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NUMBER OF SEQ ID N
SEQ ID NO 58
LENGTH: 775
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PRIOR FILING DATE: 2002-04-02
PRIOR PPLICATION NUMBER: 00/281086
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/281906
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/282020
PRIOR FILING DATE: 2001-04-06
PRIOR PRIOR DATE: 2001-04-06
PRIOR PRIOR DATE: 2001-04-10
PRIOR FILING DATE: 2001-04-10
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                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2003-01-27
PRIOR APPLICATION NUMBER: 60/350,898
PRIOR FILING DATE: 2002-01-25
                       PRIOR APPLICATION NUMBER: 60/096,319
PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: 60/095,454
PRIOR FILING DATE: 1998-08-06
                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/351,334
CURRENT FILING DATE: 2003-01-27
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CURRENT FILING DATE: 2002-04-03
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                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: 98 FILE REFERENCE: PZ031P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/283710
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Pred. No. 2e+02;
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Length 694;

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; LOCATION: (597)
; OTHER INFORMATION: Xaa
US-10-351-334-213
; ORGANISM: Homo Sapien
US-10-125-923A-60
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 213
                                                               Remaining Prior A
NUMBER OF SEQ ID
SEQ ID NO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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FEATURE:
NAME/KEY: SITE
LOCATION: (265)
OTHER INFORMATION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C79
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                                  TYPE: PRT
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les 6; Conserv
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                                                                                                                FILING DATE: 1997-10-28
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APPLICATION NUMBER: 60/063540
FILING DATE: 1997-10-28
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                                                                                                                                 APPLICATION NUMBER: 60/063544
                                                                                                                                               APPLICATION NUMBER: 60/063541
FILING DATE: 1997-10-28
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Godowski, Paul J.
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Pred. No. 2.3e+02;
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                                                                                              File Wrapper or PALM
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US-10-174-575-60
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LENGTH: 694
TYPE: PRT
ORGANISM: Homo Sapien
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Best Local
Sequence 60, Application US/10174575
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
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Best Local Similarity
Matches 6; Conser
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PRIOR FILING DATE: 1997-09-18
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FILING DATE: 1997-10-21
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Pred. No. 2.6e+02;
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Pred. No. 2.6e+02;
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APPLICANT:

Desnoyers, Luc

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; NUMBER OF SEQ ID NOS: 61
; SEQ ID NO 60
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-575-60
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US-10-174-575A-60
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Best Local Similarity
Matches 6; Conserv
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APPLICANT:
                             TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P34430R1C35
CURRENT APPLICATION NUMBER: US/10/174,575A
CURRENT FILING DATE: 2002-06-18
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: 10/052586
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CURRENT APPLICATION NUMBER: US/10/174,575
CURRENT FILING DATE: 2002-06-18
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PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
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APPLICATION
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                                                                                                                                                                    Smith, Victoria Watanabe, Colin K. Wood, William I.
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Godowski, Paul
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Godowski, Paul
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; ORGANISM: Homo Sapien
US-10-174-575A-60
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Best Local Similarity
Matches 6; Conserv
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 60
LENGTH: 694
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                                                                                                                            PRIOR
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CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US/10/052,586
PRIOR FILING DATE: 2002-01-15
PRIOR FILING DATE: 2002-01-15
                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1997-09-18
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                                                                                                       FILING DATE: 1997-10-24 APPLICATION NUMBER: 60/
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FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/063486
FILING DATE: 1997-10-21
             APPLICATION NUMBER: 60/0
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FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/063541
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Godowski, Paul J.
Gurney, Austin L.
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Pred. No. 2
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US-10-187-749-60
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US-10-187-749-60
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 60
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LENGTH: 69
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NUMBER OF SEQ ID NOS: 612
EQ ID NO 60
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CURRENT FILING DATE: 2002-07-01
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TYPE: PRT
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658 QPGPLLKKP 666
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FILING DATE: 1997-10-28
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APPLICATION NUMBER: 60/059263
FILING DATE: 1997-09-18
APPLICATION NUMBER: 60/059266
FILING DATE: 1997-09-18
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                                                               Similarity 6; Conserv
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Pred. No. 2.6e+02;
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Pred. No. 2
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2.6e+02;
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US-10-199-672-60
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NUMBER OF SEQ
NUMBER OF SEQ
; SEQ ID NO 60
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Best Local S
Matches 6
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APPLICANT: Baker, Kevin P.
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/
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CURRENT FILING DATE: 2002-07-18
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PRIOR FILING DATE: 1997-10-24
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                                                                 Godowski, Paul J. Gurney, Austin L.
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Goddard, Audrey
                                                                                                                                   Chen, Jian
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Watanabe, Colin K. Wood, William I.
                                Smith, Victoria
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                                                  Pan, James
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66.78;
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Pred. No. 2.6e+02;
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US-10-351-334-370
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-194-486-60
SOFTWARE: Pat
SEQ ID NO 370
LENGTH: 716
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Best Local Similarity 66.7

Matches 6; Conservative
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NUMBER OF SEQ ID NOS
SEQ ID NO 60
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TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: PZ031P2
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/350,898
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: 09/489,847
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CURRENT FILING DATE: 2003-01-27
                                                                                    PRIOR APPLICATION NUMBER: 60/095,455 PRIOR FILING DATE: 1998-08-06
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PRIOR APPLICATION NUMBER: PCT/US99/17130
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                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/095,454
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CURRENT APPLICATION NUMBER: US/10/194,486
CURRENT FILING DATE: 2002-07-11
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ITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ITLE OF INVENTION: ACIDS ENCODING THE SAME
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APPLICATION NUMBER: 60/059266
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                                                                                                                 ; TYPE: PRT ; ORGANISM: Mus musculus US-10-299-003-52
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PRIOR FILING DATE: 1997-01-30
PRIOR APPLICATION NUMBER: U.S. 60/057,750
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: U.S. 60/083,563
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PRIOR APPLICATION NUMBER: U.S. 09/140,749
PRIOR FILING DATE: 1998-08-26
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CURRENT FILING DATE: 2002-11-19
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ALIGNMENTS

A;Cross-references: EMBL:AC004411; NID:g3522932; PID:g3522961
A;Experimental source: Cultivar Columbia
R;Lin, X:, Kaul, S:, Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 199
Nature 402, 761-768, 199
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84910
A;Status: preliminary N;Alternate names: protein kinase homolog F14M4.11
C;Speciles: Arabidopsis thallana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001
C;Accession: T02181; F84910
C;Accession: T02181; RESULT 1 T02181 A; Map position: A; Introns: 32/1; C; Superfamily: k; 밁 Ş A; Molecule type: DNA A; Residues: 1-365 <STO> A; Status: translated from GB/EMBL/DDBJ A; Reference number: A; Accession: T02181 A; Description: Arabidopsis A; Reference number: Z14609 A; Gene: F14M4.11; At2g47060 A;Cross-references: GB:AE002093; NID:g3522961; PIDN:AAC34243.1; A; Molecule type: DNA A; Residues: 1-365 < ROU> submitted to the EMBL Data probable protein kinase [imported] -Query Match Best Local S Matches 8 Genetics 166 AQPGPVLS 173 Н AQPGPVLS 8 Similarity 8; Conserv 1; 116/3; 159/1; kinase-related Conservative 77.48; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, Library, September 1998 thaliana chromosome II BAC F14M4 genomic sequence. mported] - Arabidopsis thaliana kinase homolog F14M4.11 transforming 250/2; 294/3; 323/3 0; Score 41; Pred. No. Mismatches protein; DB 2 2 0; Length 365; protein kinase Indels GSPDB:GN00139 0 homology Gaps 0

conserved hypothetical protein - Deinococcus radiodurans (strain R1) C;Speciles: Deinococcus radiodurans C;Date: 03-Dec.1999 #sequence_revision 03-Dec.1999 #text_change 17-Mar-2000 C;Accession: A75496
C;Natcession: A75496
C;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dc, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zale S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

J.D.; Dodson, T.; Zalewski,

R.J

A75496 RESULT

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A; Map positi
A; Introns:
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22560
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                                                                                        A; Experimental source: C; Genetics:
                                                                                                   A;Cross-references: EMBL:279756; PIDN:CAB02122.1; GSPDB:GN00023; CESP:F53C11. A;Experimental source: clone F53C11
                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-891 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Stover, C.K.; Pham, X.Q.; adman, S.; Yuan, Y.; Brody, ; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
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A; Gene: DR0620
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                                                                   A; Gene: CESP:F53C11.5
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                                                                                      Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Similarity 7; Conserv
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7; Conserv
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                                 59/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                 137/1; 287/1; 313/1; 343/3; 420/1; 455/2; 637/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Erwin, A.L.; Mizoguchi, L.L.; Coulter, S.N.; Fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB; Pred. No. 41; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
 Score 37;
                                                                                                                                                                                                                     September 1996
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80;
 ВВ
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41;
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Folger, K
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Length 891
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A.; Larbig,
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                                 708/2; 831/2; 86
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; Lim,
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A;Experimental source: Strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as Neto, E.; Docana, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.; submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Lis chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palnieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa, A.Jauthors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
H72648
                                                                                                                                                                                                                                                                                                       awa, H.; Takamiya, M.; Masuda, DNA Res. 6, 83-101, 1999
                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein APE0622 - Aeropyrum pernix (strain K1)
C;Speckes: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: H72648
                                                                       A; Gene: APE0622
                                                                                                 A; Experimental C; Genetics:
                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-233 <KAW>
A; Cross-references: DDB
                                                                                                                                                                                                                                  A; Title: Complete genome se
A; Reference number: A72450;
A; Accession: H72648
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                                                                                                                                                                                                                                                                                                                                                      R;Kawarabayasi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; anonymous, The Xyle
Nature 406, 151-157,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: B82708
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Best Local S
Matches 7
  Query Match
Best Local Similarity
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Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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nes 6; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49
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7; Conser
                                                                                                                    source:
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                                                                                                                    DDBJ:AP000060; NID:g5104188; PIDN:BAA79592.1; PID:d1043378; PID:gce: strain Kl
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                                                                                                                                                                                                                                                                                                                                                    Hino, Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB:AE003956; GB:AE003849; NID:g9106196; PIDN:AAF84036.1; GSPDB:GN
                                                                                                                                                                                                                                                         sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
50; MUID:99310339; PMID:10382966
    67.9%;
87.5%;
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87.5%;
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       Score
Pred.
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l; Mismatches
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    36;
DB
41;
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2;
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T.; Kudoh, Y.
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Ja

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Proc. Natl. Acad. Sci. U.S.A. 82, 677-681, 1985
A;Title: Complete nuclectide sequence of the genome of bovine leukemia virus: it A; Rocession: A04014
A;Molecula +----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
S59531
                RESULT 9
A75373
                                                                                                                                                                                                                                                                                                           A; Molecule type: p
A; Residues: 30-59
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                manganese peroxidase (EC 1.11.1.13) precursor oyster mushroom C;Species: Pleurotus ostreatus (oyster mushroom) C;Date: 20-Jul-196 #sequence_revision 08-Nov-1996 #text_change C;Accession: S59531; S59532; S59525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-308 <SAG>
C;Superfamily: leukemia virus trans-activating transcription regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: host Bos sp. (cattle)
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 02-Jul-1998
C;Accession: A04014
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                                                                                                                                                                                                                                                                         A;Introns: 22/1; 66/3; 86/2; 132/2; 173/1; 198/2; 210/3; 213/2; 240/2; 263/3; 267/1; C;Superfamily: lignin peroxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;ASada, Y.; Watanabe, A.; Irie, T.; Nakayama, T.; Kuwahara, Biochim. Biophys. Acta 1251, 205-209, 1995
A;Title: Structures of genomic and complementary DNAs coding A;Reference number: S59525; MUID:95399442; PMID:7669812
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A; Residues: 1-361 < ASI
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   probable
                                                                                                                                                                                                           F;30-361/Product: manganese (II)
                                                                                                                                                                                                                                                                                                                                                         A; Accession: S59525
                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U21879;
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S59532
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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                                                                                                                                                                                                        ;Reywords: extracellular protein; glycoprotein; heme; manganese;
;1-22/Domain: signal sequence #status predicted <SIG>
;23-29/Domain: propeptide #status predicted <PRO>
;30-361/Product: manganese (II) peroxidase #status experimental
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   N-acetylmuramoyl-L-alanine
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                                                                                ADPGPVTSVP
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                                                                                                                                             Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukemia virus, BLV
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                                                                                 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.9%;
70.0%;
                                                                                                                                                             67.9%;
                                                                                                                                                                                                                                                                                                                                                                       NID:g732512;
                                                                                                                                                                                                                                                                                                                                                                                                                                      NID:g901983; PIDN:AAA84396.1;
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                                                                                                                                                             Score 36;
Pred. No.
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Pred. No.
     amidase
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64;
   Deinococcus
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   radiodurans
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F82971
                                                                         R;Takami, H.; Nakasone, I
Nucleic Acids Res. 28, 4:
A;Title: Complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Stover, C.K.; Pham, X.Q.; adman, S.; Yuan, Y.; Brody,
                                                                                                                                                                                                                                                        В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Complete genome see
A; Reference number: A82950;
A; Accession: F82971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position:
               A; Molecule
                            A; Status: preliminary
                                              A;Reference number: A83650;
A;Accession: B84062
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Best Local S
Matches 7
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C;Accession: A75373
C;Accession: A75373
C;Accession: A75373
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R;White, O.; Eisen, J.A.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C. Smith, H.O.: Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: PA5398
C;Superfamily: Methylophilus methylotrophus W3Al trimethylamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A75250; MUID:20036896; PMID:10567266
A; Accession: A75373
                                                                                             C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE004952; GB:AE004091; A;Experimental source: strain PAO1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable FMN oxidoreductase PA5398 [imported] - Pseudomonas aeruginosa (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE002007;
A;Experimental source: strain R1
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Science 286, 1571-1577, 1999
                                                                                                                                 hypothetical protein BH3298 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Species: Deinococcus radiodurans;Date: 03-Dec-1999 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa
                                     , K.; Takaki,
4317-4331, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence of Pseudomonas aeruginosa 50; MUID:20437337; PMID:10984043
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77.88;
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MUID: 20512582; PMID: 11058132
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Pred. No. 1.3e+02;
0; Mismatches 2;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.L.; Mizoguchi, S.D. Coulter, S.N.; Folger,
                                                    Y.; Maeno,
              the alkaliphilic bacterium
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                                                                                             01-Dec-2000 #text_change 15-Jun-2001
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1.1e+02;
2;
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                                                      G.;
                                                      Sasaki,
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                                                      R.; Masui, N.; Fuji,
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                Bacillus halodurans
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RESULT 13
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                                                                                                                                                                                                                                                                              coat protein - belladonna mottle virus
C;Species: belladonna mottle virus
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999
C;Accession: S41553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:S97776; NID:g248382; PIDN:AAB21997.1; A;Note: sequence extracted from NCBI backbone (NCBIN:97776, NA;Note: in Genbank entry S97776, release 109.0, the source is
                                                                                                                                                A; Molecule type: protein A; Residues: 1-190 <SUR>
                                                                                                                                                                                               A; Reference number: S41553; A; Accession: S41553
                                                                                                                                                                                                            R;Suryanarayana, S.; Rao, N.A.; Murthy, M.R.N.; Savithri, H.S. J. Biol. Chem. 264, 6273-6279, 1989
A;Tille: Primary structure of Belladonna mottle virus coat protein A;Reference number: S41553; MUID:89197927; PMID:2467911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Jacob, A.N.K.; Murthy, M.R.; Savithri, H.S. Arch. Virol. 123, 367-377, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Physalis mottle virus
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change
C;Accession: B45540; A46I15
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A; Residues: 1-188 <JAC>
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                                                                   Matches
                                                                               Query Match
Best Local :
                                                                                                                                 Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: turnip yellow Keywords: coat protein
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PGSILSQP
                                PGPVLSQP
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                                                             6; Conserv
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9; Conserv
                                                                                                                               turnip yellow
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24
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81.8%;
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75.0%;
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75.0%;
                                                                                                                             mosaic virus coat protein
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                                                                               Score 35;
Pred. No.
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Pred. No. 2
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No.
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5, NCBIP:97780)
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C;Species: Mus musculus (house mouse)
C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 08-Dec-2
C;Accession: E36596
R;Inoue, T.; Tamura, T.; Furuichi, T.; Mikoshiba, K.
J. Biol. Chem. 265, 19065-19070, 1990
A;Fitle: Isolation of complementary DNAs encoding a cerebellum-enriched A;Reference number: A36596; MUID:91035434; PMID:169939
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
B86939
                                                                                                                                                                                                                              A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; A;Title: Massive gene decay in the leprosy bacillus. A;Reference number: A86909; MUID:21128732; PMID:11234002
                                                                                                                                                                                                                                                                                          R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; Jämes, K.D.; Thomson, R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, i eam, M.A.; Rutherford, K.M.
                                                                                                                                                                                                                                                                                                                                                          probable isopentenyl monophosphate kinase [imported] - Mycobacter
C;Species: Mycobacterium leprae
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C;Superfamily: human nuclear f
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A; Residues: 1-311 <STO>
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A; Residues: 1-309 < INO>
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RA AIZAWA T., HARTA A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

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RA AIZAWA K., IZAWA M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

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RA Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

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RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

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RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

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RA Bluke J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,

RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashtaki Y., Storch K., Fill D., Hofmann M., Hasegawa Y., Kawaji H., Kohtsuki S.,
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"Functional annotation of a full-length mouse cDNA construct 409:685-690(2001).

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"I TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN,"

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                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest; use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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Metazoa; Chordata; C
-∵+heria; Rodentia; !
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SEQUENCE 349
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Mammalia; Eutheria;
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Primates;
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Catarrhini;
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PROSITE; PS00108;
PROSITE; PS50011;
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Am. J. Physiol. 278:C451-C462(2000)
-!- FUNCTION: PHOSPHORYLATES INHIBI
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Pfam; PF00240; ubiquitin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed.
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Nemoto S., DiDonato J.A., Lin A.;
"Coordinate regulation of IkappaB kinases by mitogen-activated
kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
Mol. Cell. Biol. 18:7336-7343(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000719; Euk_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PERIPHERAL BLOOD.

PIM: PHOSPHOTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ULTIMATELY THE DEGRADATION OF THE INHIBITOR.
SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT
ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.
HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN
ALSO BIND TO MEKKI, MAPSK14/NIK, IKAP AND IKB-ALPHA-P65-P50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Physiol. 2/8:(431-(440)).
FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THU
THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX
THE DISSOCIATION OF THE THHIRITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WEAKLY AUTOPHOSPHORYLATED.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic. TISSUE SPECIFICITY: HIGHLY EXPRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IKAPPAB KINASE SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n C., Sartor R.B.;
I kappa B/NF-kappa B system: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      603258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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AF080158; AAD08997.1;
AF031416; AAC64675.1;
BC006231; AAH06231.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:5960; IKBKB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PR00109; TYRKINASE
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                                                                                                                                                                                                                                                                                                                                                                                                                               PS00107;
      177
177
181
181
181
231
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                                                                                                                                                                                                                                                                                                                                                                                 ; Euk_pkinase; 1.
; PROTEIN_KINASE_ATP; F
; PROTEIN_KINASE_ST; 1.
; PROTEIN_KINASE_DOM; 1
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S->A: DECREASE OF ACTIVITY
S->E: FULL ACTIVATION.
S->A: DECREASE OF ACTIVITY
S->E: FULL ACTIVITION.
WHSKVRQKSEVDIVVSEDLNGTVKF
                                                                                                        K->A: LOSS OF KINASE
EFFECT ON BINDING TO
                                                                                                                                PHOSPHORYLATION
K->A: LOSS OF K:
                                                                                                                                                                        PHOSPHORYLATION (BY SIMILARITY). PHOSPHORYLATION.
                                                                                                                                                                                                                 BY SIMILARITY
                                                                                                                                                                                                                                                                               NEMO-BINDING
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LEUCINE-ZIPPER
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                      DECREASE OF ACTIVITY.
FULL ACTIVITION.
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SEQUENCE
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"NEDO human cDNA sequencing project.";
                                                                                                       "A common 11e796Val polymorphism of a common 11e796Val polymorphism of activating protein (SCAP) gene."
J. Hum. Genet. 44:421-422(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20037503; pubMed-10570913;
Nakajima T., Hamakubo T., Kodama T.
"Genomic structure and chromosomal
regulatory element binding protein
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15-JUN-2002 (Rel. 41, Last annotation update)
Sterol regulatory element binding protein cle
(SREBP cleavage-activating protein) (SCAP).
                                                                                                                                                                                                                                                                                                                                "Prediction of the coding sequences of unidentified human The coding sequences of unidentified human analysis of cDNA clones from human cell line KG-1."; DNA Res. 3:17-24(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein (SCAP)
J. Hum. Genet.
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MEDLINE=20037503;
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Q12770;
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           <del>+ +</del>
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Mammalia; Eutheria;
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                                                                                                                                                      MEDLINE=20037509;
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                                         FUNCTION: Sterol sensor. Necessary for the of SREBPs by site-I protease in the Golgi. SUBUNIT: In a tight complex with SREBP (By SUBCELLULAR LOCATION: Integral membrane prendoplasmic reticulum to the Golgi in the
          endoplasmic reticulum
similarity).
SIMILARITY: CONTAINS 1
SIMILARITY: CONTAINS 7
                                                                                                                                                                                           human cDNA sequencing tted (MAY-2001) to the
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6; Conserv
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44:402-407(1999).
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a T., Ota N., Emi M.;
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Primates;
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           STEROL SENSOR DOMAIN WD REPEATS (TRP-ASP I
                                                                                                                                                                                          project.";
EMBL/GenBank/DDBJ
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e human
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PROSITE; PS50156; SSD; 1.

PROSITE; PS50082; WD_REPEATS_2; 1.

PROSITE; PS50294; WD_REPEATS_REGION; 1.

PROSITE; PS00678; WD_REPEATS_1; 1.

Lipid metabolism; Cholesterol metabolism; Transmembrane;

Lipid metabolism; Cholesterol metabolism; Transmembrane;
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                                                                                                                                                                                                                                                                                                                            DOMAIN
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InterPro; IPR001680;
Pfam; PF00400; WD40;
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EMBL; AK027402; BAB55088.1; ALT_INIT.
MIM; 601510; -.
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
NCBI_TaxID=9606;
                                                                                                                                   TISSUE-Bone marrow;

MEDLINE-96051398; PubMed-7584044;

NOMUTA N., Nagase T., Miyajima N., Sazuka T., Tanaka A., S
Seki N., Kawarabayasi Y., Ishikawa K.-I., Tabata S.;

"Prediction of the coding sequences of unidentified human
The coding sequences of 40 new genes (KIAA0080) d
analysis of cDNA clones from human cell line KG-1.";
DNA Res. 1:223-229(1994).

--- SIMILARITY: CONTAINS 1 C3H1-TYPE ZINC FINGER.
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01-NOV-1995
15-JUN-2002
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21-JUL-1986 (Rel. 01, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
Hypothetical PXBL-I protein (Fragment).
Bovine leukemia virus (Japanese isolate BLV-1) (BLV).
Viruses; Retroid viruses; Retroviridae; Deltaretrovirus.
NCBL_TaxID=11907;
                        petween the Swiss Institute of Bioinformatics Institute by non-profit institute.
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                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
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PIR; A04014; (
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MEDLINE-85140159; PubMed-2983308;
MEDLINE-85140159; PubMed-2983308;
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Pred. No. 24;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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  PEPTIDE MOD_RES
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16-OCT-2001 (Rel. 40,
15-JUN-2002 (Rel. 41,
                                    leavage
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FUNCTION: STIMULATES FORMATION OF NAHCO(3)-RICH BILE AND INHIBITS
AND SECRETION OF NAHCO(3)-RICH BILE AND INHIBITS
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Virology 193:959-966(1993).
-I- SUBUNIT: THE VIRUS COAT IS COMPOSED OF 180 COPIES C
PROTEIN ARRANGED IN A ICOSAHEDRAL SHELL.
-I- SIMILARITY: TO COAT PROTEIN FROM OTHER TYMOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Jacob A.N.K., Murthy M.R., Savithri H.S.;
"Nucleotide sequence of the 3' terminal region
virus-Iowa (renamed Physalis mottle virus) RNA
relationships of tymoviral coat proteins.";
Arch. Virol. 123:367-377(1992).
                                                    BMDV
                                                                                                                                                                                                                                                                   modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssRNA positive-strand NCBI_TaxID=72539;
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01-JUN-1994 (Rel.
01-JUN-1994 (Rel.
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                                                                                                                                                                                    Coat protein
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                                                                                                                                                                                                                                                                                                                                                                                          Kekuda R., Karande A.A., Jacob A.N.K., Savi
"Architecture of physalis mottle tymovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=92222369;
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                                                                                                                                                                                             Pfam; PF00983; Tymo_coat;
                                                                                                                                                                                                                   HSSP; P03608;
                                                                                                                                                                                                                             PIR; B45540;
                                                                                                                                                                                                                                                           or send an
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                  Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N. Davies R.M., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                    "Massive gene decay in the leprosy
Nature 409:1007-1011(2001).
-!- FUNCTION: Catalyzes the phospho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
CONFLICT
SEQUENCE
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Bacteria; Actinobacteria;
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Suryanarayana S., Rao N.A., Murthy M.R.N., Sav
"Primary structure of belladonna mottle virus
J. Biol. Chem. 264:6273-6279(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. B101.
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Belladonna mottle virus (BMDV).
Viruses; ssRNA positive-strand viruses,
NCBI_TaxID-12149;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
1-diphosphocytidyl-2-C-methyl-D-erythritol kinase (4-(cyt.dine-5-diphospho)-2-C-methyl-D-erythritol
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                                         CATALYTIC ACTIVITY: ATP + erythritol = ADP + 2-phosp
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SUBUNIT: THE VIRUS COAT 1
                                                                                                        similarity).
                                                                                                                                    FUNCTION: Catalyzes the phosphorylation of the position group of 4-diphosphocytidyl-2C-methyl-D-erythritol (By
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Pr00983; Tymo_coat; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=11234002;
ier K., Parkhill J.,
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R -> K (IN REF. 2).
KPM -> SPQ (IN REF. 2).
; 20EEE23D2D863E14 CRC64;
                                                                     4-(cytidine 5'-diphospho)-2-C-methyl-D-
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FROM OTHER TYMOVIRUSES
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belladonna mottle virus
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01-APR-1993
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Methanol
                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrictuse by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fentities requires a license agreement (See http://www.isb-sibor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                        van Spanning R.J.M., Wansell C.W., de Boer T., Hazelaar M.J., Anazawa H., Harms N., Oltmann L.F., Stouthamer A.H.; "Isolation and characterization of the mox1, mox6, mox1, and genes of Paracoccus denitrificans: inactivation of moxJ, mox6 moxR and the resultant effect on methylotrophic growth."; J. Bacteriol. 173:6948-6961(1991).

-1- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF FORMATION
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                                          Pin; D413//; D413//.
InterPro; IPR003442; UPF0079.
Pfam; PF02367; UPF0079; 1.
                                                                                           EMBL; M57684;
PIR; D41377; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE-92041581; PubMed-1657871;
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InterPro; IPR004424; IspE.
Pfam; PF00288; GHMP_kinases;
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SIMILARITY: WITH THE CORRESPONDING PROTEIN IN M.EXTORQUENS
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Homo sapiens (Human).
Homo sapiens, Metazoa; Chordata; Metazoa; Primates;
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                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Tate G., Mitsuya T.;
Submitted (NOV-1999)
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                                                                                                             Submitted
                                                                                                                       Strausberg R
                                                                                                                                 TISSUE-Kidney;
                                                                                                                                           SEQUENCE FROM
                                                                                                                                                              hypermethylation in hum
Gene 282:151-158(2002).
                                                                                                                                                                        Namba M., Shimizu N., Shimizu K.;
"Reduced expression of the REIC/Dkk-3
hypermethylation in human tumor cells.
                                                                                                                                                                                             Kobayashi K., Ouch
Namba M., Shimizu
                                                                                                                                                                                                                PubMed-11814687;
                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                        Biochem.
                                                                                                                                                                                                                                                                                                human tumor-derived
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MEDLINE-20035735; P
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European
by non-
                                                                              nitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. FUNCTION: INHIBITOR OF WAT SIGNALING PATHWAY (POTENT SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: HIGHEST EXPRESSION IN HEART, BRJ
                                                   SIMILARITY:
       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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., Miyazaki M., Sakaguchi M.
gene shows down-regulation
mor derived cell lines.";
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6; Conserv
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LARITY: BELONGS TO THE DICKKOPF FAMILY.
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l. 41, Last
d protein-3
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rp J.D., Jiang C., Robison K., Ch
wn D.E., Guyot D., Mays G., Leiby
1 A.D.J., Gearing D.P., Sokol S.Y
tructural diversity of the human
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Catarrhini; Hominidae;
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Leiby K., Chang B.,
ol S.Y., McCarthy S.A.;
human Dickkopf gene
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     Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V. Bertero M.G., Bessieres P., Bolotin A., Borchert S., Boursier L., Brans A., Braun M., Brignell S.C., Bron Borriss R., Boursier L., Brans A., Braun M., Capuano V., Carter N.M., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A. Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.: Entian K.D., Errington J., Fabert C., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Heaaut A.
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Submitted
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                                                                                                                                                                        STRAIN-168
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; AB045207; BAA87044.2;
; AB045209; BAA87044.2;
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                                                                                                                                                  Ramon D., (XXX-1994)
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DKK-TYPE CYS-2.
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S.C., Bron S., Carter N.M., Daniel R.A.,

G., Henaut A.,

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(See http://www.isb-sib.ch/announce/
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                Length 350;
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Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Medina N., Mellado R.P., Mellado R.P., Moestl D., Nakai S., Noback M.,
None D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parev V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
A Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Naka Rieger M., Rivolta C., Rocha E., Rocha E., Schroeter R., Scoffone F.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sakiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tacconi E., Takaji T., Takahashi H., Takemaru K.,
Naka Takeuchi M., Tamakoshi A., Tanaka T., Terpptra P., Tognoni A.,
Naka Takeuchi M., Tamakoshi A., Tanaka T., Terpptra P., Vassarotti A.,
Naka Takeuchi M., Wandutt R., Wedler E., Wedler H., Weitzenegger T.,
Naka Takeuchi M., Vanamoto H., Vanane K.,
Naka Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
The complete genome sequence of the Gram-positive bacterium Bacillus
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Best Local
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InterPro; IPR001088; GH_4.
Pfam; PF02055; G1yco_hydro_4; 1.
PRINTS; PR00732; G1HYDRIASE4.
PRODOM; PD006892; GH_4; 1.
PROSITE; PS01324; GLYCOSYL_HYDROL_F4; 1.
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                                                                            Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                            NCBI_TaxID=9606
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-1- SIMILARITY: BELONGS TO FAMILY 4 OF GLYCOSYL HYDROLASES.
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Kobayashi Y., Koetter P., Koningstein G., Krogh S., F
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NPIA_RAT STANDARD; PRT; 509 AA.
P09414; Q63782;
01-MAR-1989 (Rel. 10, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nuclear factor 1 A-type (Nuclear factor 1/A) (NFI-A) (NFI-A) (NFI-A)
(CCAAT-box binding transcription factor) (CTF) (TGGCA-binding
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CONFLICT
SEQUENCE
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-I- FUNCTION: RECOGNIZES AND BINDS THE PALLIDROMIC SEQUENCE 5'-
TIGGCUNUNUNGCCAA-3' PRESENT IN VIRAL AND CELLULAR PROMOTERS AND IN
THE ORIGIN OF REPLICATION OF ADENOVIRUS TYPE 2. THESE PROTEINS AR
INDIVIDUALLY CAPABLE OF ACTIVATING TRANSCRIPTION AND REPLICATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 19-243 FROM N.A. MEDLINE-96070434; PubMed-7590749; Qian F., Kruse U., Lichter P., Si
                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                              Nuclear protein; Multigene famil
                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation; DNA replication; DNA-binding; Activator;
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-1- SUBCELLULAR LOCATION: Nuclear.
-1- SIMILARITY: BELONGS TO THE CTF/NF-I FAMILY.
-1- SIMILARITY: CONTAINS 1 DWA/MH1 DOMAIN.
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[3]
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InterPro; IPR003619; Dwarfin_A.
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509 AA;
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Pred. No. 62;
0; Mismatches
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TGPN -> PAPT (I
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cDNA clones from brain which c
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NFIA OR NFIL21. Rattus norvegicus (Rat). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;

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InterPro; IPR003619; Dwarfin_A.
Pfam; Pf00859; CTE_NFI; 1.
SMART; SM00523; DWA; 1.
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EMBL; D78017; BAA11203.1;
EMBL; X13167; CAA31565.1;
PIR; S01300; S01300.
                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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between
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"Purification of a NFI-like DNA-binding protein from rat liver cloning of the corresponding cDNA.";
EMBO J. 7:3115-3123(1988).
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                                                                                                                  Transcription regulation; DNA replication; DNA-binding; Nuclear protein; Multigene family.

DOMAIN 67 175 DWA.

SEQUENCE 509 AA; 55976 MW; 59120C7090229F87 CRC64;
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Tmagawa factor 1 family proteins bind
Nuclear factor transferase P gene.";
rat glutathione transferase P gene.";
J. Biochem. 121:355-363(1997).
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378
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                                                                         Local
                           2 QPGPVLSQP 10
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SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE CTF/NF-I FAMILY.
SIMILARITY: CONTAINS 1 DWA/MH1 DOMAIN.
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TTGGCNNNNNNGCCAA-3' PRESENT IN VIRAL AND CELLULAR PROMOTERS AND IN
THE ORIGIN OF REPLICATION OF ADENOVIRUS TYPE 2. THESE PROTEINS AR
INDIVIDUALLY CAPABLE OF ACTIVATING TRANSCRIPTION AND REPLICATION.
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S., Ikeda T., Nishihara T., Yano K., Yamasaki M.,
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                                          Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; U28007; AAC61805.1; -.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002203; Intein.
InterPro; IPR002203; Intein.
InterPro; IPR004040; SET_thr_pkinase.
InterPro; IPR004040; STY_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00221; STYKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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O1-NOV-1998 (TrEMBLrel. 08,
O1-MAR-2002 (TrEMBLrel. 20,
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MEDLINE=96107331; PubMed=8521516;
Zhou J., Loh Y.T., Bressan R.A., Martin G.B.;
"The tomato gene Ptil encodes a serine/threonine kinase that phosphoryated by Pto and is involved in the hypersensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lycopersicon esculentum (Tomato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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Martin G.B.;
                                                                                                                                                                                                                                                                                                                              response.
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PROSITE; PSU0881
ATP-binding; Kin
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Q9LKY3;
Q1-OCT-2000
Q1-OCT-2000
Q1-MAR-2002
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PRINTS; PR00109; TYKRIASE.
PRODOM; PD000001; Euk_Pkinase; 1.
SMARR; SM00221; STYKC; 1.
SMARR; SM00221; STYKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
ATP-binding; Kinase; Tansferase; Tyrosine-protein kinase.
ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
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Arch. Blochem. Blophys. 383:233:237(2000).
EMBL; AF249317; AAF91336.1;
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR004040; STY_pkinase.
InterPro; IPR001040; STY_pkinase.
Pfam; PF00069; pkinase.
Pfam; PF00069; pkinase.
Pfam; PF00069; pkinase.
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01-OCT-2000
01-MAR-2002
                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Phaseoleae; Glycine.
                                                                                                                                Glycine max (Soybean)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-21036115;
SEQUENCE
                                           NCBI_TaxID=3847;
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RESULT
Q9LUT0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
        "Full Length cDNA of gene at3 Submitted (DEC-2001) to the FIG. SIMILARITY: BELONGS TO THE EMBL; AB022216; BAB02745.1; EMBL; AY070413; AAL49909.1; HSSP; Pl1362; 1FGI.
                                                                 [3]
SEQUENCE FROM N.A.
Yamada K., Banh J., Chang C.H., Chang E., Dalto Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C. Yamamura Y., Yu G., Yu S., Bowser L., Carrinci P., Chen H., Chen Hayashizaki Y., Ishida J., Jones T., Kamiya A., Kariin-Neumann Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki Narusaka M., Shinozaki K., Davis R.W., Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                             Sato
                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry.
Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9LUT0;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000719; Euk_pkinase.
InterPro; IPR004040; STY_pkinase.
InterPro; IPR0014040; STY_pkinase.
InterPro; IPR0014045; TY_pkinase.
Pfam; PF00009; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Kinase; Transferase; Tyrosine-protein kinsequence 360 AA; 39481 MW; 0B54143D695C2B90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Two expressed soybean
Ptil kinase lack autoph
                                                                                                                                                                                                                                clones
                                                                                                                                                                                                                                                                              STRAIN-COLUMBIA;
MEDLINE-20277480;
                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnolioph; eurosids II; Brassicales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine/threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O9LUT0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000001; Euk_pkinase; SMART; SM00221; STYKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arch. Biochem. Biophys. 383:233-237(2000). EMBL; AF249318; AAF91337.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21036115; PubMed=11185558; Staswick P.;
                                                                                                                                                                                                                  DNA Res.
                                                                                                                                                                                                                                          "Structural analysis of 
features of the regions
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                         STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AT3G17410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 AQPGPVLS 167
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d (JAN-1999)
                                                                                                                                                                                                                 7:131-135(2000).
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) (TrEMBLrel. 1:
2, (TrEMBLrel. 2:
eonine protein !
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                                                                                                                                                                                                                                                                                PubMed-10819329;
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                                                                                                                                                                                                                                                                                                                                 Kaneko
to the I
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                                                                                                                                                                                                                                     Arabidopsis thaliana chromosome 3. of 4,504,864 bp covered by sixty P
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15, Last sequence update)
20, Last annotation update)
n kinase-like protein (Hypothetical
                                            At3g17410 (GI:15229035).";
he EMBL/GenBank/DDBJ databa
O THE SER/THR FAMILY OF PRO
                                                                                                                                                                                                                                                                                                                                                                                                            Brassicaceae;
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Pred. No.
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11;
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adona; core e
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                                                                                                                                                                                                                                                                                                                                             Asamizu E.,
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                                             of PROTEIN
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                                             PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    a; Tracheophyta;
eudicots; Rosid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kinase
                                                                                                                                                M., Wu H.C.,
hen H., Cheuk R.,
                                                                                                                                                                                                                                                                                                                                             Tabata
                                                                                                            Seki M.,
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ind TAC
                                                                                                                                                                        A.D.,
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IPR000719;

Euk_pkinase

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RESULT
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Best Loc
Matches
                                                                                                  Submitted (FEB-2002) to the EMBL/GenBank/
-: SIMILARITY: BELONGS TO THE SER/THR FA
EMBL; AC004411; AAC3423.1; -.
EMBL; AF325090; AAK17158.1; -.
EMBL; AF325090; AAK17158.1; -.
EMBL; AF325090; AAL87347.1; -.
HSSP; P11362; 1FG1.
InterPro; IPR007219; Euk_pkinase.
InterPro; IPR007220; Ser_thr_pkinase.
InterPro; IPR007220; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y.,
Rounsley S.D., Lin X., Fraser C.M., Somerville C.R., Vo
Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Vo
"Arabidopsis thaliana chromosome II BAC F14M4 genomic of the symbol of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                080719;
01-NOV-1998
01-NOV-1998
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TREMBLrel. 08, Created)
01-NOV-1998 (TREMBLrel. 08, Last sequence update)
01-JUN-2002 (TREMBLrel. 21, Last annotation update)
01-JUN-2002 (TREMBLrel. 21, Last annotation update)
Putative PTO kinase (Hypothetical 39.9 kDa protein).
F14M4.11 OR AT2G47060.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                          Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriuni M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SOUTHWICK A., Karlin-Neumann G., Nguyen M., Le
Palm C.J., Theologis A., Ecker J., Davis R.W.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      080719
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PTODOM; PD000001; EUK_pkinase; 1.

SMART; SM00221; STYKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP;

PROSITE; PS50011; PROTEIN_KINASE_DOM;

PROSITE; PS00108; PROTEIN_KINASE_ST; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                            Theologis A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
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                                                                               ProDom;
                                                                                                                                                                                                                                                                                                                                                            "Arabidopsis Full Length cDNA Clones.";
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                                                          SM00221;
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                                                     F00069; pkinase; 1.
PD000001; Euk_pkinase;
SM00221; STYKC; 1.
     PS00107;
PS50011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     al protein.
364 AA; 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
     PROTEIN_KINASE_ATP; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Ser_thr_pkinase.
; STY_pkinase.
; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39562 MW;
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; Pred. No.
                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62A7FE8F249F332E
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      365
       UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Embryophyta; Tracheophyta;
edons; core eudicots; Rosid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ... C.R., Venter J.C.;
M4 genomic sequence.";
3J databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lam B.,
                                                                                                                                                                                                                                                                                                            databases.
OF PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miranda
                                                                                                                                                                                                                                                                                                               KINASES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                          `\`.
RESULT
Q9U191
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Query Match
Best Local S
Matches 7
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Best Local
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01-DEC-2001 (TEMBLIFEL 19,
Hypothetical transmembrane p
L302.06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9U191
Q9U191;
01-MAY-2000
                                                                                           DJ756G23.1.
Homo sapiens (Human).
Homo sapiens (Human).
Tharvota; Metazoa; Chordata;
Tharvota; Primates;
                                                                                                                                          Q9UGS3;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DJ756G23.1 (Novel leucine rich protein) (Fragment).
DJ756G23.1.
          Submitted (JAN-2001) to the EMBL; AL035681; CAB63072.1; InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ivens A.C., Murphy L., Quail Rajandream M.A., Barrell B.G. Submitted (JUL-2001) to the F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

Hypothetical protein; ATP-binding; Serine/threonine-protein
Transferase.

SEQUENCE 365 AA; 39931 MW; ACAFEC6C79E77CAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane. SEQUENCE 258
                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 8:135-145(1998)
EMBL; AL389894; CAC22674.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                    "A physical map of the Leish
Genome Res. 8:135-145(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ivens A.C.,
Smith D.F.;
                                                                SEQUENCE FROM
                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98146435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                          AQPPPILSSP
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 IPR000483;
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                                                                                                                                                                                                                         PRELIMINARY;
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                                                                N.A.
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100.0%
LRR_Cterm
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), Last an
protein
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                          EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                        Score 39; DB
Pred. No. 19;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                               1F214B2109E0D2DB CRC64
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11;
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RESULT 9
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Best Local S
Matches 6
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Best Local S
Matches 8
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Pfam; PFO(
Pfam; PFO)
                                                                                Streptomyces avermitilis.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; S
SMART; S
NON_TER
                SEQUENCE FROM N.A.
MEDLINE=21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa J., H
                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2002 (TrEMBLrel. 20,
    Shinose
                                                                                                                                                                                                                                                                                                                                                                                                                  growth.";
Submitted (NOV-2000) to the
EMBL; AF318347; AAL55854.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam;
                                                                        NCBI_TaxID=33903;
                                                                                                                                  Thioesterase.
                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein. SEQUENCE 244 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang P.P.,
Wan D.F., G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PP147/b.
Homo sapiens (Human).
Homo sapiens (Human).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 27.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8WYV2;
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PF01463; LRRCT
PF01462; LRRNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM00013; LRRNT; 2.
SM00369; LRR_TYP; 4.
SR 797 797
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8; Conserv
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IPR003592;
IPR003591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., Zhou X.M.,
Gu J.R.;
  Takahashi
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                     PRELIMINARY;
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LRRNT; 1.
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LRRNT; 2.
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                                                                                                                                                                                                                                                                                                                                                                                        27187 MW;
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    Horikawa
                                                                                                                                            Last sequence up
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Pred. No. 28;
2; Mismatches
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Pred. No.
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  ⊮a H., Nakazawa
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                Takahashi
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  Ξ.
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                                                                                 Streptomyces
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Q96JV8
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Q96JW9
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Best Local :
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Best Local (
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
NCBI_TaxID=9606;
[1]
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RA Watanabe S., Kinura K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Watanabe S., Kinura K., Kodaira H., Kondo H.,
RA Watanabe S., Kinura K., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kinura K., Murakawa K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari Y., Saito K.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human CDMA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databasan
REMBL; AK027831; BAB55397.1; -.
RE InterPro; IPR002035: Varn
                                                              096JV8:
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ14943 fls, clone PLACE1011371, weakly similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 98:1
EMBL; AB070956; BAB69404.1; -.
InterPro; IPR001031; Thioesterase.
Pfam; PF00975; Thioesterase; 1.
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                               inter-alpha-trypsin inhibitor Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ14925 fis, clone PLACE1008643, weakly simile
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Mammalia; Eutheria;
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Homo sapiens (Human).
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6; Conserv
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7; Conserv
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Chordata;
Primates;
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 Hominidae;
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OBXPV1; O1-MAR-2002 (TrEMBLrel. 20, Cre
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01-MAR-2002 (TrEMBLrel. 20, Las
Probable activation/secretion s
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SEQUENCE
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Pfam; PF00092; vwa; 1.
Pfam; PF00092; vwa; 1.
Pfam; PF00092; vwa; 1.
Pfam; PF00092; vwa; 1.
Pfam; PF00092; vwa; 1.
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
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"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).
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Bacteria; Proteobacteria;
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
     Ralstonia solanacearum 
Plasmid megaplasmid.
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TISSUE-PLACENTA;
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583 AA;
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                               solanacearum)
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Q9BT94;
Q1-JUN-2001
Q1-JUN-2001
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Strausberg R.;

Strausberg R.;

Submitted (FEB-2001) to the EMBL/GenBa

EMBL; BC003195; AAH03195.1; -

InterPro; IPR000345; CytC_heme_bind.

R InterPro; IPR000571; Znf_CCCH.

R InterPro; IPR001841; Znf_ring.

R InterPro; IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00642; zf-CCCH; 2.
SMART; SM00184; RING; 1.
SMART; SM00356; ZnF_C3H1; 3.
PROSITE; PS00190; CYTOCHROME_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; "ature 415:497-502(2002).

EMBL; AL646085, CAD18686.1; -. Plasmid; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TIEMBLIEL 17, 01-JUN-2001 (TIEMBLIEL 17, 01-MAR-2002 (TIEMBLIEL 20, 01-MAR-2002 (TIEMBLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical 69.6 kDa protein
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1 (TremBLrel. 17, Las
2 (TremBLrel. 20, Las
al 80.6 kDa protein.
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Sciurognathi; Muridae;
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STISSUE-SKIN;

Strausberg R.;

Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC004282; AAH04282.1; -.

R InterPro; IPR002035; VWF_A.

R Pfam; PF00092; vwa; 1.

R SMARR; SM00327; VWA; 1.

R PROSITE; PS50234; VWFA; 1.

R PROSITE; PS50234; VWFA; 1.

SEQUENCE 728 AA; 80604 MW; 118A1B32F89BCECA CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human deaminase en	AA015117	23	355		٥.	44
Drosophila melanog	ABB64569	22	3169	11.9	67	43
laminin	AAB48460	21	1725	11.9	67	42
Rat laminin 5 poly	AAB48461	21	1694	11.9	67	41
Drosophila melanog	ABB68585	22	1532	11.9	67	40
	ABB05681	23	835	11.9	67	39
	AAU36734	22	792	11.9	67	38
Staphylococcus aur	AAU37199	22	748	11.9	67	37
Human protein sequ	AAB95238	22	725	11.9	67	36
Enterococcus faeca	AAU35335	22	375	11.9	67	35
Drosophila melanog	ABB61938	22	363		67	34
	ABB44556	22	2442	12.0	67.5	ü
uman	АВВ97489	23	1215	12.0	67.5	32
Fungal ZBC protein	ABP35614	23	736	12.0	67.5	31
Human homologue of	AAU82954	23	1023	•	68	30
C glutamicum prote	AAG91954	22	215	•	68.5	29
ס	ABB63410	22	1420	2	69	28
Novel human diagno	ABG05595	22	881	12.3	69	27
	AAB40945	21	1532	12.4	69.5	26
Novel human diagno	ABG08332	22	1045	۲	69.5	25
nibacter	AAU46608	22	128	12.5	70.5	24
Human PCLP1. Homo	AAB98977	22	528		71	23
Complete form of h	AAR08338	11	979	۲	71.5	22
Novel human diagno	ABG15016	22	2639	12.8	72	21
Ö	ABB59050	22	2296		~	20
Novel human diagno	ABG08165	22	1236	۲.	72.5	19
Staphylococcus epi	ABP38928	23	412	•	72.5	18
Human polypeptide	AAM40472	22	625	13.0	73	17
	AAM40471	22	625		73	16
	AAM38685	22	619	13.0	73	15
	AAM38686	22	595	ω.	73	14
an tran	ABB50171	22	591	13.0	73	13
Elf-1 polymor	AAB03190	21	615	13.2	74	12
Rat Elf-1 polymorp	AAB03191	21	579	13.2	74	11

ALIGNMENTS

RESULT 1 AAW31494 AAW31494; AAW31494 standard; Protein; 801 AA.

28-APR-1998 (first entry)

Human hTAFII105 protein.

antibodies; diagnosis; therapy; biopharmaceutical industry. TATA-binding protein associated binding factor 105; human; activator; hTAFII105; transcription factor; TFIID; transcriptional activation;

Homo sapiens.

US5710025-A

20-JAN-1998

02-OCT-1996; 96US-0725012.

02-OCT-1996; 96US-0725012

(REGC) UNIV CALIFORNIA.

Dikstein R, Tjian R;

WPI; 1998-109818/10. N-PSDB; AAV02872.

DNA encoding human tata-binding protein associated factor - producing recombinant protein

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RESULT 2
ABG09468
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Best Local
          The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                        diagnostics, forensics, responsible for genetic biodiversity -
                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           associated subunits (TAF's) are components of the transcription factor TFIID and are thought to mediate transcriptional activation. This encode protein may be produced recombinantly from transformed host cells or purified from human cells. hTAFIII05 specific binding agents such as specific antibodies could be used for diagnosis (e.g. genetic hybridisation screens for hTAFIII05 transcripts), therapy (e.g. gene hybridisation screens for hTAFIII05 gene expression) and in the biopharmaceutical industry (e.g. as immunogens, reagents for isolating cell specific activators or other transcriptional regulators).
 polynucleotides
                                                                                            Claim
                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                        31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABG09468 standard;
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                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                              WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein
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                                                                                                                                                                                                2001-639362/73.
DB; AAS73655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        supplement;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA sequence represents a human tata-binding protein associated or, hTAFIIIO5, isolated from Daudi cell nuclear extracts. Tightly clated subunits (TAF's) are components of the transcription factor
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                                                                                         20; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome mapping; gene mapping; gene therapy; forensic;
upplement; medical imaging; diagnostic; genetic disorder.
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2000US-0649167.
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   are also used in
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                                                                                         No 39827; 103pp; English.
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Pred. No. 1.6
0; Mismatches
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sequence tags
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in a supplement of a consequence of the sequences have applications in
                                        N-PSDB;
                                                                               Dikstein R,
                                                                                                                                                                                        09-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription factor subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY57279 standard;
                                                                                                                                    27-AUG-1998;
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                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                              transcription factor; apoptosis; cytostatic; immunosuppressive;
antiinflammatory; virucide; antibacterial.
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                                                                                                                                                              25-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                   98IL-0125971
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834
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                                                                                                                                                                                                                                                                                                 /label=
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Polypeptide encoding TATA box binding protein associated useful for treating e.g. cancers and inducing apoptosis

factor II 105 has a dominant

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Best 1
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            gene
                   The TATA-binding protein associated factor hTAFIII30 (including specific antibodies and fusion products) are used in drug screeni diagnostics and therapeutics. They are used in the development c specific biochemical assays for screening compounds that agonise antagonise selected transcription factors involved in regulating
                                                                                                               TATA-binding protein associated protein factors corresponding nucleotide sequence and deriv. and in screening, diagnostics and therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This represents a polypeptide comprising a (modified) fragment (I) of a TATA box-binding protein associated factor II 105 (TAFIII05). A pharmaceutical composition comprising (I) or the polynucleotide or an inhibitor or antagonist of (I) is useful for treating cancers and inducing apoptosis in pathological cells. The composition is also useful
                                                                                                                                                                 N-PSDB;
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                                                                                                                                                                                                                                                             28-JAN-1993;
30-JUN-1993;
                                                                                                                                                                                                                                                                                                                       04-AUG-1994.
                                                                                                                                                                                                                                                                                                                                                                                          diagnostic;
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                                                                                           Disclosure;
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                                                                                                                                                                                                                                    (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                              28-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                    Homo
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Local :
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DB; AAQ70731.
            expression
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Wang E, Weinzierl ROJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     852
                                                                                          Page 142; 180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune diseases, inflammatory processes and viral or fertions
                                                                                                                                                                                                                                                                                                                                                                                                     protein associated factor; hTAFII130;
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93US-0087119.
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            associated with human
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Pred. No. 1.8e-54;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                          transcription regulation.
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            pathology
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RESULT 5
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28-JAN-1993;
30-JUN-1993;
                   The invention relates to purified proteins involved in transcription by RNA polymerase II, the RNA polymerase which transcribes messenger RNA. RNA polymerase II transcription proceeds in vitro upon addition of several nuclear fractions designated TFIIA, B, D, E, F, H, I and I to RNA polymerase II holenzyme. Fraction TFIID has been shown to contains a TBP and other TAFs. Purification of TFIID and separation cits components reveals 7 proteins ranging in size from 30-250 kD.
                                                                                                                                                                                                           This is the amino acid sequence of the human TATA-binding protein (TBP) associated factor (TAF) designated TAFIII30. The protein is a component of the TFIID fraction required for reconstituting RNA polymerase II in vitro transcription activity. The encoded protein has an estimated mol.
                                                                                                                                                                                                                                                                                                                                                                                                Screen for cpds. that bind human TATA-binding protein associated factor - by testing ability to bind to polypeptide fragments of factor, useful as (ant)agonists of transcription factors involved
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28-JAN-1993;
30-JUN-1993;
09-MAY-1996;
     AAW25018 represents TATA-binding protein associated factor (TAF) polypeptide, hTAFII100 (mol. weight 100kD). TAF peptides derived from hTAFII30 alpha, hTAFII30 beta, hTAFII40, hTAFII70, hTAFII700, hTAFII100, hTAFII130 hTAFII300, hTAFII30 hTAFII110 and nucleic acids encoding them, are used to modulate transcription, including transcription initiation. TAFS are nuclear proteins involved in RNA polymerase I, I and III transcription. The peptides act by binding to a different TAF, an activator, or TBP (TATA-binding protein) or competitively inhibiting association of a TAF domain with another compound, typically a protein like TBP or another TAF, an activator, or DNA.
                                                                                                                                     Claim 1;
                                                                                                                                                                   Nucleic acids encoding human TATA-binding protein associated (TAF) peptide(s) - for production of recombinant peptide(s),
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N-PSDB; AAT79595.
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                                                                                                                                                                                                         capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and useful cell interactions in higher enkaryotes for the development of the develop
                                   The sequence data for this patent did not form part of the pri specification, but was obtained in electronic format directly at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                          insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA Sequences (ABL9737-ABL75072)
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB63947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB63947 standard; Protein; 3726
                                                                                                                  sequences (ABL01840
(ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                   genes from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        483 D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 QP-PVLSLTQPTQVGVGKQGQPTPLVIQQPPKPGALIRPPQVTLTQTPMVALRQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 QPGPVLS--QPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTM 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHIRIMLTTPQQIQLIPPLQPVPVVKPAVLPGTKALSAVSAQAAAAQKIKLKEPGGGSFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVNTIPT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  737
                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 18633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -SQFPPASILKQITLPGNKIL---SLQASPTQKNRIKENVTSCFRD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.5%;
27.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                   acid
a and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ľ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PWD,
                                                                                                                                                                                                                                                                                                                                                                                                              detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                      21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    띭
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID NO 18633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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and c
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                                                                                         printed
                                                                                                                                                                                                                                                                                                                                                                                                                0 or more cell-cell
                                                                  from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     422
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Query Match Best Local S Matches 30

Similarity

14.18;

Score 79.5; Pred. No. 51;

DΒ 22;

Length

3726;

Conservative

24

Mismatches

50;

Indels

61;

Gaps

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Sequence

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RESULT 8
ABB60384
ID ABB6
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                                                              Query Match
Best Local
                                                  Matches
                                                                                                                                                                   useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                The
                                                                                                                                                                                                                                                                      Disclosure; SEQ ID
                                                                                                                                                                                                                                                                                                        New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2953
                                                                                               Sequence
                                                                                                                                    specification,
                                                                                                                                                                                                                                  capable
                                                                                                                                                                                                                                                                                                                                                                                    Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                           (PEKE )
                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB60384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB60384 standard; Protein;
  509
                                                                                                                                                            (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87
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                          s
                                                           COCAL
                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                sequence data
                      PVLSQPAGIPTGSSSKQ--LFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVN 62
PLKINVLGGSQGNSNKMRAIFNSASSIQHENG----VTTIVPASSLA---ASNQTAAMN 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPMQQRQEPAPLSNECPVVSSPTPPKPVEQPIIHQMTSASVSKCY 3116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSLQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FVMEPQALEQQELANRVQHFSTSSSSSSSSSSSSPTNVVNPMQQQAPSTTSSSTTRPTNRV 307:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASILKQITLPGNKI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKVTISQQR-IPAQTQQQQLQQAQMIHIPQQQQPLQQQQVQVQPSMPIITLAEAPVVQSQ 3011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGPVLSQPAGIPTGSSSKQL--FSLFHVVQQPSGGNEKQV----
                                                                                                                                                                                                                                                                                                                                                          2001-656860/75
                                                                                                                                                                                                                                                                                                                                               ABL04487
                                                                                                                                                                                                                                                                                                                                                                                                           PE CORP NY
                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                 Adams
                                                                                                622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               developmental biology; cell signalling;
                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-191637P.
2000US-0614150.
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                                                                                                                                    but was
                                                                                                                                for this patent did not form twas obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                  æ
                                                                                                                                                                                                                                                                     NO 7944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                           14.0%;
27.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -ASPTQKNRIKE----NVTSCF 107
                                                                                                                                                                                                                                                                                                                                                                                  PWD,
                                                                                                                                                                                                                                                                                                        detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 622
                                               Score 78.5; D
Pred. No. 5.6;
L9; Mismatches
                                                                                                                                                                                                                                                                     21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                 Myers EW;
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6;
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                                                40;
                                                                                                                                part of the printed format directly from
                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insecticide;
                                                                       622;
                                                                                                                                                                                                                                 The invention
                                               15;
                                               Gaps
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                                                                                                                                 WIPO
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RESULT 9
AAB94560
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                                   the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                        comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the
                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                      Primer sets for synthesizing
                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; primer;
                   of the present invention
                                                                                                                                                                                                                                           The present invention describes primer sets full-length cDNAs defined in the specificati
                                                                                                                                                                                                                                                                            Claim 8; SEQ ID 15332;
                                                                                                                                                                                                                                                                                                                                                                                         Ota T,
                                                                                                                                                                                                                                                                                                                                                                                                              (HELI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB94560 standard; Protein;
                               represent oligonucleotides,
                                                                                                                                                                                                                                                                                                 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                               Ishii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIIP-TSQFPPASILKQITLPGNKILSLQ----ASPTQKNRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIAPSTYTITPSSYGKKYTYPNPKFILLKPAKFYGPASANEV
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                                                                                                                                                                                                                                                                                                                                                                                       Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                              HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                           Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                  2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-0248036
99JP-0300253
                                                                                                                                                                                                                                                                                                                                                                            'n
                                                                                                                                                                                                                                                                                                                                                                                        Nishikawa T,
                                                                                                                                                                                                                                                                           2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                            Wakamatsu
                                                                                                                                                                                                                                          cribes primer sets for synthesising 56 in the specification. Where a primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID NO:15332
                               all of which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   696 AA
                                                                                                                                                                                                                                                                                                                                                                           Hayashi K,
ı A, Nagai K
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(, Otsuki
                               used
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                                                                                                                                                                                                                                                                                                                                                                                        Yamamoto
                               exemplification
                                                                                                                                                                                                                                            set
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Query Match Best Local S Matches 37

Similarity 37; Conserv

13.5%; ilarity 23.0%; Conservative

23;

Score 76; DB Pred. No. 13; 23; Mismatches

DB 13;

22;

Length 696

41;

Indels

60;

Gaps

8

Sequence

696 AA;

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AAB03192
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                                                                                  Matches
                                                                                              Query Match
Best Local
                                                                                                                                                           The invention relates to three polymorphic variants of a rat transcriptional regulatory factor Elf-1 (ARAB33190-B03192) and nucleic acids encoding them (ARAB1645-861647). The invention also encompasses the use of Elf-1 for regulating the transcription of a gene in an expression vector. The cDNA encoding rat Elf-1 variant #1 (ARAB1645) was isolated using PCR primers (ARAB1644-861649) based on mouse Elf-1 cDNA, and the rat Elf-1 variant #2 and 3# cDNAs (ARAB1646-A61647) were subsequently isolated. The Elf-1 cDNA and protein sequences are potentially useful for the prevention and treatment of immunological and allergic diseases mediated by Elf-1. The present sequence represents a variant (#3) of rat Elf-1.
                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                       A transcription regulating factor Elf-1 cDNA and its polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                           (ASAK ) ASAHI BREWERIES LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP2000135088-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Elf-1; transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat Elf-1 polymorphic variant #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB03192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB03192 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunological disease;
                             271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 PVPSSILQHVA-----SLQMKRESQNPDQKDETNSIKRE 158
  60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 VSQAGTLTLRISPPEPQSFASKTGSETKITYSSGGQPVGTASLIPLQSGSFALLQLPGQK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۍ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           w
PVNTIIPTSQFPPASILKQITLPGNKIL---SLQASP 93
                         QPSEVLRTVQPSQAPYPT---QLFRTVHVVQPVQAIPEEATIT----STMQEEAAGSSVQ
                                                   QPGPVLS--QPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTM 59
                                                                                                                                                                                                                                                                                                                                                                                    2000-425802/37
)B; AAA61647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --PASILKQITLPGNKILSLQASPTQKNRIKENVTSCFRDE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISHSSTLTIQ------KCGQKT-----MPVNT--IIPTS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGSVMGIRLPAPSKPSETPPSSTSSSAFSVMNPVIQAVGSSSAVNVITQAPSLLSSGASF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGPVL-----SQPAGIPTGSSSKQLFSLFHVVQQPSGGN------EKQVTT
                                                                                  30;
                                                                               Similarity 30.9
30; Conservative
                                                                                                                                                                                                                                                                                                                             Page 17-18; 21pp; Japanese.
                                                                                                                                      524 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       98JP-0309595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98JP-0309595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                             13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulatory factor; rat; polymorphic variant; allergic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "This region is apparently encoded by
                                                                             b; Score 74; DB
b; Pred. No. 14;
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    524
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                                                                                          DB
14;
                                                                                                        21;
                                                                                38;
                                                                                                        Length 524;
                                                                                Indels
                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -QFP---
                                                                            Gaps
                          323
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RESULT 1:
AAB03190
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                                                                                                                                                                            Matches
                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                               The invention relates to three polymorphic variants of a rat transcriptional regulatory factor Elf-1 (AAB03190-H03192) and nucleic acids encoding them (AAB61645-A61647). The invention also encompasses the use of Elf-1 for regulating the transcription of a gene in an expression vector. The cDNA encoding rat Elf-1 variant #1 (AA61645) was isolated using PCR primers (AAA61648-A61649) based on mouse Elf-1 cDNA, and the rat Elf-1 variant #2 and 3# cDNAs (AAA61646-A61647) were subsequently isolated. The Elf-1 cDNA and protein sequences are potentially useful for the prevention and treatment of immunological an allergic diseases mediated by Elf-1. The present sequence represents a variant (#2) of rat Elf-1.
          AAB03190 standard;
                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 13-14; 21pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                 A transcription regulating factor Elf-1 cDNA and its polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAA61646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-425802/37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP2000135088-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Elf-1; transcriptional regulatory factor; rat; polymorphic variant;
immunological disease; allergic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Elf-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat Elf-1 polymorphic variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB03191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB03191 standard;
                                                                                                                           326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ASAK ) ASAHI BREWERIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-OCT-2000
                                                                       379 GIRTIQASTQVP-----VVVSPGNQQLHTVTLQTVP 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 GIRTIQASTQVP-----VVVSPGNQQLHTVTLQTVP
                                                                                               60 PVNTIIPTSQFPPASILKQITLPGNKIL---SLQASP
                                                                                                                                                                                        Local
                                                                                                                                              2 QPGPVLS--QPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTM 59
                                                                                                                       OPSEVLRTVQPSQAPYPT---QLFRTVHVVQPVQAIPEEATIT----STMQEEAAGSSVQ 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gp
                                                                                                                                                                           Similarity
30; Conserv
                                                                                                                                                                                                                             579 AA;
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98JP-0309595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98JP-0309595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "Encoded 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Encoded by GAT"
          Protein; 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                     13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIT
                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               579
                                                                                                                                                                        Score 74; DB:
Pred. No. 16;
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by GAG
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                                                                                                                                                                                    . 16;
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                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354
                                                                                                                                                                          38;
                                                                                                                                                                                                 Length 579;
                                                                                                                                                                          Indels
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                                                                                                                                                                        Gaps
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RESULT 13
ABB50171
ID ABB50
XX ABB50
XX ABB50
XX ABB50
XX ABB50
XX Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to three polymorphic variants of a rat transcriptional regulatory factor Elf-1 (AAB03190-B03192) and nucleic acids encoding them (AAB1645-A61647). The invention also encompasses the use of Elf-1 for regulating the transcription of a gene in an expression vector. The cDNA encoding rat Elf-1 variant #1 (AAB61645) was isolated using PCR primers (AAA61648-A61649) based on mouse Elf-1 CDNA, and the rat Elf-1 variant #2 and 3# cDNAs (AAA61646-A61647) were potentially useful for the prevention and treatment of immunological ar allergic diseases mediated by Elf-1. The present sequence represents a variant (#1) of rat Elf-1.
                                                                                      Human; transcription factor; TRFX; cell proliferative disease; autoimmune disease; inflammation; neurological disease; developmental disorder; cancer; AIDS; infection; cytostatic; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A transcription regulating factor Elf-1 cDNA and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP2000135088-A.
                                                                           neuroprotective;
                                                                                                                                                                   Human transcription factor TRFX-22
                                                                                                                                                                                                          05-FEB-2002
                                                                                                                                                                                                                                            АВВ50171;
                                                                                                                                                                                                                                                                               ABB50171 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 8-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ASAK ) ASAHI BREWERIES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elf-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat Elf-1 polymorphic variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  362
                                                                                                                                                                                                                                                                                                                                                                       415 GIRTIQASTQVP-----VVVSPGNQQLHTVTLQTVP
                                                                                                                                                                                                                                                                                                                                                                                                              60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QPGPVLS--QPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTM 59
                                                                                                                                                                                                                                                                                                                                                                                                          PVNTIIPTSQFPPASILKQITLPGNKIL---SLQASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                OPSEVLRTVQPSQAPYPT---QLFRTVHVVQPVQAIPEEATIT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Similarity 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                        (first
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                                                                         antiinflammatory;
                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regulatory factor; allergic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                               591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 74;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
18;
                                                                       therapy
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                                                                                                                                                                                                                                                                                                                                                                       445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polymorphic variant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              STMQEEAAGSSVQ 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            615;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   including: arteriosclerosis, cirrhosis, hepatitis, cancers, AIDS, allergies, anaemia, asthma, autoimmune thyroiditis, bronchitis, atopic dermatitis, diabetes mellitus, emphysema, Goodpasture's syndrome, gout, Grave's disease, multiple sclerosis, osteoarthritis, pancreatitis, psoriasis, rheumatoid arthritis, systemic lupus erythematosus, ulceraticolitis, uveitis, Alzheimer's disease, Huntington's disease, Parkinson' disease, stroke, and viral, bacterial, fungal and protozoal infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillman
Azimzai
                                     peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolutio, dama amount of the system of the syste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor. The transcription factor and its coding sequence are useful in the diagnosis, treatment and prevention of diseases associated with altered expression of the transcription factor e.g. cell proliferative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel transcription factor polypeptides, used to treat diseases associated with altered activity and expression of TRFX, and to for agents capable of modulating its activity - {\sf TRFX}
                                                                                                                                                                                                                                                Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-570896/64.
N-PSDB; ABA82995.
                              chemokinetic;
                                                                                                                                                                                                                                                                                                                       22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                   AAM38686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM38686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       number of specific disorders/diseases are given in the specification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune/inflammatory, neurological and developmental disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Pages 164-166; 327pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reddy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INCY-) INCYTE GENOMICS
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leukaemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTVLKENV
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37; Conserv
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Bandman
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                                 thrombolytic;
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Tang
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                              drug
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P, Au-You
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RESULT 15
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Best Local S
Matches 37
                   AAM38685;
                                   AAM38685 standard;
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                                                                                                                                                                                                                                                                                                             The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptices (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous snjuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as
  22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                   Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang
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25-APR-2000;
                                                                                                                                                                                                                                     specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao
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19-OCT-2000;
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                                                                                                                                GOKTMPUNTIIPTSQFPPASILKQITL-----
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DB; AAI57842.
                                                                                              -NRIKENV
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Zhou P,
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                                                                                                                                                                                   Conservative
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2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0652191.
2000US-0693036.
2000US-0727344.
  (first entry)
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Wehrman T, X
Goodrich R,
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Pred. No. 22;
L1; Mismatches
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Xue
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. 22;
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Yang Y,
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Zhang i
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Wang J,
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21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                            14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                              peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndromo; chemotactic; chemokinetic; thrombolytic; drug screening.
                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                   26-DEC-2000;
                                                                                                                                                                                                                                                                                                                                          WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                          2000US-0552317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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Qian xB,
, Yang Y,
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Novel nucleic acids and polypeptides, useful such as central nervous system injuries for treating disorders

2001-442253/47. DB; AAI57841.

Wang 2 Zhou Liu

, v P,

Asundi V, Wehrman T, Goodrich F

Chen R,

nen R, Ma Y, tu C, Xue AJ, Drmanac RT;

Ren Zhang

Έ, J, Wang

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Example 3; SEQ ID NO 1830; 10078pp; English.

The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activitic such as: Immune system suppression, activity, hamcatic/chemokinetic activity, hamcostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and specification. .N.S disorders. ote: The sequence data for this patent did not moot part of the printed

Sequence 619 æ

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Matches
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Best Local 9
                     417
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97
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                                                               AQPSEVLRTVQPTQSPYPT---QLFRTVHVVQPVQAVPEG--EAARTSTMQDETLNSSVQ 416
                                                                                          AQPGPVLS-
                    SIRTIQAPTQVPVVVSPRNQQLHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP
                                           GQKTMPVNTIIPTSQFPPASILKQITL-----
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Search completed: February 16, 2003, 21:55:10 Job time : 10.4325~secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/B_COMB.pep:*
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US-09-95-776B-9
US-09-913-748-4
US-09-134-001C-4461
US-07-952-853-22
US-08-914-048-22
US-09-998-901-2
US-08-476-509B-2
US-08-476-509B-2
US-08-348-510C-2
US-08-98-937-2
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US-08-188-82-16

US-08-646-715-16

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US-09-514-247A-10

US-08-588-821-2

US-08-915-214-2
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US-08-477-389-2

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ALIGNMENTS

; TYPE: amino acid ; TOPOLOGY: linear ; MOLECULE TYPE: prot US-08-725-012-2 RESULT 1 US-08-725-012-2 Query Match Best Local S Matches 110 Patent No. 5710025 GENERAL INFORMATION: TELEFAX: (415) 343-4342 INFORMATION FOR SEQ ID NO: 2: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patenth Release #1.0, Version #1.30 CURRENT APPLICATION DATA: ATTORNEY/AGENT INFORMATION: NAME: OSMAN, RICHARD A REGISTRATION NUMBER: 36, COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk APPLICANT: Dikstein, Rivka APPLICANT: Tjian, Robert TITLE OF INVENTION: B-Cell Specific Transcription NUMBER OF SEQUENCES: 2 SEQUENCE CHARACTERISTICS: REFERENCE/DOCKET NUMBER: B9 TELECOMMUNICATION INFORMATION: CORRESPONDENCE ADDRESS: ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO FILING DATE: CLASSIFICATION: LENGTH: TELEPHONE: APPLICATION NUMBER: Similarity 94104 CALIFORNIA 801 amino acids USA 100.0%; ilarity 100.0%; Conservative C (415) 343-4341 protein US/08/725,012 36,627 0, в97-005 Score 562; DB 1; Pred. No. 9e-63; Mismatches 0; 0; Length 801; Indels 0 Gaps

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VNTIIPTSQFPPASILKQITLPGNKILSLQASPTQKNRIKENVTSCFRDE 552

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US-08-646-715-16
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-188-582-16
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Best Local Similarity
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GENERAL INFORMATION:
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   GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 16:
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CLASSIFICATION:
ATTORNEY_AGENT INFORMATION:
NAME: OSMan, Richard A
NAME: OSMan, Richard A
NAME: ATTORNEY ATTORNEY
NAME: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION
TELEPHONE: (415) 781-1989
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MEDIUM TYPE: Floppy disk
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Tanese, Naoko
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27.3%;
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TATA-BINDING
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Pred. No. 0.0046;
9; Mismatches 5
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                                 GENERAL INFORMATION:

APPLICANT: LYNN DOUGETTE-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                        Sequence 3773, App Patent No. 6380370
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Best Local Similarity
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TELEX: 910 27729
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 737 amino acids
                  FILE REFERENCE:
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TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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                                                                                                                       Application US/09134001C
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Tanese, Naoko
Wang, Edith
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Comai, Lucio
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SYSTEM: PC-DOS/MS-DOS
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NUMBER: US/09/134,001C
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Pred. No. 0.0046;
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LENGTH: 2442
; TYPE: PRT
; ORGANISM: human
US-09-514-247A-10
                                                                                     RESULT 6
US-08-588-821-2
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US-09-514-247A-10
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3773
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 30; Conser
                                                       Sequence 2, Application US/08588821 Patent No. 5712097
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Best Local
                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09514247A Patent No. 6365361
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                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/514,247A CURRENT FILING DATE: 2000-02-28 PRIOR APPLICATION NUMBER: PCT/JP98/03734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: JP231084/1997 PRIOR FILING DATE: 1997-08-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1998-08-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST TO ILE REFERENCE: TANIGUCHI=6
   APPLICANT:
                                                                                                                                                                                                                                                                                          1910 QPSPVSMSPAGFPSVARTQPPTTVSTGKPTSQVPAPPPPAQPPPAAVEAARQIEREAQQQ 1969
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                                                                                                                                                                                          79
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                                                                                                                                                                                          ITLPG--NKILSLQA 91
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 Kern,
Hahn,
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Scott E.
Stephan A.
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Pred. No. 4
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Pred. No. 0.
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Best Local
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                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kern, APPLICANT: Hahn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: La Jolla
STATE: CA
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                                                                                                                                 APPLICATION NUMBER:
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APPLICATION NUMBER:
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3. 5814457
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N: NOVEL TUMOR SUPPRESSOR GENE,
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32.8%;
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Pred. No.
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; MOLECULE TYPE: US-09-005-532-2
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   Query Match
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                                                                                                                              TELEFAX: 619/678-5099
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                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS
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                                                                                                                                                                                           NAME: Haile, Lisa A. REGISTRATION NUMBER: 38,347 REFERENCE/DOCKET NUMBER: 07
                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/005,532 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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REFERENCE/DOCKET NUMBER: 07265/079001
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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Similarity 32.8%;
22; Conservative
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                                                                                                                                               619/678-5099
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                                                                                             amino acids
                                               protein
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19-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOVEL TUMOR SUPPRESSOR GENE, DPC4
   11.78;
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                                                                                                                                                                                           07265/079001
 Score 66;
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Pred. No. 7
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RESULT 10
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          GENERAL INFORMATION:
                        Sequence 9, Application US/09096776B Patent No. 6270994
                                                                                                                                                                                                                          Matches
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APPLICANT:
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APPLICATION NUMRED.
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MEDIUM TYPE: Floppy disk
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                                                                                                           278 PNLPHHQ 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: REA, Teresa Stanek REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/701,582D FILING DATE: 22-AUG-1996 CLASSIFICATION: 435
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                                                                                                                                                                                                                                       Similarity
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amino acid
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P.O. Box 1404
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ER: 024916-004
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7; Mismatches
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Pred. No. 7
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APPLICANT: Kawabata, Masahiro TITLE OF INVENTION: SMAD6 AND USES THEREOF

L0461/7038

FILE REFERENCE:

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US-09-134-001C-4461
; Sequence 4461, Application US/09134001C
; Patent No. 6380370
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                                                                              RESULT 12
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 GENERAL INFO
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 4
LENGTH: 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HOWE, JAMES R.
APPLICANT: AALTONEN, LAURI A.
TITLE OF INVENTION: A GENE FOR JUVENILE POLYPOSIS
FILE REFERENCE: IOWA.021
CURRENT APPLICATION NUMBER: US/09/312,748
CURRENT FILING DATE: 1999-05-13
EARLIER APPLICATION NUMBER: 60/085,312
EARLIER FILING DATE: 1998-05-13
UNMBER OF SEQ ID NOS: 16
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PRIOR APPLICATION NUMBER: 1997
PRIOR FILING DATE: 1997
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver.
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CURRENT FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: US 60/049,990
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                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                  INFORMATION:
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Lynn Doucette-Stamm et al
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Pred. No. 7.1;
7; Mismatches
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Pred. No. 7
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; LENGTH: 451
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4461
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SEQ ID NO 4461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186
                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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            NAME: Murashige, Kate H
REGISTRATION NUMBER: 29
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55
                                                                                                                                                                                                                                             STATE: California
ZIP: 94304-1018
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                                                                                     CLASSIFICATION:
                                                                                                     FILING DATE:
                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                            CITY: Palo Alto
                                                                                                                                                                                                                                                                                             STREET:
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24.68;
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                                                                                                                      US/07/952,853
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                246152003500
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RESULT 14
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                                                                NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tent No.
                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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                                                                                          TELEFAX:
                                                                                                                                                NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,
                                                                                                                                                                                        APPLICATION NUMBER: UFILING DATE: 25-NOV-J
                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/914,848 FILING DATE:
                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                          TELEPHONE:
                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VNTIIPTSQFPPASILKQITLPGN 84
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                                        ENGTH:
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No. 5989887
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                                                                                                                                                                                                                                                                                                                                                   94304-1018
 TYPE:
                          amino acid
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                                       628 amino acids
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huis, Janna G.
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CLONING AND EXPRESSION OF DNA
MOLECULES ENCODING ARABINAN-DEGRADING ENZYMES OF FUNGAL
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Search completed: February 16, 2003, 22:03:01 Job time: 4.82655 secs
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                                                                                                                                                                                                               Query Match
Best Local S
Matches 26
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.7%;
Best Local Similarity 26.2%;
Matches 22; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Scott, Matthew
APPLICANT: Sisson, John C.
TITLE OF INVENTION: Costal2 Genes and their Uses
FILE REFERENCE: SUN-65P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 60/051,347 EARLIER FILING DATE: 1997-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/098,901B CURRENT FILING DATE: 1998-06-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ
                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: D. Melanogaster
                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
LOCATION: (1)...(1201)
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                   1141 TTTATATTTTSTTTTGAVGKVKDKALVSFRPEQLKRLMPAPTATKVTRQKNKIIIQDAS 1198
                                                                                                                                      1081 LIKAPKPMPTGSALDKYKDKEQRSGRNIFAKFHVLTRYASAAAAGSSGSTAEESTALIES 1140
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                                                                                                  40 ----- VTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASILKQITLPGNKILSLQAS 92
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Pred. No. 26;
18; Mismatches
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GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd

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Result
No.
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1 AQPGPVLSQPAGIPTGSSSK
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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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343
813
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10 US-09-815-242-14110

9 US-09-846-899-25

10 US-09-749-601A-9

11 US-10-109-886-8

10 US-09-729-674-176

10 US-09-729-674-176

10 US-09-78-295A-496

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9 US-09-738-65-5708
9 US-09-893-519A-14
12 US-10-109-886-10
10 US-09-815-242-12928
10 US-09-815-242-12929
10 US-09-815-242-12327
10 US-09-933-922-9
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Sequence 48, Appl
Sequence 5708, Ap
Sequence 10, Appl
Sequence 10928, A
Sequence 10928, A
Sequence 12792, A.
Sequence 13327, A
Sequence 9, Appl
Sequence 33, Appl
Sequence 14110, A
Sequence 25, Appl
Sequence 9, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 176, App
Sequence 496, App
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מהלמהונה דיהו נולה	2	9, Apr	Sequence 1093, Ap	7,	2	Sequence 6, Appli	4	Sequence 2, Appli	Sequence 6, Appli	4	2, Af	Sequence 106, App	Sequence 5075, Ap	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 25, Appl	Sequence 358, App	Sequence 358, App	358	Sequence 1, Appli	•	•	•	Sequence 358, App	Sequence 496, App

ALIGNMENTS

US-09-870-759-48

GENERAL INFORMATION:

CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14

APPLICANT: TERMAN, DAVID S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759

Sequence 48, Application US/09870759 Patent No. US20020177551A1

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RESULT 2
US-09-738-626-5708
; Sequence 5708, Application US/09738626
; Publication No. US20020197605A1
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-759-48
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GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSH
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                   282 LGPV 285
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                  MIZOGUCHI, HIROSHI
ANDO, SEIKO
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SEQ ID NO 5708
SEQ THE 215
                                                     SEQ ID NO 14
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                                                                                                         APPLICANT: DAVIDOV, Eugene
TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND METHODS
FILE REFERENCE: 0342/1G548-US2
CURRENT APPLICATION NUMBER: US/09/893,519A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,164
PRIOR FILING DATE: 2000-6-29
PRIOR APPLICATION NUMBER: US 60/224,457
PRIOR FILING DATE: 2000-08-10
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
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CURRENT FILING DATE: 2000-12-18
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: JP 00/280988 PRIOR FILING DATE: 2000-08-03
                                                                                              NUMBER OF SEQ ID NOS:
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ORGANISM: Homo sapiens
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                        IYPE: PRT
                                       ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 TSHIFSLV----QPLKGPPEAVSTIRATSSRVPERKHCAMAECSEST----GMICPSFAFE 120
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                                       1023
                                                                            PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                            SANDERSON, Karen
                                                                                                                                                                                                                                                                                                                                                MCCOY, Melissa
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DESILVA, Thamara
HARRIS, Sandra
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BUURMAN, Ed T.
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SENOH, AKIHIRO
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MENDILLO, Marc
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Pred. No. 3
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                                                                                                               US-09-815-242-10928
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; LENGTH: 2442
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                                                                            Sequence 10928, Application Patent No. US20020061569A1
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Best Local Similarity
Matches 30; Conserv
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                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION
APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/514,247
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 09/514,247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1998-08-24
PRIOR APPLICATION NUMBER: JP231084/1997
PRIOR FILING DATE: 1997-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/109,886
CURRENT FILING DATE: 2002-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUBLICATION INFORMATION:
DATABASE ACCESSION WUMBER: Human Genbank/CAA72189
DATABASE ENTRY DATE: 1997-06-25
RELEVANT RESIDUES: (1)..(1023)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND TITLE OF INVENTION: ANTAGONIST TO PPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: TANIGUCHI, Tomoy APPLICANT: MIZUKAMI, Junko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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OTHER INFORMATION: Corresponds to
                                                                                                                                                                                                                                                                                                                                    1910 QPSPVSMSPAGFPSVARTQPPTTVSTGKPTSQVPAPPPPPAQPPPAAVEAARQIEREAQQQ 1969
                                                                                                                                                                                        2030 QPMPGLPRPVISMQA 2044
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22.2%; Pred. No. 94;
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                                                                                            US/09815242
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Pred. No.
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                                                                                                    TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
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CURRENT FILING DATE: 2001-03-21
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                                         APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
APPLICATION NUMBER: 60/242,578
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FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
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                                                                                                                                                                                                                                                                                                   Xu, H. Howard
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Yamamoto, Robert T.
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Zyskind, Judith W.
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SOFTWARE: Fascus
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FUGTH: 792
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SEQ ID NO 12792
LENGTH: 748
                                                                          Query Match
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Best Local Similarity
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
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CURRENT FILING DATE: 2001-03-21
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                                                     Local
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SQPAGIPTGSSSKQLF----SLFHVVQQPSGGNEKQVTTISHSST---LTIQKCGQKTMP 60
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                                        . Similarity
27; Conser
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Yamamoto, Robert T.
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Zyskind, Judith W
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                                    Score 67; DB 10; Length 792;
Pred. No. 25;
23; Mismatches 35; Indels
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Pred. No.
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61 VNTIIPTSQFPPASILKQITLPGNKILSLQASPTQKNRIKENVTSCF 107

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US-09-964-899-33
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SEQ ID NO 9
SEQ TH: 552
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Best Local S
Matches 22
                                                         Query Match
Best Local :
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                                          Matches
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                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cohen, Dalia et al.
TITLE OF INVENTION: Identification of Genes Involved in
TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
FILE REFERENCE: 4-31612 A
                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/236,893
PRIOR FILING DATE: 2000-09-29
                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/964,899
CURRENT FILING DATE: 2001-09-27
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APPLICANT: Kawabata, Masahiro
TITLE OF INVENTION: SMAD6 AND USES THEREOF
FILE REFERENCE: L0461/7120
                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/298,309 PRIOR FILING DATE: 2001-06-14
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PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: US 60/053,040
PRIOR FILING DATE: 1997-07-18
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TYPE: PRT
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TYPE: PRT
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PRIOR APPLICATION NUMBER: 09/096,776
PRIOR FILING DATE: 1998-06-12
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                                      Local Similarity
nes 27; Conserv
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AQPGPVLSQ---PAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQK 57
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                                                                                                                                                                   1249
                                                                                                                                                                                                        FastSEQ for Windows Version 4.0
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                                        Conservative
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                                                     11.7%; Score 66; 21.3%; Pred. No.
                                      22;
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Pred. No.
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                                    Mismatches
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                                                                       Length 1249;
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RESULT 11
US-09-964-899-25
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                                                                                                                                                                                                                                                                                                                                                                : NAME/KEY: VARIANT
: LOCATION: (1)...(343)
: OTHER INFORMATION: Xaa - Any Amino Acid
US-09-815-242-14110
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
Sequence 25, Application US/09964899 Patent No. US20020174446A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 14110 LENGTH: 343
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CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 TSCFRDE 110
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                                                                                                                   83 ---QIGMI-----FQHFNLLSSRTVFGNVALPLELDNTPKEEIKRRVT 122
                                                                                                                                                          57 KTMPVNTIIPTSQFPPASILKQITLPGNKILSLQASPTQKNRIKENVT 104
                                                                                                                                                                                                   26 LHVPAGQIYGVIGASGAGKSTLIRCVNLLERPTEGSVMVGGQELTTLSESGLTKARR--- 82
                                                                                                                                                                                                                                                                                       Local Similarity
mes 26; Conserv
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                                                                                                                                                                                                                             7 LSQPAGI-----PTGSSSKQLFSLFHVVQQPSGGN----EKQVTTISHSSTLTIQKCGQ 56
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Zyskind, Judith W
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                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 1
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RESULT 13
US-10-109-886-8
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US-09-749-601A-9
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US-09-964-899-25
                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Cohen, Dalia et al.
TITLE OF INVENTION: Identification of Genes Involved in
TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
FILE REFERENCE: 4-31612 A
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/749,601A CURRENT FILING DATE: 2000-12-28 PRIOR APPLICATION NUMBER: 60/183,333 PRIOR FILING DATE: 2000-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Vogelstein, Bert TITLE OF INVENTION: A method for generating hypermutable TITLE OF INVENTION: plants FILE REFERENCE: 01107.00069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2001-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Nicolaides, Nicholas
                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Arabidopsis thaliana
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 737
                                                                                                                                                                              369 EQKVEYI--QSTLTSQKSDSPVSQKPSGQKTQKVPVNKMVRTDSSDPAGRLHAFLQPKPQ 426
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                                                                                                       427
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                                                                                                                                                                                                   37 EKQVTTISHSSTLTIQK-------CGQKT--MPVNTIIPTSQFPPASIL-------KQI 79
                                                                                                                                      80 TLPGNKILSL --- QASPTQKNRIKE 101
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                                                                                                   SLP-DKVSSLSVVRSSVRQRRNPKE 450
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27.7%;
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Pred. No. 43;
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US-09-729-674-176
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                                   SEQ ID NO 176
LENGTH: 832
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CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 09/514,247
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: PCT/JP98/03734
PRIOR FILING DATE: 1998-08-24
                                                                                                                                                                                    TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING FILE: REFERENCE: 6055-64X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: JP231084/1997 PRIOR FILING DATE: 1997-08-27 NUMBER OF SEQ ID NOS: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                              PRIOR APPLICATION NUMBER: 09/539,330 PRIOR FILING DATE: 2000-03-30
                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
                                                                        SOFTWARE: PatentIn Ver.
                                                                                            PRIOR FILING DATE: 2000-03-30 NUMBER OF SEQ ID NOS: 283
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TYPE: PRT
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2027 IPQQQPMPGMPRPVMSMQA 2045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1971 QHLYRANINNGMPPGRDGMGTPGSQMTPVG----LNVPRPNQVSGPVMSSMPPGQWQQAP 2026
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 Homo sapiens
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MIZUKAMI, Junko
                                                                                                                                                                                                                          Fechtel, Kim
Genetics Institute,
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Treacy, Maurice
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Evans, Cheryl
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LaVallie, Edward R.
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US-09-864-761-43246
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Best Local Similarity
Matches 32; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: AGOMICS-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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              APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21 APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
                                                                                                                                                          FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
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FILING DATE: 2000-05-26
APPLICATION NUMBER: US 09/632,366
FILING DATE: 2000-08-03
                                                                                              APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                         FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
                                                                                                                                      FILING DATE:
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FILING DATE: 2001-01-30
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                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                             FILING DATE:
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Hanzel, David K.
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Pred. No. 57;
4; Mismatches 46
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Matches 31
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SOFTWARE: Annomax Sequence
SEQ ID NO 43246
                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005859.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.99
OTHER INFORMATION: EST_HUMAN HIT: AW867810.1, EVALUE 5.00e-13
OTHER INFORMATION: SWISSPROT HIT: Q28888, EVALUE 4.00e-14
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1: /cgn2_6/ptodata/2,
2: /ggn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
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2558
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Maximum Match 100%
Listing first 45 summaries
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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                                       4 US-09-122-400B-5
US-09-253-691-3
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US-08-928-361B-4
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US-08-625-188-19
US-08-625-188-19
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US-08-615-022A-10
US-08-615-022A-10
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US-08-615-022A-253
US-09-427-048A-10
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US-08-613-906A-18
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	.5012	ALIGNMENTS	US-08-446-915-1	US-08-250-858-1	US-08-331-394-1	US-08-900-117A-2	US-08-961-527-55	US-09-791-211-10	US-09-351-414-3	US-08-483-432-20	US-08-479-939-20	US-08-361-920-20	US-08-687-080-115	US-08-682-517-8	US-08-682-517-7	US-08-682-517-14	US-08-682-517-13	US-09-528-784A-13	US-08-723-142A-13	US-08-990-571-13

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; LOCATION:
US-08-725-012-1
                                                                                                                                                                         TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENCTH: 2556 base pairs
TYPE: nucleic acid
 Matches 2556;
                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-Lease #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: B-Cell Specific Transcription NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                              FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: B9
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,
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MEDIUM TYPE: Floppy disk
                                                                                                                             MOLECULE TYPE: CDNA
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                  Local Similarity
                                                                                                                                                TOPOLOGY:
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                  Score 2534;
Pred. No. 0;
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                  0;
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1020 1019`	61 AGCACCCAGAACTGTGTCAGTGCAAACTTTGAACCCACTTGCTGGTCCAGTGGGAGCAAA 	9 9
960 959	GGTGACAACTACAGTGTCCTCAAGCCAGTCTGAAAAGTCAATTATTGTTTCTGGAGCAAC 	y y
900	GCAGACTTCTAGTGACATGGTCATTGCTACCTGTACTACAACAGTAACAACTTCTCCTGT	& &
840 839	CGTGGTTGCCTTACGACAACTTCTGCCTAACTCCCAGAGCTTCATCCAGCAATGTGTTCA	7
780 779	ACTGTATGTTGAACTCAAGTCTTCACCTCAGCCTCACCTGGTTCCTTTTCTTAAGAAAAG 	7
720 719	GAAGAAGCTGGTGGAACAACTTTTGGATGCAAAAATCGAAGCAGAAGAATTTACTAGGAA 	σ , σ,
660 659	TGCAATGTTAATAAACTAGCATGTAGTGGATCACAGTCCCCTGAAATGGGGGCAAAATGT 	თ თ
599	TGTTCAGATTAATCTTTCTCCGACAATGCTAGAAAATGTGAAGAAATGCAAGAACTTCCT 	и и
540 539	TTTGGGAGCATCATCCACTCCTTCAAATGAGCCCAATCTTAAAGCAGAGAACTCAGCAGC	4 4
480 479	RGTCGTCACAGTTACTCCTGGAAAGCCATTGAATACTGTAACTACCCTGAAGCCTTCAAG 	4 4
420 420	ACTGTGGTAACCACTGTTCCGAAGCCTTCCTCAGTACAATCTGTGGCTGTGCCAACCAGT	w w
360	TCACAATTAATCAAGAAAGTGGCAGTGACACCTGTTAAAAAATTGGCACAAATAGGAACT 	w w
300	AGGCCAGCAGTACCAGCGAATCCTCAAACAGTCAAAATCTGTACAGTGCCGAACTCTAGC	NN
240 240	181 ATGTTGGTATCTCCTCAGCAAACTGTAACAAGAGCCGAGAGCACAAGTAACATAACCTCA 	
180	CCTGCTAATTIGCAGCTTCCTCCAGGAACCGTTTTGATTAAAAGTAACAGTGGTCCGTTG	
120 120	AGGCTGCCTCCTCAGATAGTCGCCGTGAAAGCCCCCAACACCCACGACAATCCAGTTT 	
60	1 GGGACCCTGGTGACCAAAGTGGCTCCGGTCAGCGCCCCTCCTAAAGTCAGCAGCGGCCCT	

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2160 2158	01 CAGAACAGCTGAGATTAAAGCAGAAAGCCAAAGAGTTACAGCAATTGGAACTTGCACAGA 	D Qy
2100 2098	2041 ATTTGGAAGAAAAGAGAAATGTTACTTAAGGCAGCCAAGAGTCGTTCTAATAAAGAAGATC 	Db
2040 2038	981 ATACCAGGTCACAGCTCAAATTTCTTGAAAAGCTGGATCAATTGGAGAAAGCAGAGAAAGG 	do Qy
1980 1978	21 CAATTGCTCAGCATCGAATGACTACTTACAAGGCAAGTGAAAATTACATCCTGTGTAGTG	dg Qy
1920 1918	861 TGAACTTGATCTCCCAAGCAAGCAGGACAGGACTACGAGGCCTTCTAGAAAAACTGACTG	Qу
1860 1858	801 AAAAGAGAATCTTAGACATTGGTAAAAAGCATGACATTACAGAACTTAACTCTGATGCTG	dg VQ
1800 1798	741 TGGTTGGCACACTCATTCAGTCATGTAAAGATGAACCATTTCTTTTTATTGGAGCTCTAC 	Дy
1740 1738	81 CTATGGCAGGGGTCAACCTTAATGAAGAAAATGCCTGCATCTTAGCAACAACTCTGAAT 	ру
1680 1678	621 GAATAAAAGAGAATGTAACATCATGCTTCCGAGATGAGGATGACATCAATGATGTGACTT 	ФФ
1620 1618	561 AATTACCTCTGCCTGGAAATAAAATTCTGTCACTTCAAGCATCTCCTACTCAGAAAAATA	Оy
1560 1559	501 GATGCCAGTGAACACCATAATACCTACTAGTCAGTTTCCTCCAGCTTCCATTCTAAAGCA 	Qу
1500 1499	41 ACAAGTGACCACAATTTCACATTCCTCAACATTGACCATTCAGAAATGTGGACAGAAGAC	Db dy
1440 1439	381 AAGCAAGCAACTATTCTCATTGTTTCACGTAGTTCAGGAGGCTTCAGGAGGCAATGAAAA	рь
1380 1379	1321 CAAACTTGCCCAGCCGGCCCTGTCCTTTCACAACCAGCTGGGATTCCAACAGGCAGTTC	Db Qy
1320 1319	1261 TGTTGTTTCCTTCTGCTGGGACCACATCTGCAAGCCTGTTATTGGGACTCCAGTTCAAAT	рb
1260 1259	1201 TCCAGCAGTAACTTTTGGAGAAACTTCAGGTGCAGCTATTTGTCTTCCATCTGTGAAACC	Qу
1200 1199	1141 CACGGTCTCACTGCAACCTGAAAAGCCAGTTGTCTCTGGAACAGCAGTAACACTGTCCCT	Qy db

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                    TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 3603 base pairs
TYPE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert (
TITLE OF INVENTION: TATA-BIND
TITLE OF INVENTION: NUCLEIC AN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: OSMAN, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIIM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
STREET: 4
                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
COUNTRY: USA
              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-4187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                           4 Embarcadero Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Weinzierl, Robert O.J.
VENTION: TATA-BINDING PROTEIN ASSOCIATED
VENTION: NUCLEIC ACIDS ENCODING TAFS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruppert, Siegfried
Tanese, Naoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dynlact, Brian D. Hoey, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tjian, Robert
Comai, Lucio
                                                                                                                                                                                                                                                                                                                                                                                          FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT Embarcadero Center, Suite 3400
              linear
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                                                                                                                                                    A-57650-2/AJT/RAC
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Best Local
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Local Similarity 63.9%;
es 536; Conservative
                 GGAACAGGAACGGGAGATGAAGTATTCTCGAGCTCTATACCTGGCCCTTCTGAAGTGAC 2409
                                                                                           CAAACAGTTGCATCGTCCAAGAATCACGAGAATCTGCCTCAGGGACTTGATATTTTGTAT
                                                                                                                                                                                                                                                                                                                                  TAAGGCAGCCAAGAGTCGTTCTAATAAAGAAGATCCAGAACAGCTGAGATTAAAGCAGAA
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RESULT 3 US-08-646-715-15

Sequence 15, Application US/08646715
Patent No. 5637686
GENERAL INFORMATION:
APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Dynlact, Brian D.

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US-08-646-715-15
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Best Local Similarity
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REFERENCE/DOCKET NUMBER: A-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0,
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                                                   AAAACATGGTATAACGGAATTACATCCAGATGTAGTAAGTTATGTATCACATGCCACGCA
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San Francisco
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Tanese, Naoko
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Pred. No. 6.3e-92;
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                                             APPLICATION NUMBER: US/08/
FILING DATE: 28-7AN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,62
                                                                                                                                                COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: TATA-BINDING PROTEIN AS TITLE OF INVENTION: NUCLEIC ACIDS ENCODING NUMBER OF SEQUENCES: 36
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                                                                                                                                                                                                                                                                                             CITY: San Francisco
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Weinzierl, Robert O.J
JENTION: TATA-BINDING
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Tanese, Naoko
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                                                                                                                                                                                                                                                                                                                                  Suite
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                                                                                                                                                                           Version #1.25
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TELEFAX:

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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 4615 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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hes 395;
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TGTCGCAGTTCCATGCTGTTCAAGACATACCTCAAGTGATCGCTGCTGTTGCCCCATCAA 3323
                                                                        AGAATCACGAGAATCTGCCTCAGGGACTTGATATTTTTGTATGGAACAGGAACGGGAGATG
                                                                                                                                            AACCTTCTTGCTTCTGG----GACATCCAGCCTGACAGCCACCAAACAGTTGCATCGTCCA 2309
                                                                                                                                                                        GAGATGCAACGCGCCGAAATGGAGGAGTTGCGTCAACGAGATGCCAATCTGACGGCGCTG
                                                                                                                                                                                                                                                                                                                                                                                     CTGAAGAACATCGTTGAGAAGTTGGCTGTGATAGCGGAGCACCGCATTGATGTCATCAAG
                                                                                                                GGTTCAAGTGGCGGGGGGGTGCTAAGCAGCTCGGGATCTGCGCCGACGACGTTACGGCCT
                                                                                                                                                                                                                                                                GAGTTACAGCAATTGGAACTTGCACAGATACAGCATAGAGACGCTAATCTCACAGCTCTT
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                           CGCATAAAACGTGTGAACCTGCGCGACATGCTCTTCTACATGGAGCAAGAGCGGGAGTTC
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Pred. No. 1.7e-32;
0; Mismatches 378;
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RESULT 5 US-08-646-715-1

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                                                                                                                                                                                                                                                                    Query Match 5.6%;
Best Local Similarity 50.7%;
                                                                                                                                                                                                                                                        Matches
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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2725
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                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                             2665
                                                                                                                           2608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 09-MAY-1996
                                                                                                                                                                                                                                                                                                                                     LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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GGACTGGATGAGCCGTCGCAGGATGTGGCCGTTCTGATATCGCACGCCTGTCAGGAGCGC
                          GACATTACAGAACTTAACTCTGATGCTGTGAACTTGATCTCCCAAGCAACACAGGAACGA 1892
                                                                                                                         CAGCGAATTCTCGGCTGTA----CCGAAAACATCGGCACGCAGATTCGATCCTGCAAAGAT
                                                                                                                                                       GCCTGCATCTTAGCAACAAACTCTGAATTGGTTGGCACACTCATTCAGTCATGTAAAGAT 1772
                                                            GAGGTTTTTCTTAATCTCCCCTCGCTGCAAGCTAGAATACGGGCAATTACTTCGGAGGCG
                                                                                        GAACCATTTCTTTTATTGGAGCTCTACAAAAGAGAATCTTAGACATTGGTAAAAAGCAT 1832
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Tanese, Naoko
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Comai, Lucio
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Pred. No. 1.7e-32;
                                                                                                                                                                                                                                                     Mismatches 378;
                                                                                                                                                                                                                                                                                   Length 4615;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
             FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 304
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                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                         FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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VENTION: RECOMBINANT FOWLPOX VIRUS
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; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: (1)...(2169)
; OTHER INFORMATION: n =
US-09-434-408-3
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.US-08-232-463-14
                                                                                                                                                       NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09434408 Patent No. 6440697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.3%; Score 57.6; DB 1
Best Local Similarity 3.8%; Pred. No. 9.2e-07;
Matches 15; Conservative 226; Mismatches 15
                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/434,408
CURRENT FILING DATE: 1999-11-04
EARLIER APPLICATION NUMBER: US 60/108,258
EARLIER FILING DATE: 1998-11-12
                                                                                                                                                                                                                                                                 APPLICANT: Venezia, Domenick
APPLICANT: Grossmann, Angelika
TITLE OF INVENTION: RING FINGER PROTEIN ZAPOP3
FILE REFERENCE: 98-41
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TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                       OTHER INFORMATION: Degenerate polynucleotide sequence
                                                                                              FEATURE:
                                                                                                                                           LENGTH:
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Patent No. 5766597
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                                  CLASSIFICATION DATA:
PRIOR APPLICATION UMBER: US 08/075,783
PRIOR DATE: 11-JUN 1993
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                                PRIOR APPLICATION DATA:
                                                                                                                                                                         CURRENT APPLICATION DATA:
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APPLICANT: Tine,
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hes 111;
                                                                                                                 FILING DATE: 09
CLASSIFICATION:
APPLICATION NUMBER: US 07/852,305 FILING DATE: 18-MAR-1992
                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 09-JUN-1994
                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                  COMPUTER:
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                                                                                                                                                                                                                                                                                                             UNITED STATES OF AMERICA
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Tine, John A.
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SYSTEM: PC-DOS/MS-DOS
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21.8%; Pred. No. 0.
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                                                                                                                    US-09-122-400B-5
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US-09-122-400B-5/c
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Best Local Similarity
Matches 137; Conserv
                                                                                                                                                                          SOFTWARE:
SEQ ID NO 5
                                                          Matches
                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/09122400B Patent No. 6245974
                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/122,400B
CURRENT FILING DATE: 1998-07-24
                                                                                                                                                                                                                                                                                     APPLICANT: Michalowski, Stapplicant: Spiker, Steven APPLICANT: NOTE OF INVENTION: MATRITUDE OF INVEN
                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1997-08-06
                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                             LENGTH: 998
TYPE: DNA
                                                                                                                                ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                          1768
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                   REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 20-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1812 TTAGACATTGGTAAAAAGCATGACATTACAGAACTTAACTCTGAT 1856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1708
809 CAAATTTTACTAAAAACTGAAAAAACGAAAATATTGTTTTCAAGTTTTTACAAAAAAA 750
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                                                          84;
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                                                          Conservative
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                                                                      Pred.
                                                                        Score 36; Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                             Spiker
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                                                         Mismatches
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                                                                                    DB 4; Length 998
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US-08-700-651-1
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US-09-253-691-3
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Best Local Similarity
Matches 108; Conserv
             SEQ ID NO 1
LENGTH: 5163
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                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08700651B Patent No. 6015882
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Patent No. 6124100
                                                                                                                   APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, F
TITLE OF INVENTION: FOR PROPHYLAXIS AND TRE
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-4(HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
                                                                    EARLIER FILING DATE: 1995-04-03 NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                  APPLICANT: LEECH, JAMES APPLICANT: NELSON, RICHARD, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/253,691
CURRENT FILING DATE: 1999-02-22
EARLIER APPLICATION NUMBER: KR 98-6,278
EARLIER FILING DATE: 1996-02-26
                                                 SOFTWARE: PatentIn
                                                                                                      EARLIER APPLICATION NUMBER: 08/415,751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dong Kyu JIN
TITLE OF INVENTION: Diagnostic Method and kit for Neuropsychiatric Diseases
TITLE OF INVENTION: Using Trinucleotide Repeats Sequence
FILE REFERENCE: 1942/36
                                                                                                                                                                                                                                                                                        APPLICANT: PETERSEN,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 397
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DNA
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                                                   Ver.
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                                                                                                                                                                                             TREATMENT OF Cryptosporidium
                                                                                                                                                                                                            PROTEINS, GLYCOPROTEINS, DNAS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121;
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RESULT 12
US-08-928-361B-4
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US-08-928-361B-4
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Best Local Similarity 45.5
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APPLICANT: Peters
                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
             TOPOLOGY: 1
MOLECULE TYPE:
                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 5163 base pairs
                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1103 TCAAAACCACTTGTGACATCTGTGGCAAACACAGTGA 1139
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                                                                                                                                                                               NAME: Verny, Hana
REGISTRATION NUMBER: 30
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 385 Sner
                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/928,361B FILING DATE: 12-SEP-1997
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                                                            nucleic acid
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                                                                                                                              650-324-1678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PETERS, VERNY, JONES & BIKSA
             DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08928361B
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Pred. No. 3.9;
0; Mismatches 151;
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; LENGTH: 5318
; TYPE: DNA
; ORGANISM: Cryptosporidium parvum
US-08-700-651-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NELSON, RICHARD, C.
APPLICANT: OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPTOSPORIGIUM PARVUM
TITLE OF INVENTION: INVECTIONS
FILE REFERENCE: 480.19-4(HV)
CURRENT FILING DATE: 1997-08-14
CURRENT FILING DATE: 1997-08-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: 08/415,751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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               1103
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Local Similarity 45.5%;
TCAAAACCACTTGTGACATCTGTGGCAAACACAGTGA
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Pred. No. 3.9;
0; Mismatches 151;
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5318 base pair
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NAME: Verny, Hana
REGISTRATION NUMBER: 30,
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APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
                         1103 TCAAAACCACTTGTGACATCTGTGGCAAACACAGTGA 1139
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                      AGCCAGTCTGAAAAGTCAATTATTGTTTCTGGAGCAACAGCACCCAGAACTGTGTCAGTG
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                                                      TCTGTGGGCCCAACTGCTGCAACAGGAGGAACAACAGCTGGAACTGGTTTGCTTCAGACT 1102
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94306-1840
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                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                      1.48;
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PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS, A
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n Avenue, Suite 6
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RESULT 15
US-09-512-342-1/c
; Sequence 1, Application US/09512342
; Patent No. 6388068
; Patent No. 6388068
; GENERAL INFORMATION:
   APPLICANT: MASUDA, SUSUMU
; APPLICANT: MASUDA, SUSUMU
; TITLE OF INVENTION: METHOD FOR PRODUCING FOREIGN POLYPEPTIDE IN PLANT
TITLE OF INVENTION: INTERCELLULAR FLUID
; FILE REFERENCE: 081356/0142
; CURRENT APPLICATION NUMBER: US/09/512,342
; CURRENT FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2030
; TYPE: DNA
; ORGANISM: Cucumis sativus
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Search completed: February 16, 2003, 22:29:35 Job time : 158 secs
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Title:
Perfect score:
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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1: /cgn2_6/ptodata/2/pubpna,

2: /cgn2_6/ptodata/2/pubpna,

3: /cgn2_6/ptodata/2/pubpna,
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/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
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US-09-960-352-11227
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US-09-964-761-1914
US-09-964-761-10113
US-09-964-761-12567
US-09-9864-761-12567
US-09-9815-242-3827
US-09-9815-242-3827
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US-09-9815-242-3827
US-09-974-300-101
US-09-9764-878-403
US-09-764-878-403
US-09-796-988-1
 US-09-822-846-198
US-09-864-761-286
US-09-864-761-120
                                                     US-10-118-328-3
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US-09-070-927A-516
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-864-761-28655
-864-761-12075
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                                                                                                                                                                                                                                                                                                                                                     Description
              Sequence 3, Ap
Sequence 198,
Sequence 2865
                                                                                                 Sequence 516, App
Sequence 11462, A
Sequence 1127, App
Sequence 9944, App
Sequence 10113, A
Sequence 118737, A
Sequence 12567, A
Sequence 5267, Appli
Sequence 3827, App
Sequence 6667, App
Sequence 6667, App
Sequence 101, App
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ALIGNMENTS

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; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Human Genbank/Y11354.1
; DATABASE ENTRY DATE: 1997-06-25
; RELEVANT RESIDUES: (1)..(2307)
US-09-893-519A-87
                                                                                                                                                                 SEQ ID NO 87
LENGTH: 2307
   Query Match
                                                                                                                                                                                                                            APPLICANT: DAVIDOV, Eugene
TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND METHODS OF
FILE REFERENCE: 0342/16548-US2
CURRENT APPLICATION NUMBER: US/09/893,519A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,164
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/224,457
PRIOR PILING DATE: 2000-08-10
PRIOR FILING DATE: 2000-08-10
UMBER OF SEQ ID NOS: 146
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                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                             PatentIn version 3.1
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DESILVA, Thamara
HARRIS, Sandra
KOMARNITSKY, Svetlana
MENDILLO, Marc
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MOORE, Jeffrey
BUURMAN, Ed T.
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                                                                                                                                                                                                                                                                                                                                                                                                                          LONG,
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 5.3%; Score 135.8; DB
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Length 2307;
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US-09-070-927A-516
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US-09-070-927A-516
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                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1836
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                TOPOLOGY: linear SEQUENCE DESCRIPTION:
                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Enterococcus NUMBER OF SEQUENCES: 982
                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGCTGACCCCGACTCCGCGGCCTTCATCCAGCAGAGCCAGCAGCAGCC
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                                                        STRANDEDNESS: double
                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                            NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/066,009 FILING DATE: 1997-11-14
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/044,031 FILING DATE: 1997-05-06
                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/046,655 FILING DATE: 1997-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: MSDOS version SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Rockville
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                                                                                          LENGTH: 5101 base pairs
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Patrick J. Dillon
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US-09-960-352-11227/c

; Sequence 11227, Application US/09960352

; Patent No. US20020137139A1
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APPLICANT: Mathialgan, Nagappan
TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/99/960,352
CURRENT APPLICATION UNBER: US/99/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11462
LENGTH: 438
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Best Local :
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: BOS taurus
OTHER INFORMATION: Clone ID: 49-LIB3058-045-Q1-K1-E2
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                                                                                                                                                                                                                                                                               232 AAAATACTGGAAAAATGAAAAAAGGCAGAGACTTTGTACAGACAAAAATCTAAATTTTC
                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                   CTAGCTCTAACGCTTCTAGCTGCTCAAATAATGTGGAACCT
                                                                                                                                                           TTGGATGCAAAAATCGAAGCAGAAGAATTTACTAGGAAACT 723
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                                                                                                                                                                                                  TGGAAGGGTTTTGTGTGCCCTACACACGGGGGCAATTTGTACACACTAGTGAAATGAACA 113
                                                                                                                                                                                                                                         TGTAGTGGATCACAGTCCCCTGAAATGGGGCAAAATGTGAAGAAGCTGGTGGAACAACTT 682
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Pred. No. 0.
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Pred. No. 2
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GENERAL

INFORMATION:

APPLICANT: Warren, APPLICANT: Tao, No APPLICANT:

Warren, wengbing
Tao, Nengbing
Tao, Nengbing
Tao, Nengbing
Negapan

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; LENGTH: 442; TYPE: DNA; CRGANISM: Bos taurus; OTHER INFORMATION: Clone ID: 48-LIB3058-045-Q1-K1-D8 US-09-960-352-11227
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CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICR FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                         APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
                                                                                                                                             APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
                                                                                                                                                                                  FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00667 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: GB 24263.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/207,456
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                                     APPLICATION NUMBER: PCT/US01/00662
                                                                                                   APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00661
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Chen, Wensheng
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248 CAGTACCAGCGAATCCTCAAACAGTCAAAATCTGTACAGTGCCGAACTCTAGCTCACAAT 307

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; OTHER INFORMATION:
US-09-864-761-9944
                                                                                                  US-09-967-768A-314
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US-09-967-768A-314
                                                                                                                                       SEQ ID NO 314
SEQ THE 174424
                                 Best Loc
Matches
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                                                                  Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 689290-72
CURRENT APPLICATION NUMBER: US/09/967,768A
CURRENT FILING DATE: 2001-09-28
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PRIOR FILING DATE: 2000-09-28
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PRIOR APPLICATION NUMBER: US/60/236,111
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                                                                                                              TYPE: DNA
ORGANISM: Homo
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                                 Local Similarity es 81; Conserv
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
TATCTCCTCAGCAAACTGTAACAAGAGCCGAGACCACAAGTAACATAACCTCAAGGCCAG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAAAATGCTAGGGATAAAAAAAAAAAAA 179
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Pred. No. 1
                                               Score 36.6;
Pred. No. 87;
                                 Mismatches
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    Query
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EQ ID NO 10113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                    OTHER INFORMATION: MAP TO AL035457.11
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL =
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL =
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                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                LENGTH:
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  Match
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
APPLICATION NUMBER: US 09/608,408
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APPLICATION NUMBER: PCT/US01/00669
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APPLICATION NUMBER: PCT/US01/00667
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FILING DATE: 2001-01-30
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NUMBER: PCT/US01/00668
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US-09-864-761-18737
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                                  FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00661
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NUMBER: US 09/608,408 : 2000-06-30
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US-09-864-761-12567; Sequence 12567, Application; Patent No. US20020048763A1
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SEQ ID NO 18737
LENGTH: 510
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PRIOR EILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR EILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR EILING DATE: 2000-08-03
PRIOR EILING DATE: 2000-08-03
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CURRENT FILING DATE: 2001-05-23
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.85
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.85
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4.6
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4.6
OTHER INFORMATION: EXPRESSED IN BT574L SIGNAL = 0.93
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.93
OTHER INFORMATION: NT HIT: U01287.1, EVALUE 1.30e+00
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                                            OR FILING DATE: 2000-08-03
OR APPLICATION NUMBER: GB 24263.6
OR ETLING DATE: 2000-10-04
OR APPLICATION NUMBER: US 60/236,359
OR FILING DATE: 2000-09-27
OR APPLICATION NUMBER: PGT/US01/00666
OR FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00667 FILING DATE: 2001-01-30
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Pred. No.
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RESULT 10 US-09-816-894-5/c

Sequence 5, Application US/09816894 Patent No. US20020073448A1 GENERAL INFORMATION:

APPLICANT: Michalowski, Susan

APPLICANT: Spiker, Steven
TITLE OF INVENTION: MATRIX ATTACHMENT REGIONS
FILE REFERENCE: 5051.401XXDV
CURRENT APPLICATION NUMBER: US/09/816,894
CURRENT FILING DATE: 2001-06-20

; ORGANISM: Nicotiana tabacum US-09-816-894-5

SEQ ID NO 5 LENGTH: 998 TYPE: DNA

NUMBER OF SEQ ID NOS: 22 SOFTWARE: PatentIn versi

version 3.0

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SEQ ID NO 12567
LENGTH: 591
                                                                                                                                                                                                                                           Query Match
Best Local
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.68
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.62
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.62
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                             1674
                                                                                                                                                                                 1614 AAAAATAGAATAAAAGAGAATGTAACATCATGCTTCCGAGATGAGGATGACATCAATGAT 1673
   353
                                                                          293
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00662
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FILING DATE: 2001-01-30
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                                    TCTGAATTGGTTGGCACACTCATTCAGTCATGTAAAGATGAACCATTTCTTT 1785
                                                                                                           GTGACTTCTATGGCAGGGGTCAACCTTAATGAAGAAAATGCCTGCATCTTAGCAACAAAC 1733
                                                                                                                                               AGAAATAGAGTGAGAAAACAAAACAGCACCAAGAAAACATGACAATAGAAAGTGGGAT
                                                                        TGTCAAGTAGATGGATACCTGGTACCTTCTTGACTGTAAATACAGTTTATTT
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Pred. No.
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                                                                                                                                                                                                                                                                                                                            ; LENGTH; 2391
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-815-242-3827
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Best Local Similarity 51.9%;
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Best Local Similarity
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2117 AAAGCAGAAAGCCAAAGAGTTACAGCAATTGGAACTTGCACAGA 2160
                                                                                                                   249 AGTACCAGCGAATCCTCAAACAGTCCAAAATCTGTACAGTGCCGAACTCTAGCTCACAATT 308
                                                                                                                                                                                                              189 ATCTCCTCAGCAAACTGTAACAAGAGCCGAGACCACAAGTAACATAACCTCAAGGCCAGC 248
                       466 AACCAAAACCGTGGCGGCCAAAACCGTAACAACAAT 501
                                                         309 AATCAAGAAAGTGGCAGTGACACCTGTTAAAAAATT 344
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                                                                                                                                                                         809 CAAATTTTACTAAAAACTGAAAAAAACGAAAATATTGTTTTCAAGTTTTTACAAAAAAA 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2000-11-27
                                                                                               AACAATAACGGTTCTACAACGAATCAAAATCGGACCAGCCAAAATAACAATGGCGGGAAC
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Trawick, John D.
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                                                                                                                                                                                                                                                                      Score 36; DB 10; Length 2391; Pred. No. 8.2;
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Pred. No. 4.6;
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US-09-974-300-101
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US-09-815-242-6667
                               Sequence 101, Application US/09974300
Patent No. US2002016721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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SEQ ID NO 6667
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CURRENT FILLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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CURRENT APPLICATION NUMBER: US/09/974,300 CURRENT FILING DATE: 2001-10-05
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 ATCTCCTCAGCAAACTGTAACAAGAGCCGAGACCACAAGTAACATAACCTCAAGGCCAGC 248
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                                                                                                                                                                                                                                                                        AACCAAAACCGTGGCGGCCAAAACCGTAACAACAAT
                                                                                                                                                                                                                                                                                                                                              AACAATAACGGTTCTACAACGAATCAAAATCGGACCAGCCAAAATAACAATGGCGGGAAC
                                                                                                                                                                                                                                                                                                                                                                                 AGTACCAGCGAATCCTCAAACAGTCAAAATCTGTACAGTGCCGAACTCTAGCTCACAATT 308
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US20020061569A1
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Xu, H. Howard
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Pred. No. 8.2;
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Length 2397; Indels

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Gaps

PRIOR APPLICATION NUMBER: 09/ PRIOR FILING DATE: 2000-10-06 PRIOR APPLICATION NUMBER: 60/ PRIOR EILING DATE: 2001-03-27

09/680,598 0-06 60/279,526

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; SOFTWARE: Patentin Ver. 2
; SEQ ID NO 403
; LENGTH: 2534
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-878-403
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US-09-790-988-1
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                                                   GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA121
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                                                                                                                                                                                                                                      Sequence 1, Application US/09790988 Patent No. US20020127687A1
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CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: JP2000-107160 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version
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ORGANISM: Bacillus licheniformis
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Local Similarity 56.3%;
nes 67; Conservative
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Pred. No. 9.7;
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Pred. No. 7.4;
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Search completed: February 16, Job time: 1554 secs

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Matches
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265828 AA
                                                                 265768 TAAGAAAGAATTAGAATGTTATGTAAATGGTGTAAAATTATCACAGTTAAAATTCATCAA
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ORGANISM: Buchnera
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Perfect score:
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Match
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AUTHORS
TITLE
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SOURCE
ORGANISM
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'	BE844520 EST265 Ap AW414768 48566 MAR	AW378648 PM0-HT022		AI467327 vd22a01.x	1R0-HT02	161	AG092765 Pan trogl	AV965961 AV965961	BE940003 RC1-UT003	AW785378 116368 MA	BF135081 601780119	BM853763 K-EST0135	BG514288 dc96d09.x	AI503691 vk77g01.x	AA549039 vk77g01.s	BE698723 RC1-UT003	вм938537 UI-м-CG0p	вE986487 UI-м-CG0р	BE939960 RC1-UT003	AA438072 vd22a01.s	во560102 н4062С09-	BG198225 RST17369	BG191106 RST10076	AW964632 EST376705	AL668344	DKFZp762C) ik51d07.	•	60239337	73-36	•	1 H4C	RST3723	BC026493 Mus muscu	7 RST3337	20171 AGENCOUR	391

ALIGNMENTS

EQ952832

BQ952832

DEFINITION

AGENCOURT_8949744 NCI_CGAP_Mam2 Mus musculus cDNA clone

IMAGE:6442204 5', mRNA sequence.

ACCESSION

RESTON

RESTON

EST.

ORGANISM

Mus musculus

Eutharyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; house mouse.

ORGANISM

AUTHORS

TITLE

JOURNAL

COMMENT

COMMENT

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bloscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM13966 row: k column: 05

High quality sequence stop: 666.

FEATURES

SOURCE

ACCESSION

AGENCOURT_8949744 NCI_CGAP_Mam2 Mus musculus cDNA clone

IMAGE:642204 5', mRNA sequence.

PAGENCOURT B993

BQ952832

1 GI:22368310

EST.

SCURCE

AUTHORS

AUTHORS

AUTHORS

AUTHORS

AUTHORS

AUTHORS

AUTHORS

NIH-MGC http://mgc.ncl.nlh.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CONTACT: Robert Strausberg, Ph.D.

CDNA Library Preparation: Life Technologles, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bloscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM13966 row: k column: 05

High quality sequence stop: 666.

Location/Qualifiers

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BASE COUNT
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                                                                             GAAAGCCAAAGAGTTACAGCAATTGGAACTTGCACAGATACAGCATAGAGACGCTAATCT 2182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCATTGAGCACTCAGAACTGTGGGCAGAAGAC---ACCAGTAAATGCTGTGATGCCTACT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACATTGACCATTCAGAAATGTGGACAGAAGACGATGCCAGTGAACACCATAATACCTACT 1528
                                                                                                                                                                                                                                                TATTTACAAGGGAAGTGAAAATTATATCTTGTCTACTGATACCAGATCACAGCTCAAATT
                                                                                                                                                                                                                                                                                                                                                                  ACAGGAGAGTTACGAGGCCTTCTAGAGAAACTAACTACAATTGCTCAGCATCGAATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAAAAAGCATGACATTACAGAACTTAACTCTGATGCTGTGAACTTGATCTCCCAAGCAAC 1882
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                                                       AAAAGCCAAAGAGTTGCAGCAGTTGGAGCTTGCCCAGATCCAGTACAGAGATGCTAATCT
                                                                                                                                   ACTAAAGGCAGCCAAGAGTCGCTCCAATAAAGAAGATCCAGAGCAGCTGAGATTAAAACA
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203 c 193 g 226 t 2 others
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/dev_stage="5 months"
/lab_host="DH10B"
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/clone="IMAGE:6442204"
/clone_11b="NCI_CGAP_Mam2"
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/strain="FVB/N-3"
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                                                                                                                                                                                                CTTAAAAGACAACCTTCTTGCTTCTGGGACATCCAGCCTGACAGCCACCAAACAGTTGC 2301
  GCATAGAGACGCTAATCTCACAGCTCTTGCAGCTATTGGACCAAGGAAGAAGAGACCACT
                                     ACAGCTGAGATTAAAGCAGAAAGCCAAAGAGTTACAGCAAGTGGAACTTGCACAGATACA
                                                          ACAGCTGAGATTAAAGCAGAAAGCCAAAGAGTTACAGCAATTGGAACTTGCACAGATACA 2164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://imagg.llnl.gov
Plate: LLAM11404 row: j column:
High quality sequence stop: 673.
Location/Qualifiers
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603041813F1 NIH_MGC_116 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 673)
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORF6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 3 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MCC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:5162978"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 6.3e-142;
0; Mismatches 9;
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                                                                                         Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishila,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                       Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTC; CAP trapper.

Mus musculus (strain:C57BL/6J) 10 days embryo cDNA to mRNA.

clone_lib:RIKEN full-length enriched mouse cDNA library
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1116 bp mRNA linear HTC 19-JAN-2002
Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2610524804; homolog to TRANSCRIPTION
INITIATION FACTOR TFIID 105 KDA SUBUNIT (TAFII-105) (TAFII105),
                                                                           Genome Res.
20530913
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   Kawai,J., S
Arakawa,T.,
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 Shinagawa, A., Shibata, K., , Hara, A., Fukunishi, Y.,
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Eutheria; Rodentia;
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 Yoshino, M., Itoh, M.
Konno, H., Adachi, J.,
                   Itoh, M.,
 Fukuda,S.,
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Alachi, J., Alawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunlshi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiracka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Sogabe, Y., Szuuki, H., Tagami, M., Tagawa, A., Tayawa, A., Shiraki, T., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasaunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
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GGGACCCTGGTGACCAAAGTGGCTCCGGTCAGCGCCCCTCTAAAGTCAGCAGCGGCCCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yol
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL.http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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/db_xref="McD:MGI:1919754"
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/strain="C57BL/6J"
/db_xref="FANTOM_DB:2610524B04"
/db_xref="NGD:MGI:1905330"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="2610524B04"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="10 days embryo"
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             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDN
prepare full-length cDNA libraries for rapid discovery of
genes. Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                       Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Itc,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M., and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BB616334 599 bp mRNA linear EST 31-AUG-2001 BB616334 RIKEN full-length enriched, adult male testis Mus musculus cDNA clone 4932409F03 5', mRNA sequence.
                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0
                                                                                                                                                                                                                                                     RIKEN Mouse ESTs (Arakawa,T., et al. Unpublished (2001)
Contact: Yoshihide Hayashizaki
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 Fujiwake, S.,
 Inoue, K.,
Togawa,Y.,
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Izawa, M.,
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Ohara, E.,
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2243 CTTAAAAGACCATCCTTGCTTGCTGGGACATCCAGCCTGACAGCCACCAACAGTTGCA
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                                                                                                         CACAGCTCTTGCAGCTATTGGACCAAGGAAGAAGAGACCACTAGAATCTGGAATTGAGGG
                                                                                                                                                     AAAAGCCAAAGAGTTGCAGCAGTTGGAGCTTGCCCAGATCCAGTACAGATGCTAATCT
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Yamanaka,I., Kiyosawa,H., Kondo,S., Salto,T., Shinagawa,A., Alzawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T., Ishii,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequencing pipeline with 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tane,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 86.:
75; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="testis"
/dev_stage="adult"
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/clone="4932409F03"
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Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Mc,
Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schellenberg,K., Steptoe,M.,
,T., Waterston,R. and Wilson,R.
Washd-Merck EST project 1997
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/db_xref="taxon:9606"
/clone="IMAGE:838408"
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427 bp mRNA linear EUI-H-BW0-aji-c-11-0-UI.sl NCI_CGAP_Sub6 Homo sapiens IMAGE:2731796 3', mRNA sequence.
AW297262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; V. Mammalia; Eutheria; Primates; Catarrhini; 1 (bases 1 to 427)
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www-bio.llnl.gov/bbrp/image/image.html
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National Cancer Institute, Cancer Genome Anat
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            /Clone_lib="NCI_CGAP_Sub6"
//Clone_lib="NCI_CGAP_Sub6"
//Lab_host="DH10B (Life Technologies)"
//Lab_host="DH10B (Life Technologies)
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                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:2731796"
                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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LLAM 3575-3582,
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Best Local Similarity 92.6
Matches 411; Conservative
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Canis familiaris
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
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hb05c07.91 Canis cDNAs from testes
clone hb05c07 5', mRNA sequence.
BM539135
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pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE
CloneIDs 1257096-1258631,1469064-1470983, 1475592-1476743
); NCI_CGAP_Pr22 pool 1 LLAM 2457-2459, 2758-2759,
3062-3068 (IMAGE CloneIDs 985608-986759, 1101192-1101959,
1217928-1220615); NCI_CGAP_CO10 pool 1 LLAM 2644-2653,
2871-2872 (IMAGE CloneIDs 1057416-1061255,1144584-1145351), (50% of the driver population), plus a pool of 3,840
arrayed clones from NCI_CGAP_Sub1 (IMAGE CloneIDs 2708616-271035) and NCI_CGAP_Sub2 (IMAGE CloneIDs 2708616-2712455) (20% of the driver population), plus a pool of 11,136 clones from NCI_CGAP_Sub2 (IMAGE CloneIDs 2712456-2723591) (30% of the driver population).
Subtraction was performed as previously described (Bonaldo, Lennon & Soares (1996): Normalization and Subtraction:
Two Approaches To Facilitate Gene Discovery. Genome
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Tel: 516 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O'Shaughnessy, A.L., McCombie, W.R., Baker, J.P., Balija, V., Cunniu. D., Dedhia, N.N., de la Bastide, M., Katzenberger, F., King, L., Kirchoff, K.A., Miller, B., Muller, S., Nascimento, L.U., Palmer, L., Santos, L., Shah, R.S., Splegel, L.A., Zutavern, T., Preston, R. and Hannon, G.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expressed sequence tags from Canis familiaris (dog) (2002) Unpublished (2002) Contact: W. Richard McCombie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mccombie@cshl.org
Plate: hb05 row: c column:
Seq primer: -21M13UnivRev
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/note="Vector: Lambda ap II; The library was produced by
Greg Hannon and Raymond Preston (Cold Spring Harbor
Laboratory). This library is oligo(dT) primed using
stratagene zap cDNA synthesis kit. It was made from dog
testes. Please contact Greg Hannon (hannon@cshl.org) with
any library related inquiries."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Canis familiaris"
/db_xref="taxon:9615"
/clone="hb05c07"
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                                                                                        562
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                                                                                                                                                                                                                                                                                                                                                                                   1 CCAACTGCTGCAAC--GGAGGAACACAGCTGGAACTGGTTTGCTTCAGACTTCAAAACCA 58
                                                                                                                                             CAAGCCTGTTATTGGGACTCCAGTTCAAATCAAACTTGCCCAGCCGGGCCCTGTCCTTTC
                                                                                                                                                                                                        GCAGCTATTTGTCTTCCATCTGTGAAACCTGTTGTTTCCTTCTGCTTGGTAGGACCACATCTG- 1290
                                                                                                                                                                                                                                                                                                                    CTTGTGACATCTGTGGCAAACACAGTGACCACGGTCTCACTGCAACCTGAAAAGCCAGTT 1171
                AGTTCAGCAGCCTTCAGGAGGCAATGAAAAACAAGTGACCACAATTTCACATTCCTCAAC 1470
                                                                                                                                                                                                                                                          GTCTCTGGAACAGCAGTAACACTGTCCCTTCCAGCAGTAACTTTTGGAGAAACTTCAGGT
                                                                                                                                                                                                                                                                      GTCTCTGGAACAGCAGTAACACTGTCCCTTCCCAGCAGTAACTTTTGGAGAAACTTCAGGT 1231
                                                                                           CAAGCCTGTTATTGGGACTCCAGTTCAAATCAAACTTGCCCATCCGGGGCCTGTCCTTTC
                                                                                                                                                                                         GCAGCTATTTGTCTTCCATCTGTGAAACCTGTTGTTT-CTTCTGCTGGGACCACATCTGA 237
                                                               ACAAACCACCTGGGATTCCACCGGCACTTCAA - -
AGTTCAGCATCCTTCTGGACGCAGTGAAAAACCAGGCACCACGTTTTCACATTCCCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence start: 14
High quality sequence stop: 184.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM13307 row: a column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 LU 1722),
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BQ220171 GI:20401571 BQ220171.1 GI:20401571 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                National Institutes of Health, Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGENCOURT_7571205 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:60521075', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MCC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIH_MGC_92"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

a 423 c 330 g 307 t
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/db_xref="taxon:9606"
/clone="IMAGE:6052107"
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84.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 288.6; DB 14; Length 1410; Pred. No. 1.8e-70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Scott J. Cain Athersys, Inc.
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E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3201 Carnegie Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence
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Fax: 216 361 9596
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                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                            GAAATTTCAATTTCTGGAAAATAA-CACCAACATGAAAGAGCATTGTTTACGATTAG-AA 2538
                                                                                                                                                                                                                                                           TCCATCCACATCCTTGCTATTTACTGCCAAAGAAGACACAAAGCATTGTTGCACTGTCCT 2480
                                                                                                                                                                                                                                                                                                                             CGGGAGATGAAGTATTCTCGAGCTCTATACCTGGCCCTTCTGAAGTGACCACTCCACTCT 183
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                                                                                                                                                                                                 TCCATCCAGATCCTTGCTATTTACTGCCAAAGAAGACACAAAGCATTGTTGCACTGTCCT
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Creation of genome-wide protein expression libraries using random
activation of gene expression
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
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1 (bases 1 to 787)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inote="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression'.

Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

176 c 160 g 227 t 1 others
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/cell_line="HT1080"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 286.4; DB 1
Pred. No. 4.9e-70;
0; Mismatches 6
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Best Local
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                       1910
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                                                                         CTCTGATGCTGTGAACTTGATCTCCCCAAGCAACACAGGAACGACTACGAGGCCTTCTAGA 1909
                                                                                                                                               TGGAGCTCTACAAAAGAGAATCTTAGACATTGGTAAAAAGCATGACATTACAGAACTTAA 1849
AAAACTGACTGCCAATTGCTCAGCATCGAATGACTACCTTACAAGGCAAGTGAAAATTACAT 1969
                                                                                                                           CGCGCCTTTGCAGAGGAGGATACTGGAGATAGGTAAAAAAGCACGGCATCACGGAACTGCA 141
                                                       CTTTATTAACTCTTACCTAT
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Mus musculus, Similar to TAF4 RN.
protein (TBP)-associated factor,
BC026493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution informat through the I.M.A.G.E. Consortium/LLMI at: http://i Series: IRAK Plate: 44 Row: g Column: 12
This clone was selected for full length sequencing passed the following selection criteria: Hexamer fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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/tissue_type="Eye, retina, mc/clone_lib="NuH_MGC_94"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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                                                                                                                                                                                                                                                                                                                                                                                                                            creation of genome-wide protein expression libraries using random activation of gene expression
                                                                                                                                                                                                                               High quality sequence
                                                                                                                                                                                                                                                      Email: scain@athersys.com
                                                                                                                                                                                                                                                                                                                     3201 Carnegie Ave,
                                                                                                                                                                                                                                                                                                                                                Athersys,
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib-"Athersys RAGE Library"
/cell_line="HT1080"
/note-"See 'Creation of Genome-wide Protein Expression
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Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BQ560074
BQ560074.1
                                                                                                                                           National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA Email: cdnaelysun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details. Plate: H4062 row: B column: 07
Seq primer: -21M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                           CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ560074 507 bg
H4062B07-5 NIA Mouse 7.4K cDNA
H4062B07 5', mRNA sequence.
                                                                                                                                                                                                                                                Contact: Yong Qian
Laboratory of Genetics
                                                                                                                                                                                                                                                                            Unpublished (2002)
Other_ESTs: H4062B07-3
                                                                                                                                                                                                                                                                                                                       Luo, A.G. and Ko, M.S.H. Assembly, verification,
                                                                                                                                                                                                                                                                                                                                                VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G., Martin, P.R., Stagg, C.A., Bassey, U., Alba, K., Hamatani, T., Kargul, G.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST
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1 (bases 1 to 507)
                                                                                                                                                                                                                                                                                                                                                                                                                                         house mouse.
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172 c 156 g 223 t 1 others
/clone="H4062B07"
/clone_lib="NIA Mouse
                           /db_xref="niaEST:H4062B07-5"
/db_xref="taxon:1000"
                                                         /strain="C57BL,
                                                                       /organism="Mus musculus
                                                                                                   Location/Qualifiers
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REFERENCE
AUTHORS
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JOURNAL
                                                                                                                                                                                                                                            SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
AW390057
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                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Res
Rua Prof. Antonio Prudente 109,
                                                                                                                                     HCGP http://www.ludwig.org.br/ORESTES
The FAPESP/LICR Human Cancer Genome Pu
Unpublished (1999)
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                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                            Homo sapiens
                  Fax: +55-11-2707001
                                Tel: +55-11-2704922
                                                                                                                                                                                           (bases 1 to 545)
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asimpson@ludwig.org.br
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145 c 112 g 126 t
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/dev_stage="mixed"
/lab_host="DH10B"
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73.7%;
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D; Mismatches 111;
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2 ST0178
                                                                                   Research
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                                                                                                                                                                                ACAGCTCTTGCAGCTATTGGACCAAGGAAGAAGAGACCACTAGAATCTGGAATTGAGGGC 2243
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 B1986567
3173-36 Mouse E14.5 I
mRNA sequence.
B1986567
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                                                                                                               544
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Seq primer: puc 18 forward
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111 c 145 g 93 t 1 others
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mRNA sequence.
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602393377F1 NIH_MGC_94
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/dev_stage="ombryonic day 14; 5 post-fertilization"
/dev_stage="ombryonic day 14; 5 post-fertilization"
/note="Vector: pAMP10 (Gibco); Cloned unidirectionally.
/note="Vector: pAMP10 (Gibco); Cloned unidirectionally.
/note="vector: pAMP10 (Gibco); Cloned (Cloned RNA preps)
(Manniatis); Cloning Technique: CIA Cloning (CloneAmp,
Life Technologies); Average insert size: 1.8 Kb;
Insertion site: TACGTCCACTGAATTCTGAGTG--->. Other
information regarding entire library may be found at
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GGAAGAAGAGACCACTAGAATCTGGAATTGAGGGCTTAAAAGACAACCTTCTTGCTTCTG 2268
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                                                                    AACTTGCACAGATACAGCATAGAGAGACGCTAATCTCACAGCTCTTGCAGCTATTGGACCAA 2208
                                                                                                                                                               ATAAAGAAGATCCAGAACAGCTGAGATTAAAGCAGAAAGCCCAAAGAGTTACAGCAATTGG 2148
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                                          AGCTGGCACAGATGCGACAACGAGATGCCAACCTCACTGCACTGGCAGCGATCGGGCCCA
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10378 row: i column: 20
High quality sequence stop: 721.
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1 (bases 1 to 734)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: The Cepko Laboratory
CONNA Library Preparation: Life Technologies, Inc.
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_NGC Library."
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/clone="IMAGE:4505179"
/clone_lib="NIH_MGC_94"
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                            2375 TTCTCGAGCTCTATACCTGGCCCTTCTGAAGTGAC 2409
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680 TTCACTGTGGCTCTACAAAGCATTCCTTAAGTAAC 714
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                                                                                         CACGAGAATCTGCCTCAGGGACTTGATATTTTGTATGGAACAGGAACGGGAGATGAAGTA 2374
                                                                                                                                             GGACA-----TCCAGCCTGACAGCCACCAAACAGTTGCATCGTCCAAGAAT 2314
                                                           CACGCGGGTCAACCTCAGGGACCTCATA-TTTGTGTAGAAAACGAGCGTGAGACAAGCCA
                                                                                                                                                                                     GCGCAGCAGTCCCAGGCGGTCCGGCGTGGGAACCCCCCAGACAGTTCACACGGCAAAGAAT 620
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Scoring table:

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ABB66631 ABG66702 ABG66756 AAB4252 ABG66756 AAB426078 AAB94078 AAB94078 AAB63947 AAB50363
FLO1 protein, invo Human protein sequ Yeast 2.6 kB agglu S cerevisiae apopt Drosophila melanog Human SRCAP. Homo

Human novel polype Human novel polype Human ORFX ORF2414

864 1296 1296 1322

2781 2907 2035 1795 1920 2135 1328 1331 5179

ABB69806 AAB65656 AAE21714

ABB61528 ABB66055 AAY57453 AAY57452 AAR57141

Drosophila melanog Drosophila melanog

Host cell

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AAM78519 AAM79503 AAM24516

Drosophila melanog Novel protein kina Human PKIN-9 prote Human protein SEQ Human protein SEQ C899P predicted am Drosophila melanog

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Human protein sequ Drosophila melanog Human ORFX ORF995 Human EXMAD-20 SEQ

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ABB69480 AAR47578 AAR58754 ABB60186 ABB65772

Drosophila melanog Drosophila melanog Drosophila melanog Flocculation prote S. cerevisiae FLO1

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                                  Novel human diagno TATA-binding prote Human TATA-binding prote Human homologue of TATA-binding prote Drosophila TATA-bi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATA box-binding protein associated factor II 105; TAFIII105; cancer; transcription factor; apoptosis; cytostatic; immunosuppressive; antiinflammatory; virucide; antibacterial.
      (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                         09-MAR-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide encoding TATA box binding protein associated factor useful for treating e.g. cancers and inducing apoptosis has a do negative effect on the normal biological activity of the binding
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                                                                                                                                                                                                                                                                                            TRSQLKFLEKLDQLEKQRKDLEEREMLLKAAKSRSNKEDPEQLRLKQKAKELQQLELAQI
                                                             KRILDIGKKHDITELNSDAVNLISQATQERLRGLLEKLTAIAQHRMTTYKASENYILCSD
                                                                                                                          IKENVTSCFRDEDDINDVTSMAGVNLNEENACILATNSELVGTLIQSCKDEPFLFIGALQ
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                                             KRILDIGKKHDITELNSDAVNLISQATQERLRGLLEKLTAIAQHRMTTYKASENYILCSD
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                    associated subunits (TAR's) are components of the transcription farming and are thought to mediate transcriptional activation. This protein may be produced recombinantly from transformed host cells purified from human cells. hTAFIII05 specific binding agents such specific antibodies could be used for diagnosis (e.g. genetic hybridisation screens for hTAFIII05 transcripts), therapy (e.g. genetic therapy to modulate hTAFIII05 gene expression) and in the biopharmaceutical industry (e.g. as immunogens, reagents for isola cell specific activators or other transcriptional regulators).
                                                                                                                            This cDNA sequence represents a human tata-binding protein associated factor, hTAFTII105, isolated from Daudi cell nuclear extracts. Tightly associated subunits (TAF's) are components of the transcription factor
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                                                                                                                                                                                                          DNA encoding human tata-binding protein producing recombinant protein
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                                                                                                                                                                                   Claim 1; Col 17-22;
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upplement; medical i
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maging; diagnostic; genetic disorder.
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CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at fit, wipo.int/pub/published_pct_sequences.
 Query Match
Best Local S
Matches 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                           Sequence
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23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide (II) sequences.
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The TATA-binding protein associated factor hTAFII130 (including specific antibodies and fusion products) are used in drug screening, diagnostics and therapeutics. They are used in the development of specific biochemical assays for screening compounds that agonise or antagonise selected transcription factors involved in regulating
                                                                                                                                                     Comai L,
Tjian R,
                                                                               TATA-binding protein associated protein factors - and corresponding nucleotide sequence and deriv. antibodies, in screening, diagnostics and therapeutics
                                                              Disclosure; Page 142;
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30-JUN-1993;
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                                                                                                                                                                                                                                                                                                                            TATA-binding
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DB; AAQ70731.
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                                                                                                                                                                                                                                                                                                                  therapeutic;
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93US-0087119.
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                                                                                                                                            BD, now, Weinzierl ROJ;
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            GTSSLTATKQLHRPRITRICLRDLIFCMEQEREMKYSRALYLALLK
                                                         EQLRLKQKAKELQQLELAQIQHRDANLTATAAIGPRKKRPLE-----SGIEGLKDNLLAS
                                                                                        VGTLTRSCKDETFLLQAPLQRRILEIGKKHGITELHPDVVSYVSHATQQRLQNLVEKISE
                                                                                                                                                  VGTLIQSCKDEPFLFIGALQKRILDIGKKHDITELNSDAVNLISQATQERLRGLLEKLTA
                                                                                                                                                                                                 PGNKIL---SLQASPTQKNRIKENVTSCFRDEDDINDVTSMAGVNLNEENACILATNSEL
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                                                                                                                                                                                                                                                                                                                                                                                                                       AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS
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 GSSGVGTPRQFTRQRITRVNLRDLIFCLENERETSHSLLLYKAFLK
                                            EQLRLKQKAKEMQQQELAQMRQRDANLTALAAIGPRKKRKVDCPGPGSGAEGSGPGSVVP
                                                                                                                                                                                                                                                                                  TLTQT-----PMVALRQPH-NRIMLTTPQQIQL------
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                                                                                                                                                                                      PGTKALSAVSAQAAAAQKNKLKEPGGGSFRDDDDINDVASMAGVNLSEESARILATNSEL
                                                                                                                                                                                                                                                                                                                               RTVPGATTTSSAATE-----TMENVKKCKNFLSTLIKLASSGKOSTETAANVKELVONL
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Pred. No. 2.4e-79;
13; Mismatches 200; 1
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Human TATA-binding

protein associated factor hTAFII130

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Tjian R,
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28-JAN-1993;
30-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                             This is the amino acid sequence of the human TATA-binding protein (TBP) associated factor (TAF) designated TAFIII30. The protein is a component of the TFIID fraction required for reconstituting RNA polymerase II in vitro transcription activity. The encoded protein has an estimated mol. wt. of 130 kD by SDS-PAGE.

The invention relates to purified proteins involved in transcription by RNA polymerase II, the RNA polymerase which transcribes messenger RNA. RNA polymerase II transcription proceeds in vitro upon addition of several nuclear fractions designated TFIIA, B, D, E, F, H, I and J to RNA polymerase II holoenzyme. Fraction TFIID has been shown to contains a TBP and other TAFs. Purification of TFIID and separation of its components reveals 7 proteins ranging in size from 30-250 kD. Serum raised against the TFIID fraction allowed cloning of the corresp. genes from lambda-gtll expression libraries.
                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Screen for cpds. that bind human TATA-binding protein associated factor - by testing ability to bind to polypeptide fragments of the factor, useful as (ant)agonists of transcription factors involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REGC ) UNIV CALIFORNIA.
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les 330; Conserv
NE-PNIKAENSAAVQINISPTMIENVKKCKNFIAMLIKLACSGSQSPEMGQNVKKIVEQI
                                                                                                                                                                                     LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
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DB; AAT42217.
                                                                                                                               AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS
                                                                                                                                                                    MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
                                                                                                                                                                                                                        RTVPGATTTSSAATE-----TMENVKKCKNFLSTLIKLASSGKQSTETAANVKELVQNL
                                                                                                            ----TTIIKQV----SQAQTTVQPSATLQRSPGVQPQLVLGGAAQTASLGTATAVQTGTPQ
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                                                                                                                                                                                                                                                                                                                                         737
                                                                                                                                                                                                                                                                             30.7%; Score 1307.5; DB 17; Length 737; ilarity 40.0%; Pred. No. 2.4e-79; Conservative 103; Mismatches 200; Indels 193;
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ō	340	Q3TTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL
Y	344	VTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAV 403
ŏ	377	QPPKPGALIRPPQV 410
¥	404	TEGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPAGIPTGSSSKQ 463
ŏ	411	TLTQT
У	464	LFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASILKQITL 523
6	438	NPLQPVPVVKPAVL 451
Y	524	PGNKILSLQASPTQKNRIKENVTSCFRDEDDINDVTSMAGVNLNEENACILATNSEL 580
Ď	452	PGTKALSAVSAQAAAAQKNKLKEPGGGSFRDDDDINDVASMAGVNLSEESARILATNSEL 511
Ÿ	581	VGTLIQSCKDEPFLFIGALQKRILDIGKKHDITELNSDAVNLISQATQERLRGLLEKLTA 640
ō	512	VGTLTRSCKDETFLLQAPLQRRILEIGKKHGITELHPDVVSIVSHATQQRLQNLVEKISE 571
Ÿ	641	IAQHRMTTYKASENYILCSDTRSQLKFLEKLDQLEKQRKDLEEREMLLKAAKSRSNKEDP 700
σ	572	TAQQKNFSYKDDDRYEQASDVRAQLKFFEQLDQIEKQRKDEQEREILMRAAKSRSRQEDP 631
7 4	701	EQLRLKQKAKELQQLELAQIQHRDANLTATAAIGPRKKRPLESGIEGLKDNLLAS 755
4	л	801
₽.	692	GSSGVGTPRQFTRQRITRVNLRDLIFCLENERETSHSLLLYKAFLK 737
SUI W25	T 6 5019 AAW2501	5019 standard; Protein; 737 AA.
× ∩ :	AAW25	5019;
(i i)	08-00	-OCT-1997 (first entry)
< m >	TATA-	-binding protein associated factor, hTAFII130.
	TATA	TATA-binding protein associated factor; TAF; nuclear protein; RNA polymerase transcription: TATA-binding protein:
	init	
ל מֹס;	Ното	Homo sapiens.
׿:	US56:	US5637686-A.
₹ ⊕ ;	10-JUN-	UN-1997.
र म्हे	28-л	-JAN-1993; 93US-0013412.
	28-л	1994; 94US-01885
	30-JUN-	AN-1993; 93US-0013412. UN-1993; 93US-0087119.
	1M-60	1996; 96US-06467
× > ;	(REGC	C) UNIV CALIFORNIA.
: i i i i	Comai Tjian	<pre>1 L, Dynlact BD, Hoey T, Ruppert S, Tanese N; n R, Wang E, Weinzierl ROJ;</pre>
	WPI; 19	1997-319113/29. DB: AAT79595.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for modulating transcription of TAFs
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                                                                                                                                                                                                   VGTLIQSCKDEPFLFIGALQKRILDIGKKHDITELNSDAVNLISQATQERLRGLLEKLTA
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                                                                         TAQQKNFSYKDDDRYEQASDVRAQLKFFEQLDQIEKQRKDEQEREILMRAAKSRSRQEDP
                                                                                                IAQHRMTTYKASENYILCSDTRSQLKFLEKLDQLEKQRKDLEEREMLLKAAKSRSNKEDP
                                                                                                                                                                                                                                                                        PGTKALSAVSAQAAAAQKNKLKEPGGGSFRDDDDINDVASMAGVNLSEESARILATNSEL
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Query Match Best Local Similarity

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                         or more test compounds and determining the effects on the growth or viability of the culture of cells which preferably comprises fungal cells or yeast cells. Preferably the identified compounds interact with, or modulate (preferably inhibit) activity of C. albicans Ep. The inhibitor compounds identified by the method are useful for preventing or inhibiting fungal, particularly C. albicans growth in culture or in a mammal. The antifungal agents interact with essential fungal elements that can be used to treat fungal infection by preventing the growth and preferentially killing the fungal infection by preventing the growth and preferentially killing the fungi, but does not inhibit the biological activity of mammalian homologues. This amino acid sequence represents a target protein used to test the antifungal compounds, described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moore J, Bu
Mendillo M,
                                                                                                                                                                                                             The invention describes a method of screening a candidate antifungal compound for interaction with essential proteins (EP) or for modulation of EP activity e.g fungal gene transcription. The proteins tested in the invention include RPC34, POP3, TFA2, NAB2, MPT1, MTR2, BOS1, POL30, RSA2 SQT1, MTW1, TFB1, SPC98, BFR2, RNA1, GCD7, SKI6, NIP1, LCP5, NCE103, ECO1, ORC2, CNS1, YPD1, TIM10 and SRB4 from S. cerevisiae, C. albicans and human homologues. The method involves contacting a culture with one
                                                                                                                                                                                                                                                                                                                                                                            Screening candidate antifungal compound for interaction with essential protein, modulation of essential protein activity, binding to essentia protein, by contacting protein with test compound and determining efforts.
                                                                                                                                                                                                                                                                                                                                       Claim 1; Figure 79;
                                                                                                                                                                                                                                                                                                                                                                     effects
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                                                                                                                                                                                                                                                                                                                    SGVGTPROFTRORITRVNLRDLIFCLENERETSHSLLLYKAFLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDGKIEAEDFTSRLYRELNSSPQPYLVPFLKRSLPALRQLTPDSAAFIQQSQQQPPPP--
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therapeutic; gene transcription regulation.
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Tjian R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specific antibodies and fusion products) are used in drug screenin diagnostics and therapeutics. They are used in the development of specific blochemical assays for screening compounds that agonise antagonise selected transcription factors involved in regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATA-binding protein associated protein factors corresponding nucleotide sequence and deriv. and in screening, diagnostics and therapeutics
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30-JUN-1993;
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              SVLSTLNSASTTTLPIPSLPTVHLPPEALRAREQMQNSLNHNSNHFDAKLVEIKAPSLHP
                                                                                                                                                                         QIP-SLQVPGQANIVQIR--GPQHAQLQRTGSVQIRATTRP-----PNSVPTAN-----
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                                                   SQPAGIPTGSSSK----QLFSLFHVVQQPSGGNEKQVTTISHSS-----
                                                                                                                 VVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVL 449
                                                                                                                                                                                                              LNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKP
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            This is the amino acid sequence of the Drosophila TATA-binding protein (TBP) associated factor (TAF) designated TAFTII10. The protein is a component of the TFIID fraction required for reconstituting RNA polymerase II in vitro transcription activity. The encoded protein has an estimated mol. wt. of 110 kD by SDS-PAGE, a calculated mol. wt. based on sequence of the gene of 99.4 kD and an estimated pI of 10.1.
                                                                                                                                                                                                                                                                                                            28-JAN-1994;
28-JAN-1993;
30-JUN-1993;
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                                                       LELAQIQHRDANLTATAAIGPRKKRPLE----SGIEGLKDNLLASGTSSLTATKQLHRP
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                                                                                                                                                             VVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVL
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                                         AEMEELRQRDANLTALQAIGPRKKLKLDGETVSSGAGSSGGGVLSSSGSAPTTL---
                                                                                                                                                                                                                                                     PHMERINASLTPIGAKTM-----ARPPPAINKAIGKKKRDAMEMDAKLNTSSGGAA
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                                                                                                                                                                                                                                                                                                                                   SQPAGIPTGSSSK---QLFSLFHVVQQPSGGNEKQVTTISHSS-------
                                                                                                                                                                                                                                                                                                                                                            ------KLTAVKVGQTQIKAI-TPSLHP-----PSLAAISGGP------PPTPTL
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Pred. No. 2.2e
L28; Mismatches
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?.2e-43;
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Tjian R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW25028 represents TATA-binding protein associated factor (TAF) polypeptide, dTAFIII0 (mol. weight 110kD). TAF peptides derived from dTAFII30 alpha, dTAFII30 beta, dTAFII40, dTAFII60, dTAFII60, dTAFII60, dTAFII10, dTAFII10, dTAFII10, dTAFII10, dTAFII10, and dTAFII250, their human equivalents and nucleic acids encoding them, are used to modulate transcription, including transcription initiation. TAFS are nuclear proteins involved in RNA polymerase I, II and III transcription. The peptides act by binding to a different TAF, an activator, or TBP (TATA-binding protein) or competitively inhibiting association of a TAF domain with another compound, typically a protein like TBP or another TAF, an activator,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JAN-1994;
28-JAN-1993;
30-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding human TATA-binding (TAF) peptide(s) - for production of recommodulating transcription of TAFs
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DB; AAT79604.
APQLPQITQIQTIPAQQSQQQQVNNVSSAGGTATAVSSTTA-----
                                                KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSP 187
                                                                                                    NTTSTTNHPTTTQ-IRLQTVPAAASMTNTTATSNIIVNSVASSGYANSSQPPHLTQLNAQ
                                                                                                                                                       NITSRPAVPANPQTVKICTVPNSSSQ------LIKKVAVTPVKKLAQIGTTVVTTVP
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ROJ;
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Pred. No. 2.2e-43;
28; Mismatches 308;
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                                                                                                  RITRICLRDLIFCMEQEREMKYSRALYLALLK
                                                                                                                                AEMEELRQRDANLTALQAIGPRKKLKLDGETVSSGAGSSGGGVLSSSGSAPTTL----RP
                                                                                                                                                    LELAQIQHRDANLTATAAIGPRKKRPLE----SGIEGLKDNLLASGTSSLTATKQLHRP
                                                                                                                                                                                         YEPAKDVRGQIKFLEELDKAEQKRHEELEREMLLRAAKSRSRVEDPEQAKMKARAKEMQR
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26-MAR-2002 (first entry)

ABB61528;

Drosophila melanogaster polypeptide SEQ ID NO 11376

pharmaceutical. Drosophila; developmental biology; cel1 signalling; insecticide;

Drosophila melanogaster

WO200171042-A2

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23-MAR-2001; 2001WO-US09231

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[ABB57737-ABB72072].
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                                                                                 SVLSTLNSASTTTLPIPSLPTVHLPPEALRAREQMQNSLNHNSNHFDAKLVEIKAPSLHP
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                                                                                                                                                                                                                       LNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKP
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DB; ABL05631.
PTQKNRIKENVTSCFRDEDDINDVTSMAGVNLNEENACILATNSELVGTLIQSCKDEPFL
                                                                                                           SQPAGIPTGSSSK---QLFSLFHVVQQPSGGNEKQVTTISHSS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVL 449
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        VVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEK 480
                                                                      GTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAVTFGETSGAAICLPSVKP
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                                       ----QSSKPQVAAQS------QPQSNVQGQSPVRVQSPSQTRIRPSTPSQLSPGQQS
                                                                                                   PAKAQPQTAQPSARPQPQTQPQSPAQPEVQTQPEVQTQTTVSSHVPSEAQPTHA-----
                                                                                                                                  PRTVSVQTLNPLAGP------VGAKAGVVTLHSVG-----PTAATGGTTA
                                                                                                                                                                                                TSSDMVIATCTTTVTTSPVVTTTVSSS----
                                                                                                                                                                                                                            LTQGHGGNQGLTVVIQGQGQ------TTGQLQLIPQGVTVLPGPGQQLMQAAMPNG
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                                               Query Match
Best Local S
Matches 181
                                                                                                                                                                                                   The present sequence represents a human transcriptional regulatory factor containing a bromo domain. The factor interacts with proteins involved in the chromatin-mediated transcription regulatory mechanism. It binds to hswr2H, hswr2L and NCOA-62/Skip. It can be used for screening compounds binding to it and acting as agonists or antagonists, which are potentially useful for the treatment and prevention of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2460
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                                                                                                                                                                                          cell
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                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                   Page 48-68; 154pp; Japanese.
                                                                                                                                                                                     proliferation disorders.
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No. le-07;
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                            Homo sapiens
                                                        transcription
                                                                   Herpes simplex virus; herpes virus; vP16; immediate early gene; host cell factor; virus infection therapy; cellular protein;
                                                                                                                  Host cell factor protein.
                                                                                                                                               19-MAR-1995
                                                                                                                                                                          AAR57141;
                                                                                                                                                                                                      AAR57141 standard;
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                                                                                                                                                                                                                                                                             KRSKQNATKLSAL
                                                                                                                                                                                                                                                                                                         LRLKQKAKELQQL 715
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New Host Cell Factor polypeptide(s) and nucleic acid - to develop agents for diagnosis or treatment of disease associated with expression of a HCF-modulated gene e.g.
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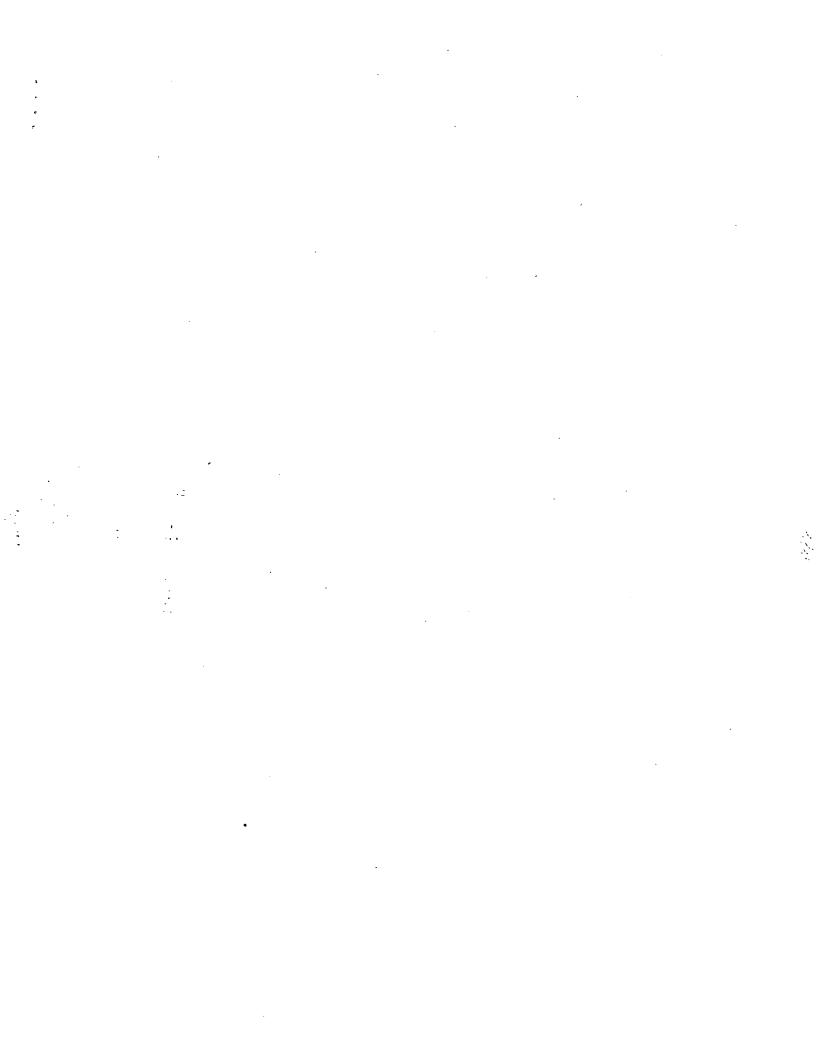
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                                                                                                                                         SQPTQVTLITAPSGVEAQPVHDLPVS
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Pred. No. 1.1e-06;
4; Mismatches 239;
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Sequence 14, Appl
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Sequence 1068, App
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Sequence 1068, App
Sequence 104, App
Sequence 104, App
Sequence 100, App
Sequence 110, Appl
Sequence 21, Appl
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US-09-893-519A-14
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APPLICANT: ANADYS PHARMACEUTICALS, INC.
APPLICANT: THOMPSON, Craig
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ALIGNMENTS

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SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 1023
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: CORRESPONDS to SEQ ID NO: 87
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Human Genbank/CAA72189
DATABASE ENTRY DATE: 1997-06-25
                                                                                                                                                                                                                                                   APPLICANT: DAVIDOV, Eugene
TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND METHODS OF
FILE REFERENCE: 0342/16548-082
CURRENT APPLICATION NUMBER: US/09/893,519A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,164
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/224,457
PRIOR APPLICATION NUMBER: US 60/224,457
PRIOR APPLICATION NUMBER: US 60/224,457
PRIOR FILING DATE: 2000-08-10
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MOORE, Jeffrey
BUURMAN, Ed T.
BRADLEY, John
DESILVA, Thamara
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ZHU, Shuhao
LONG, Fan
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KOMARNITSKY, Svetlana
MENDILLO, Marc
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RESULT 2
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                                                                                           GENERAL INFORMATION:
                                                                                                          Sequence 108, Application US/09801368 Patent No. US20020128250A1
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Best Local Similarity
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                  APPLICANT:
                                                      APPLICANT: Busby, Robert APPLICANT: Cali, Brian
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                Holtzman, Doug
                                   Hecht, Peter
 Madden, Kevin
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SOFTWARE: PatentIn version
SEQ ID NO 108
LENGTH: 1367
Sequence 1068, Application US/10025380 Publication No. US20020182191A1
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Best Local Similarity
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APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving
FILE REFERENCE: 109272.147
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                                                                                                                                                                                                                                                                                                                                                                                              -----YPGSQT--EISVSSTIETTIVPTKTTTSVTTPSTTTITTTVCSTGTN
                                                                                                          -AGETTSGCSPKTVTTTVPCSTGT----GEYTTEATTLVTTA
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                                                                                                                                                                                  LTTIAPTPSVTTVTNF----
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Salama, Sofie
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Milne, Todd
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Best Local Similarity
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TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C14
CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILING DATE: 2001-12-19
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ORGANISM: Homo sapiens
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                               SKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIP----TSQFPPAS
                                                                                                PAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPAGIPTGSS
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                                                               PTPTGTQT-----PTTTPITT-----TTTVTPT-----PTPTGTQ-TGPPTHTS
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Vedvick Thomas S.
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Skeiky, Yasir A. W.
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CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1068
LENGTH: 5179
TYPE: PRT
ORGANISM: Homo sapiens
US-09-922-217-1068
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US-09-922-217-1068
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Best Local S
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APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR US:
FILE REFERENCE: 210121.471C13
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                                                                    4106 TEPITTTTVTPTPTPTGTQTPTTTPITTTTVTPTPTGTQTPTTTPITTTTTTVT-PT
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PAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPAGIPTGSS 460
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                                                                                                                                             ----TAGTGLLQTSKPL-----VTSVANTVTTVSLQP------EKPVVSGTAVTLSL 400
                                                                                                                                                                                                                                                                                   SSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAK----AGVVTLHSVGPTAATGGT----
                                                                                                                                                                                                                                                                                                                                                                                                                                             KKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTT-----TVTTSPVVTTTVS
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Smith, Carole Lynn
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Benson, Darin R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -TTPITTTTTTPTP-----
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; ORGANISM: Homo sapiens
US-09-833-263-1068
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Best Local Similarity
Matches 136; Conserv
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 1068
LENGTH: 5179
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CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT FILING DATE: 2001-04-10
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APPLICANT: Stolk, John A.
APPLICANT: Medgher, Madeleine J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND |
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PTPTGTQT---
                            PAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPAGIPTGSS
                                                                TTPITTTTTVTPTPTGTQTPTTTPITTTTVTPTPTPTGTQTPTTTPITTTTTVT-PT
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                                                                                               ----TAGTGLLQTSKPL-----VTSVANTVTTVSLQP------EKPVVSGTAVTLSL
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                                                                                                                                                                                                                                                                                                                                                          ------GKPLNTVTTLKPS-SLGASSTPSNEPNLKAENSAAVQINLSPTMLENVKKCK 197
                                                                                                                                                                                                                                                                                                                                                                                                                          ----VPNSSSQLIKKVAVTPVKKLAQIGTTVVTTVPKPSSVQS-VAVP-TSVVTVTP---
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21.9%;
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Pred. No. 3.9e-05;
3; Mismatches 227;
-TTTVTPT---
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PTPTGTQ-TGPPTHTS
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SOFTWARE: Patentin version 3.0
SEQ ID NO 114
LENGTH: 1322
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CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
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APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving
FILE REFERENCE: 109272.147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/160,587 PRIOR FILING DATE: 1999-10-20
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                                                                                                                                                                                                                                                                                                                                                                                                                 663 LPTDETIIVIRTPTTATTAMTTTQPWNDTFTSTSTEITTVTGTNGLPTDETIIVIRTPTT 722
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AKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVA--NTVTTVSLQPEKPVVSGTAV
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                                                                        S--SDMVIATCTTT--VTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVG
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Milne, Todd
No. US20020128250Alman,
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Madden, Kevin
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                                                                                                                                                                 Query Match
Best Local
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Summers, Eric TITLE OF INVENTION: Methods for Improving FILE REFERENCE: 109272.147
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                                     KKVAVTPVKKLAQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLN-TVTTLK-PSSLG 162
                                                                         TVIVIRTPTSEGLISTTTEPWTGTFTSTSTEVTTITGTNGQPTDETVIVIRTPTSE----
                                                                                                          TVLI---KSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANP--QTVKICTVPNSSSQLI 104
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No. US20020128250Alman,
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Holtzman, Doug
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   -GLISTTTEPWTGTFTSTSTEMTTVTGTNGQPTDETVIVIRTPTSEG
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                                                                                                                                            257; Indels
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Patent No. US20020142428A1
GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: No. US20020142428A1e1 Kinases
FILE REFERENCE: 35800/234862
                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                         SOFTWARE: F
                                                                                                                                              Matches 136;
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/862,027
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                         TYPE: PRT
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NIPAMSPTSAQPQPVLS--PTSAAVPVPTTMIHVPKPSEIPVQNVATT----AAPVAANN 613
                                 --POOTVTRAETTSNITSRPAVPANPOTVKICTVPNSSSOLIKKVAVTPVKKLAQIGTTV 122
                                                                       TPIPPTPATPH-SSAQQQPIPPPLSTQ----TSAEIQQSAQQP-----
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                                                                                                                                                                                                                                      elegans
                                                                                                                                            Conservative 115;
                                                                                                                                                                                                                                                                                                         NOS: 82
for Windows Version
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                                                                                                                                            4.3%; Score 182.5; DB
19.4%; Pred. No. 0.0016;
rative 115; Mismatches 29
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                                              PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: P##~~~~
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 110, Application Patent No. US20020128250A1 GENERAL INFORMATION:
SOFTWARE: PatentIn version 3.0
SEQ ID NO 110
LENGTH: 1075
TYPE: PRT
                                                                                                                                             APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
                                                                                                                                                                                                                             APPLICANT:
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APPLICANT: Cali, Brian
APPLICANT: Hecht, Pete
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Milne, Todd
No. US20020128250Alman, Canana
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Silva, Jeff
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                                                                                                                                                                                                                                                                                                                                                                                                             Robert
                                                                                                                                                                                                                                                                                                                                              Kevin
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RESULT 10 US-09-864-761-34248

US/09864761

Sequence 34248, Application Patent No. US20020048763A1 GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ATTILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-x-1

ACID PROBES USEFUL

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CURRENT APPLICATION NUMBER: US/09/864,761

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Best Local Similarity 20.9
Matches 158; Conservative
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                                                                                          564 --VNLNEENACILATNSELVGTLIQSCKDEPFLFIGALQKRILDIGKKHDITELNSDAVN 621
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                                                               SVVSVSETGNTMSLTSSGL-STMSQQPRSTP---
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                              LISQATQERLRGLLEKLTATAQHRMTTYKASENYIL
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Pred. No. 0.00096;
5; Mismatches 279;
 1058
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APPLICATION NUMBER:

US 60/207,456

FILING DATE:

2000-02-04

APPLICATION NUMBER: US

FILING DATE:

2001-05-23

60/180,312

FILING DATE: 2000-05-26

APPLICATION NUMBER: US 09/632,366

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                                                                                                                                                                                              Best Local Similarity
Matches 133; Conserv
                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: Annomax Sequ
SEQ ID NO 34248
                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: I                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: I OTHER INFORMATION: I OTHER INFORMATION: I OTHER INFORMATION: I OTHER INFORMATION: I OTHER INFORMATION: I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                       1888
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                  125
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APPLICATION NUMBER: PCT/US01/00666
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FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: GB 24263.6
                                                                                                                                                          PVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLVS--PQ
                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
              TVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQIN 184
                                                                                                                         PVTPP----SDPSIPIPTLPSVTA-----AKLSPPVASGGIPHQSPPTKVTEWITR 1887
                                                  QEEPRAQSTPS-----PALPPDTKASDVDTSSSTL-RKILMDPKYVSATSVTSTSVTT
                                                                                     QTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTP--VKKLAQIGTTVVT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2665
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                        N: EXPRESSED IN FETAL LIVER, SIGNAL = N: EXPRESSED IN ADULT LIVER, SIGNAL = N: EXPRESSED IN HEACENTA, SIGNAL = 7.2 N: EXPRESSED IN HEART, SIGNAL = 7.2 N: EXPRESSED IN HELA, SIGNAL = 9.5 N: EXPRESSED IN HELA, SIGNAL = 9.5 N: EXPRESSED IN LUNG, SIGNAL = 9.3
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SWISSPROT
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EXPRESSED IN BONE MARROW,
EXPRESSED IN FETAL LIVER,
EXPRESSED IN ADULT LIVER,
                                                                                                                                                                                                                                                                                                                         EXPRESSED
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22.2%;
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                                                                                                                                                                                                                                                                                     HIT:
                                                                                                                                                                                                              Score 182; DB 10
Pred. No. 0.0035;
                                                                                                                                                                                                                                                                                     IN HBL100, SIGNAL = 7.7
IN BT474, SIGNAL = 12.00e+00
HIT: AU117052.1, EVALUE 0.00e+00
HIT: P08640, EVALUE 3.00e-10
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                                                                                                                                                                                              Mismatches 230;
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IGNAL = 14
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                                                                                                                                                       ; ORGANISM: Saccharomyces cerevisiae US-09-801-368-106
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                                                                                                                                                                                                                                                                    APPLICANT: Summers, Eric
FILLE OF INVENTION: Methods for Improving Se
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
                                                                                                                                                                                                             SEQ ID NO 106
LENGTH: 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 106, Application US/09801368 Patent No. US20020128250A1
                                                                            Matches
                                                                                                                Query Match
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                                                                                                                                                                                                                                                      SOFTWARE:
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                                                                                                                                                                                             TYPE: PRT
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                                                                                            Local
VTSSSVVSTPITSESSESSASVTIL----PSTITSEFKPSTMK----TKVVSISSSPTNL 740
                                    VTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQF-PANLQLPPGTVLIKSNSGPLML 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQVKPDSVTA----SQPPSKGPQAPAGYANVATHSTLVLTAQTYNASPVISSVKADRPSL 2292
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                                                                        4.0%; Score 172; DB 10;
al Similarity 21.4%; Pred. No. 0.0047;
112; Conservative 85; Mismatches 191
                                                                                                                                                                                                                                                   PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Busby, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sherman, Amir
Silva, Jeff
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Salama, Sofie
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No. US20020128250Alman,
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Holtzman, Doug
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                                                                            191;
                                                                                                            Length 1169;
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                                                                          136;
                                                                      Gaps
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; ORGANISM: Homo sapiens
US-10-161-510-10
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US-10-161-510-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/161,510
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/328,605
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/357,253
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                              Query Match 3.9%; Score 167; DB 9; Length 1056; Best Local Similarity 21.4%; Pred. No. 0.0086; Matches 134; Conservative 61; Mismatches 238; Indels 192;
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APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: PIBS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE FILE REFERENCE: EXO2-074C
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 1056
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133 GPKPPPATTGSVLAPTSLGLVMPASAGPRSPPVTLGPNLAPTSRDQKQEP------PA 184
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                                           124 TTVPKPSSVQSVAVPTSVVTVTPGK--PLNTVTTLKPSSLGASSTPSNEPNLKAENSAAV 181
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                                                                                                                                                                                         39 VAOTGAPSKVDSSFQLPAKKNAAL-GPSEPRL---ALAPVGPRAAMSASSEGPRLALASP
                                                                                                                                                                                                                                7 VAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGP-LMLVSP 65
                                                                                                                                        QQTVTRAETTSNITSRP--AVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTVV 123
                                                                                          ------RPILAPLCTPEGQKTATAHRSSS-----LAPTSVGQL--VMSASA 132
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194	Qy 149PLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSPTMLENVK	
1163	Db 1109 VKKPAETTVGTLLDKDTTTVTTTPRQKVA-PSSTMSTHPSRRRPNGRRRLRPNKFR	
148	QY 104 IKKVAVTPVKKLAQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGK	
103 1108	QY 50 TVLIKSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQL	
aps 30;	Query Match 3.7%; Score 159.5; DB 10; Length 2828; Best Local Similarity 20.4%; Pred. No. 0.1; Matches 144; Conservative 77; Mismatches 241; Indels 245; Ga	
ION PRODUCTS	US-09-905-129-21 Sequence 21, Application US/09905129 Patent No. US20020137705A1 GENERAL INFORMATION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION TITLE OF INVENTION: AND USES THEREOF FILE REFERENCE: 540579-2007.2 CURRENT APPLICATION NUMBER: US/09/905,129 CURRENT APPLICATION NUMBER: 09/207,821 PRIOR APPLICATION NUMBER: 60/207,821 PRIOR FILING DATE: 2001-03-08 PRIOR FILING DATE: 2000-05-30 PRIOR APPLICATION NUMBER: 60/084,944 PRIOR FILING DATE: 1998-05-11 PRIOR APPLICATION NUMBER: 60/084,944 PRIOR FILING DATE: 1998-05-11 PRIOR APPLICATION NUMBER: 60/085,673 PRIOR APPLICATION NUMBER: 60/085,782 PRIOR APPLICATION NUMB	the same and
	183NKRLKDALFTDQWSELF	
	Qy 575 ATNSELVGTLIQSCKDEPFLFIGAL 599	
574 482	Qy 521 ITLPGNKILSLQASPTQKNRIKENVTSCFRDEDDINDVTSMAGVNLNEENACIL	
439	G	
520	Qy 461 SKQLESLEHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTTIPTSQFPPASILKQ	
460 392	OY 402 AVTEGETSGAAICLESVKPVVSECMDHICKPVIGTPVQIKLAQPGPVLSQP-AGIPTGSS Db 338 TEREGAPSGQTVPPPLPKPPRSPSRSPSHSPNRSPCVPPAPDMALPRLGTQSTGP	
337	278	
401		
361 277	Qy 302 TTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTAG :	
222	Db 209 ELPSTPSPVPSPVL	
208	185	
241	182 QINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL	

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                                                                                       Query Match 3.7%; Score 159.5;
Best Local Similarity 20.4%; Pred. No. 0.1
Matches 144; Conservative 77; Mismatches
                                                                                                                                                                                                                                                                        SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS THERE
FILE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 540579-2007.3
CURRENT APPLICATION NUMBER: US/09/991,630
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: 09/905,129
PRIOR APPLICATION NUMBER: 09/905,129
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 09/802,318
PRIOR APPLICATION NUMBER: 09/802,318
PRIOR APPLICATION NUMBER: 09/729,485
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SOFTWARE: PatentIn versi
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                                                                                                                                                                                                                                                   ENGTH:
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1053 TLLIKKGMKEMSQTLQGGNMLEGDPTHSRSSE----SEGQESKSITLPDSTLGIMSSMSP 1108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         471 ------VQQPSGGNE-----KQVTTISHSSTLTIQKCGQKTM------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       397 TLSLPAVT---FGETSGAAICLPSVKPVV-----SFCWDHI-----CKPVIG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             337 VGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAV 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195
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                                        50 TYLIKSNSGPLMLYSPQQTYTRAETTSNITSRPAVPANPQTYKICTYPN-----SSSQL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KCK------LVEQ 226
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                                                                                                                                                                                                                                                                                                                                           2000-12-04
                                                                                                                               DB 10;
                                                                                     241; Indels
                                                                                                                                  Length 2828;
                                                                                     245; Gaps
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JULT 15 J9-905- Squence squence riffle FITTLE FITTL	521 1662	502 1602	471 1542	436 1482	397 1422	337 1372	279 1334	227 1281	195 1221	149 1164	1109
5-129-2 5-129-2 RO. US20020137705A1 L INFORMATION: CANT: Elnat, et al OF INVENTION: GENES ASSOCIATED WITH MECHANICAL STRESS, EXPRESSION PRODUCTS TH OF INVENTION: AND USES THEREOF REFERENCE: 540579-2007.2 NT APPLICATION NUMBER: 09/09/905,129 NT FILING DATE: 2001-07-13 APPLICATION NUMBER: 09/02/318 FILING DATE: 2001-03-08 APPLICATION NUMBER: 60/08/4 FILING DATE: 2000-05-30 APPLICATION NUMBER: 60/08/4 FILING DATE: 1998-05-11 FILING DATE: 1998-05-11 APPLICATION NUMBER: 60/085,673 FILING DATE: 1998-05-15 RO FSEQ ID NOS: 25 ARE: PATENTIN version 3.0 NO 2 TH: 2597 TH: 2597 TH: 2597 TRE: misc_feature TION: (1)(2597)	ITLPGNKILSLQASPTQKNRIKENVTSCFRDEDDINDVTSMAGVN 565 	PVNTIIPTSQFPPASILKQ 520 	VQQPSGGNEKQVTTISHSSTLTIQKCGQKTM	TPVQTKLAQPG	TLSLPAVTÉGETSGAAICLPSVKPVVSFCWDHICKPVIG 435 - - - - - - - - - - - -	VGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAV 396 	VQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGP 336 : :: : : : : : VDKHKSDILVTGESITNAIPTSRSLVSTMGEEKEESS	LLDAKIEAEEFTRKLYVELKSSPQ-PHLVPFLKKSVVALRQLLPNSQSFIQQC 278	KCK	PLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSPTMLENVK 194	IKKVAVTEVKKLAQIGTTVTTVPKPSSVQSVAVPTSVTVTPGK

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 3.7%; Score 158.5; DB 10; Length 2597; Best Local Similarity 20.5%; Pred. No. 0.11; Matches 143; Conservative 81; Mismatches 242; Indels 231; Gaps
1517 SPSNLFPSTSVPALRVDKPQNSKWKPSPWPEHKYQLK 1553
                                                                                                         1464 TKGVVTDSKVTSAFQM-----TSNRVVTIYESSRHNTDLQQPSAEASPNPEIITGTTD 1516
                                                                                                                                                                                                                                                                                                                 1366 SAYSALTTADTPLAFSHSPRQDDGGN------VSAVAYHSTTSLLAITELFEK 1412
                                                                                                                                                                                                                                                                                                                                                                                                                       1317 PTVTSPTATASVIMSETQ------RTRSKEAKDQIKGPRKNRNNANTTPRQVSGY 1365
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                                                   508 -PTSQFPPASI-LKQITLPGNKILSLQASPTQKNRIK 542
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                                                                                                                                                                                                                                                                                                                                                                       352 TAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAV--TLSLPAVT---- 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 TVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAK--AGVVTLHSVGP 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     989 SSLFHIPRNNNTGNFPLSRHLGRERTIWSRGRVKNPHRTPVLRRHRHRTVRPAIKGPANK 1048
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                                                                                                                                                                                                          YTQTLGNTTALETTL------LSKSQESTTVKRASDTPPPLLSSGAPPVPTPSPPPF' 1463
                                                                                                                                                                                                                                                             FGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPA-GIPTGS---- 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPOPHL------VPFLKKSVVALROLLPNSQSFTQQCVQQTSSDMVIATCTT 293
                                                                                                                                                         ----SSKQLFSLFHVVQQPSGGNEKQVTTISHSS--TLTIQKCGQKTMPVNTII----- 507
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Search completed: February 16, 2003, 22:01:37 Job time: 60.7846 secs

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ALIGNMENTS

transcription initiation factor IID 110K chain - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 15-Oct-1999 C;Accession: A48184 R;Kokubo, T.; Gong, D.W.; Roeder, R.G.; Horikoshi, M.; Nakatani, Y. Proc. Natl. Acad. Sci. U.S.A. 90, 5896-5900, 1993 A;Title: The Drosophila 110-kDa transcription factor TFIID subunit directly interacts A;Reference number: A48184; MUID:93317591; PMID:8327460 A;Accession: A48184 A;Cross-references: GB:S63550; NID:g398432; PID:g398433 A;Experimental source: embryo nuclear extract A;Note: sequence extracted from NCBI backbone (NCBIN:13-C;Genetics: C; Keywords: transcription A;Gene: FlyBase:Taf110
A;Cross-references: FlyBase:FBgn0010280 A; Molecule type: mRNA; protein A; Residues: 1-921 < KOK> LNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKP 389 PSQTTTIGQTQVRMI---TPNALGTPRPTIGHTTISKQPPN---IRLPTAPRLVNTGGIRT TQQGNTKEKCRKFLANLIEL--STREPKPVEKNVRTLIQELVNANVEPEEFCDRLERLLN TMLENVK-KCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELK APQLPQITQIQTIPAQQSQQQQVNNVSSAGGTATAVSSTTA-----ATT KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSP NTTSTTNHPTTTQ-IRLQTVPAAASMTNTTATSNIIVNSVASSGYANSSQPPHLTQLNAQ NITSRPAVPANPQTVKICTVPNSSSQ------LIKKVAVTPVKKLAQIGTTVVTTVP PQSPSITLSTLNTGQTPA------LLVKTDNGFQLLRVGTTTGPPTVTQTITNTSNNS PQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLML-----VSPQQTVTRAETTS 76 ----QCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVS----VQT ASPQPCLIGFLKKSLPLLRQALYTKELVIEGIKPPPQHVLGLAGLSQQLPKIQAQIRPIG h 18.2%; Score 775; DB 2; Similarity 29.6%; Pred. No. 2.1e-33; 58; Conservative 128; Mismatches 308 initiation (NCBIN:134863, NCBIP:134864) Length 921; Indels 178; Gaps 329 405 345 246 187 243 127 184 276 287 26;

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C;Species: Drosophila sp.
C;Date: 10-Jun-1993 #sequence_revision
C;Accession: A45183
R;Hoey, T.; Weinzlerl, R.O.; Gill, G.;
Cell 72, 247-260, 1993
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C;Species: Drosophila sp.
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 16-Feb-1997
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                                                                                                                   KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSP
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RESULT C87719

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; A;Accession: C87719

Status: preliminary DNA

position:

A; Molecule type: I A; Residues: 1-549 A; Cross-references: Gene: R119.6 <STO GB:chr_I; PIDN:AAC16427.1; PID:g3133007; GSPDB:GN00019; CESP:R119

Matches Query Match Best Local al Similarity 145; Conserv Conservative 8.1%; 22.7%; Score 344; DB Pred. No. 6.9e 77; Mismatches DB 2; .9e-11; Length Indels 224; Gaps

20;

158 PSSLGASSTPSNEPNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEM- 216

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nascent polypeptide-associated complex alpha N; Alternate names: alpha-NAC protein C; Species: Mus musculus (house mouse) C; Date: 22-Oct-1999 #sequence_revision 22-Oct C; Accession: T30826
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A; Introns: 24/1; 1996/1;
A; Note: differential spl:
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                                                                                                                                                                                                                                                                                                                         R;Yotov, W.V.; St-Arnaud, R. Genes Dev. 10, 1763-1772, 1996
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C; Keywords: alternative
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                                                                                                                                                                                                            A; Cross-references:
                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-2187 <YOT>
                                                                                                                                                                                                                                                         A;Status:
                                                                                                                                                                                                                                                                            A;Reference number: Z20889;
A;Accession: T30826
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                  N
TLVTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTT-IQFPANLQLPPGTVLIKSNSGPL 60
                                                                                                                                                                                                                                                         preliminary;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAAKSR-SNKEDPEOLRLKOKAKELOOLELAQIQHRDANLTATAAIGPRKKRPLESGIEG 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHLRELITLMAGVAEHRVESLRIPENYVAIDDVKRQLRFLEDLDRQEEELRESREKESLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERLRGLLEKLTAIAQHRMTTYKASENYILCSDTRSQLKFLEKLDQLEKQRKDLEEREMLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENACILATNSELVGTLIQSCKDEPFLFIGALQKRILDIGKKHDITELNSDAVNLISQATQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RMSKNKNSGKETIE
                                                                Similarity
                                                Conservative
                                                                                                                                                                                                         EMBL:U48363;
                                                                                                          6/1; 2024/3; 2050/3; 2099/3; 2142/3; 2183/3
splicing converts alphaNAC into a tissue-specific
ive splicing; DNA binding; transcription factor
                                                                                                                                                                                                                                                         translated
                                                                5.7%;
21.8%;
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                                                120;
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                                                                                                                                                                                                                                                         from
                                                                Pred.
                                                                              Score 244.5;
                                              Mismatches
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Db 1566	6 TIELKEAPATLPPSPTKSPKIPSSKKAPRTSAPKEFPASPSIKPVITSLAQTAPPS 1621
0у 61	
Db 1622	2 IQKAPSTTIPKENLAAPAVLPVSSKSPAAPARASASISPATAAPQTAPKEATTI 1675
Qy 110	0 TPVKKLAQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLG 162
Db 1676	6 PSCKKAAATETPIETSTAPSLEGAPKETSETSVSKVLMSSPPKKASSSKR 1725
Оу 163	ASSTPSNE-PNIKAENSAAVQINISPTMLENVKKCKNFLAMLIKLACSGSQ
Db 172	6 ASTLPATTLPSLKEASVLSPTATSSGKDSHISPVSDACSTGTTTPQASEK 1775
Qу 222	KLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSV
Db 1776	6LPSKKGPTAFTEMLAAPAPESALAITAPIQKSPG 1809
Qy 282	TSSDMVIATCTTTVTTSPVVTTTV
Db 1810	0ANSNSASSPKCPDP-SSKKDTKGLPSAVALAPQTVPVEKDTSKAIETLL 1857
Оу 334	4 AGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSG 393
Db 1858	8 VSPAKGSDCLHSPKGPVGSQVATPLAAFTSDKVPPEAVSA 1897
Оу 394	TAVTLSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPO
Db 1898	SVAPKPAPAASLTLAPSPVAPLPPKQ
Qy 454	
Db 1939	9 KLPVPAEEDELPPLI-PPEAVSGGEPFQPILVNMPAPKPAGTPA 1981
Qу 514	4 PASILKQITLPGNKILSLQASPTQKNRIKENVTSCFRDEDDINDVTSMAGVNLNEENACI 573
Db 1982	2 PAPSAKQPVLKNNKGSGTESDS-DESVPE-LEEQDSTQTATQQAQ 2024
Qy 574	LATNSELVGTLIQSCKDEPFLFIGALQKRILDIGKKHDITELNSDAVNLI
Db 2025	5 LAAAAETDEEPVSKAKQSRSEKKARK-AMSKLGLRQVTGVTRVTIRKSKN 2073
Qу 634	LLEKLTAIAQHRMTTYKASENYILCSDTRSQLKFLEKLDQLE
рь 2074	ILFVITKPDVYKSPASD
Оу 69	2 KSRSNKEDPEQLRLKQKAKELQQLELAQIQHRDANLTATAAIGPRKKRPLESGIEGLK
рь 212	O EAVSNIQENTQTPTVQEESEEEEVDETGVEVKDIELVMSQANVSRAKAVRALKNN 2174
RESULT 5	
N; Alternate C; Species:	ate names: s: Homo sap
C; Date: C; Access	16-Feb-1994 #sequence_revision 18-Nov-1994 ion: A40718; G02511; A56088; I37453
Wilson	A.C.; LaMarco, K.; Peterson, M.G.; Herr, W. 115-125, 1993
Title: Refere	The VP16 accessory protein HCF is a family of polypeptides processed number: A40718; MUID:93327419; PMID:8392914
A; Status	Accession: A40/16 Status: preliminary; not compared with conceptual translation

A; Molecule type: mRNA; protein
A; Residues: 1-2035 <WIL
A; Residues: 1-2035 <WIL
A; Cross references: PIDN:AAB27583.1; PID:g399752
A; Experimental source: HeLa cell
A; Note: sequence extracted from NCBI backbone (NCBIP:135349)
R; Platzer, M.; Bauer, D.; Drescher, B.
submitted to the EMBL Data Library, March 1995 >>> 0 x 0 0 0 0 x 2 2 2 A;Reference number: H01368

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-CDRQEAAASLYTSTVG----QQN-----

-GSVVRVCSNPP 1079

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A;Residues: 100-563,'R',565-603,'VS',604-1163,'P',1165-1872,'A',1874-2035 <FRA>
A;Cross-references: EMBL:X79198; NID:g558348; PIDN:CAA55790.1; PID:g558349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Genomic organization of the human VP16 accessory protein (HCF), a housekeeping A;Reference number: I37453; MUID:95130085; PMID:7829076 A;Accession: I37453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-664,'T',666-1637,'E',1639-1684,'A',1686-1734,'Q',1736-2035 </br>
R;Frattini, A.; Faranda, S.; Redolfi, E.; Zucchi, I.; Villa, A.; Patrosso,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: GDB: HCFC1; HFC1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Cross-references: GDB:388714; OMIM:600196;Map position: xq28-xq28;Introns: 65/1; 114/3; 168/2; 238/1; 266/2;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                     TSSDMVIATCTTTVTT------SPVVT-----TTVSSSQSEKSIIVSGA-----TA
KNRIKENVTSCFRDEDDINDVTSMAGVNLNEENACILATNSELVGTLIQSCKDEP
                                     EQPTATVTIADSGQGDVQPGTVTLVCSNPPCETHETGTTNTATTTVVAN--LGGHPQPTQ
                                                                                                                                                                                                  ASLATPITTLGTIATLSSQ----VINPTAITVSAAQTTLTAAGGLTTPTITMQPV-----
                                                                                                                                                                                                                                          KPLVTSVA--NTVTTVSLQPEKPVVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCW
                                                                                                                                                                                                                                                                                  LRTVPMGGVRLVTPVTVSAVKPAVTTLVVKGTTGVTTLGTVTGTVST--SLAGAGGHSTS
                                                                                                                                                                                                                                                                                                                                                                VTSSPGIKSPITIITTKVMTSGTGAPAKIITAVPKIATGHGQQGVTQVVLKGAPGQPGTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QTKPVQTSAVTGQASTGPVTQIIQTKGPLPAGTILKLVTSADGKPTTIITTTQASGAGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --KAENSAAVQINLSPTMLENVKKCKNFL--AMLIKLACSGSQSP-----EMGQNVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRPIITVHKSGTV-TVAQQAQVVTTVVGGVTKTTTLVKSPISVPGGSALISNLGKVMSVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTV-----
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                                                                             ISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASI--
                                                                                                                                                           DHICKPVIGTPVQIKL-AQPGPVLSQPA-GIPTGSSSKQLFSLFHVVQQPSGGNEKQVTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---VTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLK-PSSL-GASSTPSNEPNL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148;
                                                                                                                       ----SQPTQVTLITAPSGVEAQPVHDLPVS
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                                                                                                                                                                                                                                                                                                                          ---VSVQTLNPLAGPVGAK--AGVVTLHSVGPTAATGGTTAGTGLLQTS
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22.6%;
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Pred. No. 0.0002;
                                                                                                                                                                                                                                                                                                                                                                                                                                             -SSVSPSTT---KPGTTTIKTIPMSAIITQAGATG
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                                                                           ---LKQITLPGNKILSLQASPTQ
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A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1343-1350,'L',1352-1411,'S',1413-1448,'P',1450-1503,'T',1505-1915
A:Residues: 1343-1350,'L',1352-1411,'S',1413-1448,'P',1450-1503,'T',1505-1915
A:Cross-references: GB:M74027; NID:g188863; PIDN:AAA59875.1; PID:g188864
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:55749, NCBIP:55750)
R:Gum, J.R.; Byrd, J.C.; Hicks, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.
J. Biol. Chem. 264, 6480-6487, 1989
A:Title: Molecular cloning of human intestinal mucin cDNAs. Sequence analysis
A:Reference number: A33532; MUID:89197956; PMID:2703501
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A; Residues: 626-1895 <GU2>
A; Residues: 626-1895 <GU2>
A; Cross-references: GB: M94131; NID: g186395; PIDN: AAA59163.1;
A; Cross-references: GB: M94131; NID: g186395; PIDN: AAA59163.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M94132; NID:g186397; PIDN:AAA59164.1; PID:g186398 A;Experimental source: colon A;Note: sequence extracted from NCBI backbone (NCBIP:116698) R;Toribara, N.W.; Gum Jr., J.R.; Culhane, P.J.; Lagace, R.E.; Hicks, J.W. J. Clin. Invest. 88, 1005-1013, 1991
A;Title: MUC-2 human small intestinal mucin gene structure. Repeated arr. A;Reference number: A43932; MUID:91358717; PMID:1885763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Gum Jr., J.R.; Hicks, J.W.; Toribara, N.W.; Rothe, E.M.; J. Biol. Chem. 267, 21375-21383, 1992
A;Title: The human MUC2 intestinal mucin has cysteine-rich A.Reference number: A45106; MUID:93016075; PMID:1400449
A;Accession: A45106
                                                                                                                                                                                                                                                                                                                                                                                                   J. Clin. Invest. 87, 77-82, 1991
A; Title: Human bronchus and intestine express the A; Reference number: A61257; MUID:91086481; PMID:19 A; Accession: A61257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 10-Mar-1993 #sequence_revision 12-Apr-1996 #text_change 05-Nov-1999 C;Accession: A49963; A45106; B45106; A43932; B33532; A61257; PQ0328; PQ0329 R;Gum Jr., Jr.; Hicks, J. W.; Toribara, N.W.; Siddiki, B.; Kim, Y.S. J. Biol. Chem. 269, 2440-2446, 1994 A;Title: Molecular cloning of human intestinal mucin (MUC2) cDNA. Identification A;Reference number: A49963; MUID:94132002; PMID:8300571 A;Accession: A49963
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A; Experimental
                                                       A; Molecule type: mRNA
A; Residues: 2328-2468 < XUG>
                                                                                                                                                                                                                  Blochem. Biophys. Res. Commun. 183,
                                                                                                                                                                                       A; Title: Human intestinal mucin-like
                                                                                                                                                                                                                                                                                A; Experimental source: bronchus
                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 'T',1925-1948,'TTS',1952-1954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Jany, B.H.; Gallup, M.W.; Yan, P.S.; Gum, J.R.;
J. Clin. Invest. 87, 77-82, 1991
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A; Residues: 1916-2193 <GU4>
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A; Residues: 2037-3020 <GU3>
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A; Residues: 1-639 <GU1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: intestine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: B33532
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                          Cross-references: GB:M86523
                                                                                                                                                       Reference number:
                                                                                                                      Accession: PQ0328
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                                                                                                                                                                                                                                               G.; Huan, L.; Khatri, I.;
source:
                                                                                                                                                          PQ0328;
small intestine
                                                                                                                                                   ucin-like protein (MLP) is homologous MUID:92198477; PMID:1550588
                                                                                                                                                                                                                                               Sajjan,
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                                                                                                                                                                                                                  jan, U.S.; McCool, D.; Wang,
821-828, 1992
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                                                                                                                                                                                                                                                                                                                 <JAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                          PMID:1985113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y.S.;
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                                                                                                                                                                                                                                         D.; Jones,
                                                                                                                                                                                    with
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A; Nessentics:
C; Genetics:
A; Gene: GDB: MUC2
A; Cross-references: GDB: 120203; OMIM: 158370
A; Cross-references: GDB: 120203; OMIM: 120203; OM
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147141

127141

137141

C; Species: Sus scrofa domestica (domestic plg)
C; Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 03-Nov-2000
C; Accession: 147141; S55315
R; Turner, B.S.; Bhaskar, K.R.; Hadzopoulou-Cladaras, M.; Specian, R.D.; LaM: Gastroenterology 106, 200, 1994
A; Title: Pig gastric mucin: isolation and characterization of a cDNA clone 1
     Biochem.
A; Title:
                                                                                                                                                                     A; Reference number: 147141; MUID:94102478; A; Accession: 147141
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                          A;Cross-references: EMBL:U10281; NID:g915205; PIDN:AAC48526.1; PIIR;Turner, B.S.; Bhaskar, K.R.; Hadzopoulou-Cladaras, M.; Specian, Biochem. J. 308, 89-96, 1995
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A; Residues: 2328-2342, 'K', 2344-2354 < XUG1>
                                                                                                      A; Residues:
                                                                                                                           A; Molecule type: mRNA
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       Isolation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SCRATMYPDVPIGQLGQTVVCDVSVGLICKNEDQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LACSGSQSP-----EMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKS
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137; Conserv
                                                                                                   1-528 <TUR>
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                                                                                                                                                        GB/EMBL/DDBJ
     of.
     cDNA clones
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encoding pig gastric
                                                 PID:g915208
an, R.D.; Lai
                                                                                                                                                                                                                                 cDNA clone with
                                                                                                                                                                                                                                                                              R.D.; LaMont,
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A;Gene: CESP:H02F09.3
A;Map position: X
A;Introns: 42/1; 78/3
                                                                      A; Experimental source: C; Genetics:
                                                                         A;Residues: 1-1275 <GEI>
A;Cross-references: EMBL:AF077538; PIDN:AAC64622.1; GSPDB:GN00028;
A·Fxnerimental source: strain Bristol N2; clone H02F09
                                                                                                                                                                                                                                                                 C)ACCESSION. C.; Harmon, G.
R;Gelsel, C.; Harmon, G.
submitted to the EMBL Data Library, July 1998
submitted to the EMBL Data Library, July 1998
cos:
                                                                                                                                                                                                                                                                                                                                                     hypothetical protein H0ZF09.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #te:C;Accession: T33369
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A; Residues: 1-1275 <
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78/3; 106/3; 135/2;

from GB/EMBL/DDBJ

cosmid H02F09

29-Oct-1999 #text_change

17-Mar-2000

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A;Molecule type: mRNA
A;Residues: 1-528 <TU2>
A;Cross-references: GB:U10281; NID:g915205; PIDN:AAC48526.1; PID:g915208
C;Superfamily: pig submaxillary mucin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: S:
A; Accession: S55315
A; Status: preliminary
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LKQITLPGNKILSLQASPTQKNRI
                                                                                                                                                                                          LSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPAGIPT
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                                                            SSGSAPTTSATSV--QPSSS----SSVPTTSATSVRSSSSSTPIPT--
                                                                                                      GSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASI 517
                                                                                                                                                     TSATSVQPSSSSS----PPISSTIS----
                                                                                                                                                                                                                                           PSSSSSAPTTSATSVQPSSSSSSPPISSTISVQPSSSSSSPTTSTTSVQPSS---
                                                                                                                                                                                                                                                                                  PTAATGG-TTAGTGLLQTS--------KPLVTSVANTVTTVSLQPEKPVVSGTAVT
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Pred. No. 4.7e:
93; Mismatches
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glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) N;Alternate names: extracellular glucoamylase; mucin-like protein MUC1; prote C;Species: Saccharomyces cerevisiae C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Nov-1999 C;Accession: S48478; A26877; B26877; S27281; JC6123 R;Rowley, K. submitted to the EMBL Data Library, October 1994 A;Reference number: S48478 A;Accession: S48478
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 A; Cross-references:
                A; Molecule type: DNA
A; Residues: 1-1367 < ROW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SGPLMLVS-PQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLVTKVAPVSAPPKVSSGP----RLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSN-
                                                                                                                                                                                                                                                                                                               -----EPFLFIGALQKRIL-----DIGKKHDITELNSDAVNLISQATQERLRGLLEK
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 GB: 247047;
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Pred. No. 0.0
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 NID:g603997;
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PID:9763364; GSPDB:GN00009;
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A;Reference number: A91831; MUID:87194600; PMID:3106330 A;Accession: A26877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: nucleic acid sequence not shown A;Molecule type: DNA A;Residues: 1-1367 <LAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Lambrechts, M.G.; Bauer, F.F.; Marmur, J.; Pretorius, Proc. Natl. Acad. Sci. U.S.A. 93, 8419-8424, 1996 A;Title: Mucl, a mucin-like protein that is regulated by A;Reference number: JC6123; MUID:96323237; PMID:8710886 A;Accession: JC6123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:M16164; NID:g172522; A;Accession: B26877
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J. Bacteriol. 169, 2142-2149, 1987
A:Title: Gene fusion is a possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: SGD:MUC1; STA2; MAL5; DEX2; A;Cross-references: MIPS:YIR019c; SC
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A;Cross-references: EMBL:X13857; NID:g4551; PIDN:CAA32069.1;
A;Cross-references: EMBL:X13857; NID:g4551; Pretorius, I.S.
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A; Residues: 762-1331
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A; Residues: 1-31 <PAR>
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Best Local Similarity
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TVPCSTSPSETASESTTTSPTTPVTTVVSTTVVTTEYSTSTKPGGEITTTFVTKNIPTTY
                                                                                                                                                                                                                                                                                                                                                                                                                  SSSTTESSVAPVPTPSSSNITSSAPSSTPFSSSTESSSVPV---PTPSSSTTESSS---
                                                  SKPLVTSVANT----VTTVSLQPEKPVVSGTAVTLSLPAVT--FGETSGAAIC-----
                                                                                                     SAGETTSGCSPKTVTTTVPTTTTTSVTTSSTTTITTTVCSTGTNSAGETTSGCSPKTITT
                                                                                                                                                  KSIIVSGATAPRTV--SVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTG--LLQT
                                                                                                                                                                                                                                                                                                            --APVSSSTTESSVAPVPTPSSSSNITSSAPSSIPFSSTTESFSTGTTVTPSSSK----
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                                                                                                                                                                                                                                                       PFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSP----VVTTTVSSSQSE
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                                                                                                                                                                                                       -YPGSOT--ETSVSSTTETTIVPTKTTTSVTTPSTTTITTTVCSTGTN
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Pred. No. 0.00
77; Mismatches
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s, M.G.; Jimenez,
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A:Description: functions in multiple cell adhesion processes A:Note: found exclusively on the apical region of the sperm C:Keywords: cell adhesion
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C:Species: Mus musculus (house mouse)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T42215
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J. Biol. Chem. 273, 3415-3421, 1998
A;Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane A;Reference number: Z22080; MUID:98123114; PMID:9452463
A;Accession: T42215
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A; Residues: 1-5376 <GAO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVTTV-PKPSSV-QSVAVPTSVVTVTPGKPLNTVTTLKPSSL-GASSTPSNEPNLKAE-N 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTS
: || : | || || || ||: |: |:
                                 LAQPGPVLSQPAGI----PTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSST------
                                                                                                                   PVVSGTAVTLSLPAVTFGETSGAAICLPSVKP------VVSFCWDHICKPVIGTPVQIK 441
                                                                                                                                                                                              AKAGVVTLHSVGPTAATGGTTAGTGLL-----QTSKPLVTSVANTVTTVS-----LQPEK
                                                                                                                                                                                                                                                                          -SDMVIATCTTTV----TTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVG
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                                                                                                                                                                                                                                                                                                                                                                                                  TVPTEVTGVHTEVTNV---
                                                                                                                                                                                                                                                                                                                                                                                                                                     SAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAK---IEA
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-PTEVLTVPIEVTTFPTGETT--VPTEVPTVSTEMTGVHTEVTTVFPEETSIPTEVAT
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Pred. No. 0.014;
9; Mismatches 2
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R;Gelsel, C;; Gattung, S.
submitted to the EMBL Data Library, December 1996
submitted to the sequence of C. elegans cosmid
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A;Reference number: Z21525
A;Accession: T34434
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A;Experimental source: strain Bristol N2; clone K06A9
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A; Residues: 1-2232 <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                SLPAVTFGETSG-----AAICLPSVKPVVSFCWD-HICKPVIGTPVQIKLAQPGPVLS 450
                                                   GSGSTSTSGEITSQGSTQTPRSSLSTSPAISTSTQQSVSTNS--PGSTVTQPSTVRGSTS 1228
                                                                                                                                                                         TCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSV 349
                                                                                                                                                                                                                                                                                             TSP-VESSTSGATSSSGSPGTTLTSISPSPSSPSSTIGSSQGSTSPVVSTISQGSTETPGS 1055
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                                                                                                                                      TTLTSISPSPSQSSTIGSSQGSTSPVVSTTSGDMTSQGSTQIP----
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138; Conserv
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21.9%; Pred. No. 0.0
                                                                                             GGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAV---TL
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3; Mismatches
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hypothetical protein T19D12.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;nate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #te: C;Accession: T34369 R;Favello, A.
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A;Molecule type: DNA
A;Residues: 1-1777 <FAV>
A;Cross-references: EMBL:U41263; PIDN:AAC24428.1; GSPDB:GN00020;
A;Experimental source: strain Bristol N2; clone T19D12
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       KLAQPGPVLSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCG---
                                          LTSSSAQSTASTGVSTVASSTTIPQGSSS-
                                                                                                                 STTTSP---
                                                                                                                                               VQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQ-
                                                                                                                                                                                    TTQGSSSQAPSSTVTVPTTGTTSGAASTTGSITSTQQATSTSSVITTGSTSAPQSSTAVS
                                                                                                                                                                                                                     CVQQTSSDMVIATCT--TTVTTSPVVTTT--VSSSQ---SEKSIIVSGAT-APRT---VS
                                                                                                                                                                                                                                                                                                                               --NITR-KGYQGFVILVA------NSDESVQASVDSATNLKAQGF-NVITVAFKS
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                                                                                                                                                                                                                                                                                              ----PQPH----LVPFLKKSVVA-----
                                                                          -PEKPVVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQI
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                                                                                                             -STTTGSTPAPOSSTVASTTTVSPYTTTECICTTVSNTFGTSTTQG
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A;Note: sequence extracted from NCBI backbone (NCBIN:124958, NCBIP:124959)
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           calphotin - fruit fly (Drosophila melanogaster)
(;Species: Drosophila melanogaster
C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_ch
C;Accession: A47283
R;Ballinger, D.G.; Xue, N.; Harshman, K.D.
Proc. Natl. Acad. Sci. U.S.A. 90, 1536-1540, 1993
A;Title: A Drosophila photoreceptor cell-specific protein,
A;Reference number: A47283; MUID:93165730; PMID:8434015
A;Constants: photoreceptor cells
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LSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIP
                                                     AVTDPDVTASAV--PELPPVIAPSPVPSAVAETPVDLAPPVLPPVAAEPVPAVVAEETPE
                                                                                                                                                             GVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLP
                                                                                                                                                                                                   TEPPVAAATLTTAPET-PALAPVVAESQVAANTVVATPPTP-APEPETIAP-----
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Pred. No. 0.0017;
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R;Martin, J.H.; Benzer, S.; Rudnicka, M.; Miller, C.A. Proc. Natl. Acad. Sci. U.S.A. 90, 1531-1535, 1993
A;Title: Calphotin: a Drosophila photoreceptor cell calcium-binding A;Reference number: A47282; MUID:93165729; PMID:8094559
A;Accession: A47282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               calcium-binding protein calphotin - fruit fly (Drosophila melanogaster)
C; Species: Drosophila melanogaster
C; Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
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C;Superfamily: collagen alpha 1(I) chain;
C;Keywords: calcium binding
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A;Note: sequence extracted from NCBI backbone (NCBIN:124955,
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A; Residues: 1-865 < MAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GTLVTKV-APVSAP-----PKVSSGPRLPAP----QIVAVKAPNTTTIQFPANLQ 45
                                                                                                                                                                                           VVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVS-----FCWDHICKPVIGT
                                                                                                                                                                                                                                                                     LNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPVAATPTPVVQIPVAAPVIATPPVAASAPTPAAVTPVISPVIASPPVVPANTTVPVAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKVAVTPVKKL-AQIGTTVVTTVPKPSSVQSVAVPTSVVT-VTPGKPLNTVTTLKPSSLG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTIPSPVSAPVAAPVTPSAVAAPVQVVSPAAVAPAPAAPIAVTPVAPPPTLASVQPATVT 63
                                         GQKTMPVNTIIPTSQFPPASI 517
                                                                                                                 PVQIKLAQPGPVLSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKC 496
                                                                                                                                                                                                                                                                                                           VSAS-----TEPPVAAATLTTAPET-PALAPVVAESQVAANTVVATPPTP-APEPET
                                                                                                                                                                                                                                                                                                                                               NSQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQT
                                                                                                                                                                                                                                                                                                                                                                                       ----PEVSVVATKPLAAAEPVVVAPPATETPVVAPAAASPHVSVAPAVETAVVA----P
                                                                                                                                                                                                                                                                                                                                                                                                                             GSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAAVPAAVPVVAPVLAPAVAPAVAPVVAETPAPPPVAEIPVATIPEC---VAPLI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASSTPSNEPNLKAENSAAVQINLSPTMLE------NVKKCKNFLAMLIKLACS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPAPAPIAAASVTPVASVAP---VVVAAPTP-----PAASPVSTPVAVAQIPVAVSAPVA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPPGTVLIKSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNS-SSQLI 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETTAPPAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSQFPPASI
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                                                                           PVPAVVAEETPETPAPASAPVTIAALDIPEVAPVIAAPSDAPAE----APSAAAPI---
                                                                                                                                                         VVATTPVPATL-AVTDPDVTASAV--PELPPVIAPSPVPSAVAETPVDLAPPVLPPVAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 4.8%;
Similarity 21.7%;
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                                                                                                                                                                                                                                   -PVVAETPEVASVAVAETTPPVVPPVA----AESIPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 206.5; DB 2; Pred. No. 0.0025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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T34433
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A;Cross-references: EMBL:U80846; PIDN:AAC70889.1; GSPDB:GN00028;
A;Experimental source: strain Bristol N2; clone K06A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A; Accession: T34433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Geisel, C.; Gattung, S. submitted to the EMBL Data Library, December 1996 A;Description: The sequence of C. elegans cosmid in A;Reference number: Z21525
 Search completed:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 1
A; Introns: 38/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP: K06A9.la
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 AASSSSYATVSTIAGSTGSTIT---PVPGSSSTIGSSTPSASSSSSGTMSTIS----GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 SISTSALPI-ASSSASSSPSAASSTTPVVLSSSTIQSSSGTFPSSVASSPSTV--GSTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TLVTKVAPVSAPPKVSSGPRLPA---PQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                             TPSASSSSAGTASTISGSTGSTATIVPGSSSSSVGSSTQSASPSSPGTMSTVSGPTGSTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNP------LAGPVGAKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNIKAENSAAVQINISPTMIENVKKCKNFLAMLIKLACSGSQSPEMGONVKKLVEQLIDA 230
                                                                                             AGVNLNEENACILATNSELVGTLIQS 587
                                                                                                                                                                       I---PTSQFPPASILKQITLPGNKILSLQASP--TQKNRIKENVTSCFRDEDDINDVTSM
                                                                                                                                                                                                           MNPSSSTPTGSSQSTITPEGSTASSPTG-----STGSTFSVATEVTSQSTVPSGSS
                                                                                                                                                                                                                                                                                     SGSTGTSQSTLASSTATPGSSSTVPSSSSPQPS---SQSPAPNTGSTTPSQTSSQSPSPS
                                                                                                                                                                                                                                                                                                                           SGTAVTLSLPAVTFGETSGAAICLP-SVKPVVSFCWDHICKPVIG--TPVQIKLAQPGPV 448
                                                                                                                                                                                                                                                                                                                                                                   VVPGSSTSPAPSSSPNPSSSPASTGSTTTISG---SSSIIVSTVSGS
                                                                                                                                                                                                                                                                                                                                                                                                       VVTLHSVGPT-----AATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVSSSTFG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGTTVVTTVPKPSS------VQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLMLVSPQQTVTRAETT-SNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141;
                                                         SSLESSTSGA---TTSSGSAGTTMTS
                                                                                                                                   LGTQSTNSSPSPSSLSPST-SGMSTLTSEPSPSSTQSSGAQSTLTT---
                                                                                                                                                                                                                                               LSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTI--QKCGQKTMPVNTI
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February 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103/3; 132/2; 158/2; 222/1; 839/1; 849/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.8%; Score 206; DB 2; Length 1032;
22.5%; Pred. No. 0.0034;
7ative 79; Mismatches 246; Indels 16
 2003,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from GB/EMBL/DDBJ
22:00:16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---- ASSSSSGTMSTNSGSTGSTVTVA
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26;

Job time : 51.8257 secs

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Result
No.
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
    1277.5
753.5
257.5
257.5
244.5
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length: 2000000000
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6: ...
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110: ...
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
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Gapop 10.0 , Gapext 0.5
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4264
1 GTLVTKVAPVSAPPKVSSGP......KZHQHERALFTIRTLLTLTY 852
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Match Length DB
      30.0
177.0
6.01.7
5.33.34.4
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sp_rodent:*
sp_virus:*
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sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_bacteria:*
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851
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11275
      1 Q91W6
Q819E0
Q61797
Q81UG2
Q9UG2
Q9UG3
Q9UG7
1 Q9QX35
Q Q9G7
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ALIGNMENTS

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Qy Db Qy 1	Db Qy	Query Best Matc	SQ SI		RT "C				GN TI		1MM TOS
74 TTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTVVTTVPKPSSVQ 133	20 PRLPAPQIVAVKAPNTTTIOFPANLQLPPGTVLIKSNSGPLMLVSPQQTVTRAE 73	Query Match 30.0%; Score 1277.5; DB 11; Length 662; Best Local Similarity 39.7%; Pred. No. 3e-64; Matches 319; Conservative 105; Mismatches 204; Indels 175; Gaps 21;	MGD; MG1:2152346; T8148. NON_TER 1 1 SEQUENCE 662 AA; 71398 MW; 91A75F38CB0D0DA4 CRC64;	EXP. Cell Res. 0:0-0(2001). EXBL: AV038601; AAK94779.1;	Metsis M., Biunkhoust A., Neuman T.; "Cell Type Specific Expression of the TFIID Component TAFII135 in the Norvous System.":	SEQUENCE FROM N.A. STRAIN-BALB/C; TISSUE-PO BRAIN;	malia; Eutheria; Rodentia; I_TaxID=10090;	sculus (Mouse). ota; Metazoa; Chordata;	UI-JUN-JUNZ (TEMBLIEL ZI, Last annotation update) TATA-binding protein associated factor TAFII135 (Fragment). TAFAA.	(TrEMBLrel. 19, (TrEMBLrel. 19,	T 1 6 91106 PRELIMINARY; PRT; 662 AA.

Best Loc Matches

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SD04735p.
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                                                            SEQUENCE FROM N.A.

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.

Champe M., Chavez C., Dorsett V., Farfan D., Frise E., Georg

Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall

Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S.,

Yu C., Lewis S.E., Rubin G.M., Celniker S.,

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AY069807, AAL39952.1; -
                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                SEQUENCE
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                                                                                                                                          MLFYMEQEREFCRSSMLFKTYLK
                                                                                                                                                                                                                  DANLTATAAIGPRKKRPLE-----SGIEGLKDNLLASGTSSLTATKQLHRPRITRICLRD
                                                                                                                                                                                                                                                            QLKFLEKLDQLEKQRKDLEEREMLLKAAKSRSNKEDPEQLRLKQKAKELQQLELAQIQHR
                                                                                                                                                                                                                                                                                                                         LDIGKKHDITELNSDAVNLISQATQERLRGLLEKLTAIAQHRMTTYKASENYILCSDTRS
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                                                                                                                                                                  LIFCMEQEREMKYSRALYLALLK
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                                                                                                                                                                                                                                                                                                RAITSEAGLDEPSQDVAVLISHACQERLKNIVEKLAVIAEHRIDVIKLDPRYEPAKDVRG
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                                                                                                                                                                                                                                                                                                                                                                                                                              IQKCGQKTMPVNTIIPTSQFPPASILKQITLPGNKILSLQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSSK---QLFSLFHVVQQPSGGNEKQVTTISHSS---------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQANIVQIR--GPQHAQLQRTGSVQIRATTRP----PNSVPTAN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVS---VQTLNPLAGPVG
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01-AUG-1998 (01-AUG-1998 (01-MAR-2002 (Hypothetical R119.6.

8 (TrEMBLrel. 07, Cre
8 (TrEMBLrel. 07, Las
2 (TrEMBLrel. 20, Las
al 60.4 kDa protein.

Created)
Last sequence up
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update)

061707 061707;

PRELIMINARY;

PRT;

549 B

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Query Match
Best Local 9
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SMART; SM00549; TAFH; 1.
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"The sequence of C. elec
Submitted (MAY-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=BRISTOL N2; MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             investigating biology. The C
Science 282:2012-2018(1998).
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                                                     388
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                 KAAKSR-SNKEDPEQLRLKQKAKELQQLELAQIQHRDANLTATAAIGPRKKRPLESGIEG
                                                  GPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKAARVKELIRGVIYLETTAEEFTRNLQQVLKSQAQPHLLPFLQNTLPALRNAVRNG----
                                                                      ERLRGLLEKLTAIAQHRMTTYKASENYILCSDTRSQLKFLEKLDQLEKQRKDLEEREMLL
                                                                                                                                                                                                                                                             GARPMIRPMGPGGPSPMGLQGPVRGPMGHQMVQM----
                                                                                                                                                                                                                                                                                           LSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIP
                                                                                                                                                                                                                                                                                                                                 QQSQQQPPLEMRQ
                                                                                                                                                                                                                                                                                                                                                              AVTLSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQI--KLAQPGP----V
                                                                                                                                                                                                                                                                                                                                                                                                   GYV----FNNGRTPGPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSPMAPQGPPGT-----PQNSAAAAAAASDD--KNVTKCVRFLKTLINL--SNNDDPEMP
                                                                                                                      PTAAATATRQYPEGSLKSSIL-KPDEVLNRITKRMM----
                                                                                                                                                     ENACILATINSELVGTLIQSCKDEPFLFIGALQKRILDIGKKHDITELNSDAVNLISQATQ
                                                                                                                                                                                       ---HPPP-----PPQQIQQQHPAPPVEMEVEENL-----
                                                                                                                                                                                                                           TSQFPPASILKQITLPGNKILSLQASPTQKNRIKENVTSCFRDEDDINDVTSMAGVNLNE
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145; Conserv
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.. elegans
)8) to the
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22.7%;
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cosmid R119.";
EMBL/GenBank/DDBJ
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Pred. No. 1.2e-11;
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182; Conservative
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01-MAY-2000
01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-20130111; PubMed-10662542;
Jones M.H., Hamana N., Shimane M.;
"Iedentification and charcterization"
                                                                                                                              1977
                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00297; BROMO; 1. SMART; SM00249; PHD; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
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                                                                                                                                                                                                                                                                                                  VAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLI--KSNSGPLMLVS
                                                                                                                                                                                                                            VQQKVLGIIPSSTGTSQQTFTSFQPRTATVTIRPNTSGSGGTTSNSQVITGPQIRP----
                                                                                                                                                                                                                                                                             VAPISG--SVTTGTKMVL--TTKVGSPATVTFQQNKNFHQTFATWVKQGQSNSG---VVQ
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                        TVQRFLFTPLATTATTASTTTTVSTTAAGTGEQRQSKLSPQMQVHQDKTLPPAQSSSVG
                                                                                                                                                   PNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDA
                                                                                                                                                                             ---GMTVIRT-PLQQSTLGKAIIRTPVMVQPGAPQQVMTQIIRGQPVSTAVSAPNTVSST
  PRTVSVQTLNPLAGP---
                                                TSSDMVIATCTTTVTTSPVVTTTVSSS----
                                                                                                  KIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFI----QQCVQQ-----
                                                                                                                                                                                                  AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTL - -- KP - - SSLGASSTPSNE
                                                                                                                                                                                                                                                    PQQTVTRAETTSNITSRPAVPA-NPQTVKICTVPN-----SSSQLIKKVAVTPVKKL
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                                                                                                                            PGQKSLTSA-----
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(TrEMBLrel. 13, Last seque)
(TrEMBLrel. 21, Last annotation)
PHD finger transcription
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                                                                                                                                                                                                                                                                                                                                                                                EGF_2; UNKNOWN_1.
A; 311210 MW; 7B3BE0C1C4C3CFBE CRC64;
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EGF-like.
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-----VGAKAGVVTLHSVG----
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%; Pred. No. 7.7
104; Mismatches
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Best Local S
Matches 207
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                                                                                                                                                                                                                                                                                                                                                                                                                         Q8TE50;
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                      damage
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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stughes-Davies L.;
EMSY is amplified in
amage response.";
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TTQKP-PVVITASQSSLVSNSSSGSSSSTPSPIPNTVAVTAVVSSTPSVVMSTVÅQGVST
                         TPGKPLNTVTTLKPSSL-----GASSTPSNEPN-----
                                                              DEKPRK----RRRTNSSSSSPVVLKEVPKAVVPVSKTITVPVSGSPKMSNIMQSIANSLPP
                                                                                                                    LVSPQQTVTRAETTSNITSRPAVPANPQTV----KICTVPNSS----SQLIKKVA-----
                                                                                                                                                  TTSTPTSTP------VPSGSIATVKSPRPAS---PASNVVVLPSGSTVYVKSVSCSDE
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                                               HMSPVKITFTKPSTQTTNTTTQKVIIVTTSPSSTFVPNILSKSHNYAAVTKLVPTSVIAS
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20.0%; Pred. No. 7.4e-06;
ive 157; Mismatches 370
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01-FEB-1997 (TrEMBLrel. 02, Created)

01-FEB-1997 (TrEMBLrel. 02, Last sequence update)

01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

NASCENT polypeptide-associated complex alpha polypeptide
muscle-specific form GP220).
Eukaryota; Metazoa; Chordata; Mammalla; Eutheria; Rodentia; NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESQSATSTIKALLELQQTTVKEKLES--KPRQPTIDLSQMAVPIQMTQEKRHSPESPSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGNKILSLQAS--PTQKNRIKENVTSCFRDEDDINDVTSMA-GVNLNE-----
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Sciurognathi; Muridae;
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InterPro; IPR002715; NAC.
InterPro; IPR000449; UBA_domain.
Pfam; PF01849; NAC; 1.
Pfam; PF00527; UBA; 1.
SEQUENCE 2187 AA; 220599 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Differential splicing-in of a proline-rich exon converts alphaNAC into a muscle-specific transcription factor."; Genes Dev. 10:1763-1772(1996).
EMBL; U48364; AAB18734.1; -.
EMBL; U48363; AAB18732.1; -.
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MEDLINE-96312450; PubMed-8698236;
Yotov W.V., St-Arnaud R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASSTPSNE-PNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSCKKAAATETPIETSTAPSLEGAPKETSETSV---SKVLMSSPPKKAS-----SSKR 1725
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EAVSNIQENTQTPTVQEESEEEEVDETGVEVKDIELVMSQANVSRAK-----AVRALKNN
                                       KSRSNKEDPEQLRLKQKAKELQQLELAQIQHRDANLTATAAIGPRKKRPLESGIEGLKDN 751
                                                                                                                               LLEKLTAIAQHRMTTYK - - ASENYILCSDTRSQLKFLEKLDQLEKQRKDLEEREMLLKAA
                                                                                                                                                                        LAAAAEI------DEEP--VSKAKQSRSEKKARK-AMSKLGLRQVTGVTRVTIRKSKN
                                                                                                                                                                                                                                                                PAPSAKQPVLKNNK-----GSGTESDS-DESVPE-LEEQDSTQTATQQAQ------
                                                                                                                                                                                                                                                                                                          PASILKQITLPGNKILSLQASPTQKNRIKENVTSCFRDEDDINDVTSMAGVNLNEENACI
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^a: 220599 MW;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Host cell factor C1 (Fragment).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00041; fn3; 2.
Pfam; PF01344; Kelch; 4.
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InterPro; IPR001798; Kelch.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:105942; Hcfcl.
MGI:1349215; Abcdl.
                                                                                                                                            VVKGTTGVTTLGTVTGTVST---SLAGAGAHSTSASLATPITTLGTIATLSSQ----VINP
                                                                                                                                                                                                                     KIITAVPKIATGHGQQGVTQVVLKGAPGQPGTILRTVPMGGVRLVTPVTVSAVKPAVTTL
                                                                                                                                                                                                                                                                                           VSPSTT----KPGTTTIKTIPMSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPQMSGMAALAAAAATQKIPPSSAPTVLSVPAGTT----IVKTVAVTPGTTTLPATVKV
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 VHDLPVS---
                                  A-GIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQ
                                                                       TAITVSAAQTTLTAAGGLTTPTITMQPV
                                                                                                                                                                                 GAK - - AGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVA - - NTVTTVSLQPEKPVVSG
                                                                                                                                                                                                                                                            PVVT----TTVSSSQSEKSIIVSGA----TAPRT-----VSVQTLNPLAGPV
                                                                                                                                                                                                                                                                                                                               PQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTT----
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Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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DNA Res. 4:401-414(1997).
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Nakamura Y., Sato S., Kaneko T., Kotani H.,
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                                                                                                                                                      ST--PNNMAPASSVSPSMTTQLDASTTMNSRGPLGTSQGGANARMPPKKPSVGQKKPLET
TLIQSCKDEPFLFIGALQKRILDIGKKHDITELNSDAVNLISQATQERLRGLLEKLTAIA
                                                      LGSSPPPPSK-KQKVAGNSMDQSIEQLNDVTAVSGVNLREEEEQLFSGAKEDGRVSEASR
                                                                                                     LQASPTQKNRIKENVTSCFRDE--DDINDVTSMAGVNLNEENACILA----TNSELVG
                                                                                                                                                                                                                NTIIPTSQFPPASILKQIT------
                                                                                                                                                                                                                                                                                                                  GPV--LSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPV
                                                                                                                                                                                                                                                                                                                                                                              LGGPPQSTTNM-MTMP--KFERPSS----
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ICE 689 AA; 7568
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19.7%;
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Pred. No. 2
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Best Local Sin
Matches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U10281;
NON_TER 52
SEQUENCE 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Pig gastric mucin: isolation and with a novel tandem repeat."; Gastroenterology 106.200-200(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-YORKSHIRE/CHESTER WHITE/HAMPSHIRE CROSS;
MEDLINE-95275264; PubMed-7755593;
Turner B.S., Bhaskar K.R., Hadzopoulou-Cladaras
Lamont J.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 0.
01-NOV-1996 (TrEMBLrel. 0.
01-DEC-2001 (TrEMBLrel. 1.
Gastric mucin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Turner B.S., Bhaskar K.R., Hadzopoulou-Cladaras
LaMont J.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=YORKSHIRE/CHESTER WHITE/HAMPSHIRE MEDLINE=94102478; PubMed=7506218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mucin."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Isolation and characterization of cDNA clones encoding pig gastric
                    184
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NLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYV 243
                                                                                                                                                                                                                                                             PISVQPSSSSS--PTTSTTSVQSSSSSSVPIPSTTSVQP-----SSSGS----APTTS 48
                                                                                                                                                                                                                                                                                                            PVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLVSPQQT 68
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                                                                                                            PSSVQSVAVPTSVVT-----VTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQI 183
                                                                                                                                                                     ATSVQTSS--SSSPPISS---TISVQTSSSSS--
                                                                                                                                                                                                                 VTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTVVTTVPK 128
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                                                                PSS--SSSAPTTRATSVQSSSSSSAPISSTTSVQPSSSGSVPTTSATSVQSSSSSSA---
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26; Conservative
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; 49907 MW;
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22.3%; Pred. No. 2.1e
tive 93; Mismatches
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2.1e-05;
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Sus.
                                                                                                                                                                -VPTTSTTSV-Q
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                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 158
                                                                                                                                                                                                                                                                                                    Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U53925; AAB01163.1; -.
MGD; MGI:105942; Hcfc1.
InterPro; IPR003961; FN_III.
InterPro; IPR001798; Kelch.
Pfam; PF00041; fn3; 2.
Pfam; PF001344; Kelch; 5.
SMART: SM00060; FN3; 1.
SEQUENCE 2045 AA; 210537 MW; B89CC2FDA35B969F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-LIVER;
Kristle T.M., Dashner R.;
"cDNAs_encoding the mouse homolog of the human transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q61191 PRELIMINARY; PRT; 2045 AA. Q61191; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Transcription factor C1 (HCF).
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                                 600 VMVSNPATRMLKTAAAQVGTSVSSAANTSTRPIITVHKSGTV-TVAQQAQVVTTVVGGVT 658
                                                                                                                                                                    486 VLKVTGPQATTGTPLVTMRPASQ--AGKAPVTVT-SLPASVRM---VVPTQSAQGTVIGS 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 ELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTV---TTSPV 300
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hes 158;
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                                                                                                                                   64 SPQQT-----PQTVKICTVP 97
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NTVTTLK-PSSL-GASSTPSNEPNL-----KAENSAAVQINLSPTMLENVKKCKNFL--
                                                                   ----NSSSQLIKKVAV---TPVKKLAQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPL 150
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RESULT 12
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AC Q9QWH
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01-MAY-2000 (TrEMBLrel. 13
01-JUN-2002 (TrEMBLrel. 2)
             Submitted (DEC-1996) to t) EMBL; U80821; AAD09225.1; MGD; MGI:105942; Hcfcl.
                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                           Kristie T.M.;
                                                                                  SEQUENCE FROM N.A.
                                                                                                             NCBI_TaxID-10090;
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                                                           cDNAs encoding the mouse homolog
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                                                                                                                                                                                  Last sequence update)
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                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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01-DEC-2001 (TrEMBLrel. 19, Last annotation
Hypothetical 122.9 kDa protein.
H02F09.3.
Caenorhabditis elegans
 NCBI_TaxID=6239; [1]
                      Eukaryota; Metazoa; Nemata
Rhabditidae; Peloderinae;
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PRELIMINARY;

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Nematoda;

oda; Chromadorea; Caenorhabditis.

Rhabditida; Rhabditoidea;

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Query Match
Best Local Sim
Matches 158;
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                                                                                 ENACILATNSELVGTLIOSCKDEP
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                                                                                                                   ETHETGTTNTATTTVVAN--LGGHPQPTQVQFV-----CDRQETAASLVTSAVG----Q
                                                                                                                                                     SI-----LKQITLPGNKILSLQASPTQKNRIKENVTSCFRDEDDINDVTSMAGVNLNE
                                                                                                                                                                                        PVS-----ILASP-----TTEQPTATVTIADSGQGDVQPGTVTLVCSNPPC
                                                                                                                                                                                                          PTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPA
                                                                                                                                                                                                                                                              VSAAQTTLTAAGGLTTPTITMQPV---
                                                                                                                                                                                                                                                                                       LSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKL-AQPGPVLSQPA-GI
                                                                                                                                                                                                                                                                                                                               TTGVTTLGTVTGTVST--SLAGAGAHSTSASLATPITTLGTIATLSSQ----VINPTAIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTILKLYTSADGKPTTIITTTQASGAGTKPTILGI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMLIKLACSGSQSP-----EMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KTITLVKSPISVPGGSALISNLGKVMSVVQTKPVQTSAVTGQASTGPVTQIIHTKGPLPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTVTTLK-PSSL-GASSTPSNEPNL-----KAENSAAVQINLSPTMLENVKKCKNFL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VMVSNPATRMLKTAAAQVGTSVSSAANTSTRPIITVHKSGTV-TVAQQAQVVTTVVGGVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---NSSSQLIKKVAV---TPVKKLAQIGTTVVTTVPKPSSVQSVAVPTSVVTVTVPGKPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 5.4%;
Similarity 23.1%;
58; Conservative 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPGTTTIIKTIPMSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAPAKIIT
                                                  -GNVVRVCSNPP
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; Pred. No. 0.00016;
B4; Mismatches 254;
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                                                    1079
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Best Local :
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STRAIN-BRISTOL N2;
Geisel C., Harmon G.;
"The sequence of C. elegans
"The sequence of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen J.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Smith A., Sonnhammer E., Staden R., Sulston J.,
Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A., Smith A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watson A., Weinstock L., Wliming Spicer C., The C. "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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                          497
                                                                                                                                                                                                                                                                                                         332
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                                                                                                                   437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SGPLMLVS-PQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVK
  GQKTMPVNTIIPTSQFPPASILKQITLPGNKILSLQAS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TVTVTTVTTNPSTVTAPSTV--VTVPTTVMTSRSTVITTPTTGGSSPSTAGTSLAST 440
                                                                                                                                                                                                                                                                                                                                                  SSTATAGTSPQASTVTTVTDISTVSGSTVTSQTAESSLSTESPTSAGSSI-STVSTVSSQ
                                                                                                                                                                                                                                                                                                                                                                               KLAQIGTTVV----TTVPKPSSVQSVAVPTSVVT------VTPGKPLNTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVTAPSTVVTVPSTVVTKPNTV--VTSSPTVATTPTTV--VTTPST-----VVTVPS
                                                                                                               PVQIKLAQPGPVLSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKC
                                                                                                                                                                                                        NTVTTVSLQPEKPVVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGT
                                                                                                                                                                                                                                                      PSTYIPVSSASSIYSTLSGSTGSTA-----SPGTTESSGSSTSGPSTISGSS-----A
                                                                                                                                                                                                                                                                                                                                                                                                                                           PATQOSTKPTIGTSMSSGPTTVAPGASTESTVLQSSTPSGTTV-----TLPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEMGQNVKKLVEQLLDA--KIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tted (OCT-1998) to the AF077538; AAC64622.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity
153; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368:32-38(1994).
                                                                                                                                                             -STVTEASTISGSTESSTIPGSTESTVSEASTVSGSSVSTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                        -GSTESTSAGASTVSGS----
                                                                                                                                                                                                                                                                                                 ------LAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122924 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPSQSTSLSMSSLSTYTPSS-----STAGATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             %; Score 230.5;
%; Pred. No. 9.5;
111; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cosmid H02F09.";
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CB59B70C05959E25 CRC64;
                                                                   -----TG-----STVSDSSTIS-DST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .5e-05;
les 268;
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-PTQKNRIKENVTSCFRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215;
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                                                                                                                                                                                                                                                                                                    376
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RESULT 14
076894
                                   RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Golle R.F.,
RA Bannatides P.G., Scherer S.E., Holt R.A., Evans C.A., Galle R.F.,
RA Bannatides P.G., Vortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Buttin G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barladon R.C., Rogers Y.H.C., Blaze R.G., Champe M., Pfelffer B.D.,
RA Barlil J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Bessley E.M.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gepablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Ferraz C., Ferriera S., Fleischmann W.,
RA Colster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Malush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kilmenl B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,
RA McIsulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nount S.M., Moy M., Murphy B., Murphy B., Murphy L., Mury D.M., Nelson D.L.,
RA Ra Harris R.D., Spradling A.C., Stapleton M., Strong R., Snn E.,
RA Svirskas R., Trector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Steng Y.-Yh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhang W., Zhao Q., Zhao Q., Zheng L.,
Ra Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
Ra Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., S
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EG:56G7.1 protein.
EG:56G7.1 OR CG14796.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQL------PPGTVLIKSNSG
                         TNSELVGTLIQSCKDEPFLFIGALQKRILDI-----GKKHDITELNSDAVNLISQATQER
                                                  PAVPSTTTEREPQKTSSSPSPTKATSSTTTQPIETTTGDLEYDSSGSSDYVNDAN-----
                                                                        QASPTQKNRIKENVTSCFRDEDDINDVTSMAGVN------LNEENACILA
                                                                                                 STOKRSIPPKTLYTHNTTKEPEDSEYYDSETSEQYTDEDNEVLDKTQPRAMSSTTVAAVL
                                                                                                                                                  HIISTTPPSREHAPTQRPSSQPSSSQRSRGVTIAQMARHNLATSKPFIAHSLRLSIQQLA 1248
                                                                                                                                                                                                    THTRTHTALTGSRNTLGGQEVPDYMDDAPSSAEAESGQATTAKAPTMSTLAAAHLLQKLF
                                                                                                                                                                                                                            CWDHICKPVIGT-------PVQIKLAQPGPVLSQPAGIPTGSSSKQLFSLF
                                                                                                                                                                                                                                                                            VTSVANTVTTVSLQPEKP------VVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSF
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172; Conserv
-DISSGVVNSLEARKNFLLSLLKQRLTQIERTEAKKPATSTSTTTDAPKTSSSSTSP-
                                                                                                                         QKTMPVNTII-----PTSQFPPASILKQITLPGNKILS-----L
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18.9%;
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21; Mismatches
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Prediction of the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain we code for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          code for large proteins in vitro. DNA Res. 4:141-150(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97349984; PubMed-9205841;
Nagase T., Ishikawa K., Nakajima D., Ohira
Tanaka A., Kotani H., Nomura N., Ohara O.;
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TSKPLVTSVANTVTTVSLQPEKPVVSGTAVTL---
                                                                                                               VALRQLLPNSQSFIQQCVQQTSSDMV-----IATCTTTVTTSPVVTTTVSSSQSEKSII-
                                                                                                                                                                     LIKL-ACSGSQSPEMGQNVKKLVEOLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSV
                                                                                                                                                                                                             TEEGIAGVATSTG---VVTSGGLPIPPVSESPVLSSVVSSITIPA---VVSISTTSPSLQV
                                                                                                                                                                                                                                                                                                                                                                                  PVSAPPKVS-SGPRLP------APQIVAVKAP-----NTTTIQFPANLQ
                                      NQPHTHCPEVDSDTQPKAPGIDDIKTLE-----EKLRSLFSEHSSSGAQHASVSLE
                                                                                                                                             AFSLSAPSSSSSPGAGVS----SYISQPGGLHPLVIP----SV
                                                                                                                                                                                               SVST-----TTSFPSTASQLSIQLSSSTS---TPTLAETVVVSAHSLDKTSHSSTTGL
                                                                                                                                                                                                                                                                            PNSSSQLIKK-----VAVTPVKKLAQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLN 151
                                                                                                                                                                                                                                                                                                                               LPPGTVLIKSNSGPLMLVS----PQQTVTRAETTSNITSRPAVPANPQTVKICT-----V
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NCE 1246 AA; 129137 MW;
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Search completed: February 16, 2003, 21:58:41 Job time: 81.8407 secs

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ALIGNMENTS

RESULT 1
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AAW31494 standard; Protein; 801 AA.

28-APR-1998 (first entry)

, , TATA-binding protein associated binding factor 105; human; activator; hTAFII105; transcription factor; TFIID; transcriptional activation; antibodies; diagnosis; therapy; biopharmaceutical industry. DNA encoding human tata-binding protein associated factor - producing recombinant protein WPI; 1998-109818/10. N-PSDB; AAV02872. Dikstein R, (REGC) UNIV CALIFORNIA 02-OCT-1996; 02-OCT-1996; 20-JAN-1998 US5710025-A Homo sapiens. Human hTAFII105 protein. Tjian 96US-0725012 96US-0725012

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  Drmanac
                                                                                                          31-MAR-2000;
23-AUG-2000;
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medical imaging; diagnostic; genetic disorder
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Pred. No. 7.8
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Sequence

801 AA;

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CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or cc quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in acidernosic format directly from WIPO at the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; SEQ ID No 39827; 103pp; English
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                                                 ftp.wipo.int/pub/published_pct_sequences.
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VQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRK 240
                                                                                                                                                                      TVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAA 180
                                                   LYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPV
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                                                                                                        VQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRK
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AAY57279
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 Transcription
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factor subunit TAFII105 polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATA box-binding protein associated factor II 105; TAFIII105; catranscription factor; apoptosis; cytostatic; immunosuppressive; antiinflammatory; virucide; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptide encoding TATA box binding protein associated factor II useful for treating e.g. cancers and inducing apoptosis has a domin negative effect on the normal biological activity of the binding
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           VTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTT
                                LYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPV
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                                                                                                 VQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRK
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359;
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ilarity 100.0%;
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Pred. No. 8.5
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                                                                                                                                                                                                                                                                                                                                                                                                           TATA-binding protein associated protein factors corresponding nucleotide sequence and deriv. ant in screening, diagnostics and therapeutics
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                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
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30-JUN-1993;
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DB; AAQ70731.
         LDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ----TS
                                                                                                                                      MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
                                                                                                                                                            LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
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LDGKIEAEDFTSRLYRELNSSPQPYLVPFLKRSLPALRQLTPDSAAFIQQSQQQPPPPPTS
                                             RTVPGATTTSSAATE-
                                                        NE-PNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL
                                                                                                               AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS
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Wang E,
                                                                                                                                                                                                                                                                                 737
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                                                                                                                                                                                                                                                                                                                                                                                       Page 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein associated factor; hTAFII130; scre therapeutic; gene transcription regulation.
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93US-0087119
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                                                                                          -SQAQTTVQPSATLQRSPGVQPQLVLGGAAQTASLGTATAVQTGTPQ
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                                          -TMENVKKCKNFLSTLIKLASSGKQSTETAANVKELVQNL
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28-JAN-1993;
30-JUN-1993;
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The invention relates to purified proteins involved in transcription by RNA polymerase II, the RNA polymerase which transcribes messenger RNA. RNA polymerase II transcription proceeds in vitro upon addition of several nuclear fractions designated TFIIA, B, D, E, F, H, I and J to RNA polymerase II holoenzyme. Fraction of IIID has been shown to contains a TBP and other TAPS Purification of TPIID and separation of its components reveals 7 proteins ranging in size from 30-250 kD. serum raised against the TFIID fraction allowed cloning of the corresp.
                                                                                                                                                                                                                                                                                             This is the amino acid sequence of the human TATA-binding protein (TBP) associated factor (TAF) designated TAFILI30. The protein is a component of the TFILD fraction required for reconstituting RNA polymerase II in vitro transcription activity. The encoded protein has an estimated mol.
                                                                                                                                     Sequence
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N-PSDB; AAT42217.
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  62
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                                                      13
                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL
                         PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q-----ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL
                                                                                al Similarity
132; Conserv
                                                                                                                                                             from lambda-gtll expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   꼇ᠸ
                                                                                                                                                                                                                                                                                                                                                                                                    for cpds. that bind human TATA-binding protein associated by testing ability to bind to polypeptide fragments of the useful as (ant)agonists of transcription factors involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dynlacht
Wang E, W
                                                                                                                                                                                                                                                                                                                                                                Column 105-112;
                                                                                                                                     737 AA;
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94US-0188582.
93US-0013412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93US-0087119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9308-0013412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weinzierl ROJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                          27.78;
                                                    --PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM
                                                                                                                                                                                                                                                                                                                                                             86pp;
                                                                                52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associated
                                                                             Score 491; DB
Pred. No. 6.9e
52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruppert S,
                                                                                                                                                                libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  factor
                                                                                          DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hTAFII130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nuclear fraction;
                                                                                                        Length
                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z
                                                                                                        737;
                                                                               64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     holoenzyme;
                                                                             Gaps
 115
                                                   61
                           118
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RESULT 6
AAW25019
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                                                                                                                                                                                                                                                                                                                                       28-JAN-1994;
28-JAN-1993;
30-JUN-1993;
09-MAY-1996;
                            polypeptide, hTAFTI100 (mol. weight 100kD). TAF peptides derived from hTAFTI30 alpha, hTAFTI30 beta, hTAFTI40, hTAFTI70, hTAFTI70, hTAFTI100, hTAFTI70, hTAFTI250, hTAFTI30 beta, hTAFTI110, and nucleic acids encoding them, are used to modulate transcription, including transcription initiation. TAFS are nuclear proteins involved in RNA polymerase I, II and III transcription. The peptides act by binding to a different TAF, an activator, or TBP (TATA-binding protein) or competitively inhibiting association of a TAF domain with another compound, typical
                                                                                                                                                                                   Nucleic acids encoding human TATA-binding (TAF) peptide(s) - for production of record for modulating transcription of TAFs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA polymerase transcription; TATA-binding protein; TBP; initiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-OCT-1997
                                                                                                                                   AAW25018 represents TATA-binding protein associated factor (TAF)
                                                                                                                                                             Claim 1; Column 111-116; 86pp; English.
                                                                                                                                                                                                                                                                            Tjian
                                                                                                                                                                                                                                                                                          Coma1
                                                                                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                      28-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5637686-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW25019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW25019 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 Q-----ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
                       protein
                                                                                                                                                                                                                                        1997-319113/29.
DB; AAT79595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ----TS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTVPGATTTSSAATE----TMENVKKCKNFLSTLIKLASSGKQSTETAANVKELVQNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NE-PNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---TTIIKQV---
                                                                                                                                                                                                                                                                           Dynlact BD, Hoey Wang E, Weinzierl
                       like TBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                       94US-0188582.
93US-0013412.
93US-0087119.
96US-0646715.
                                                                                                                                                                                                                                                                                                                                                                                                      93US-0013412
                       or
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -SQAQTTVQPSATLQRSPGVQPQLVLGGAAQTASLGTATAVQTGTPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        associated
                       another TAF,
                                                                                                                                                                                                                                                                            ROJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ⋧
                                                                                                                                                                                                                                                                                       Ruppert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor,
                       an activator,
                                                                                                                                                                                                recombinant peptide(s), used
                                                                                                                                                                                                                                                                                       ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAF; nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hTAFII130
                                                                                                                                                                                                                                                                                       Tanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376
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                      compound,
                                  typically
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Sequence

737

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RESULT 7
AAUG2254
AUG2254
AUG2254
AC AAUG
AC AC AC AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antifungal;
MPT1; MTR2;
GCD7; SKI6;
                                                                                                                                                                                                                                                                                            Moore J,
Mendillo
                                                                                                          Screening candidate antifungal compound for interaction with essential protein, modulation of essential protein activity, binding to essential protein, by contacting protein with test compound and determining
    The
                                                                                                                                                                                                                                                                                                                                                                                                      29-JUN-2000;
10-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human homologue of MPT1 protein target for antifungal compound
                                              Claim 1; Figure 79;
                                                                                                                                                                                                                                                                                                                                                          (ANAD-) ANADYS PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUN-2001; 2001WO-US20592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200202055-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU82954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU82954 standard; Protein;
                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                       Davidov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yeast;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 PPKVSSG------PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
    invention
                                                                                                                                                                                                    2002-147962/19.
DB; ABK32842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NE-PNIKAENSAAVQINISPTMIENVKKCKNFIAMLIKIACSGSQSPEMGQNVKKIVEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q----ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ----TS
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                                                                                                                                                                                                                                                                                                              Buurman ET,
                                                                                                                                                                                                                                                                Thompson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fungal gene transcription; RPC34; POP3; TFA2; NAB2;
BOS1; POL30; RSA2; SQT1; MTW1; TFB1; SPC98; BFR2; R
NIP1; LCP5; NCE103; ECO1; ORC2; CNS1; YPD1; TIM10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    2000US-215164P
2000US-224457P
                                                                                                                                                                                                                                                                                            Moore D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
    describes a
                                              522pp;
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                                                                                                                                                                                                                                                                     CM;
                                                                                                                                                                                                                                                                                                                                                          INC
                                                                                                                                                                                                                                                                                       Desilva '
  method of screening
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                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 491; DB 18;
Pred. No. 6.9e-33;
2; Mismatches 96;
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                                                                                                                                                                                                                                                                                       Sanderson
                                                                                                                                                                                                                                                                                                              Harris S,
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  ρ
                                                                                                                                                                                                                                                                                                              Komarnitsky S;
                                                                                                                                                                                                                                                                                       Haq
candidate antifungal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BFR2; RNA1;
TIM10; SRB4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64;
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                                                                                                                                   essential
                                                                                                                                                                                                                                                                                       Long
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cc compound for interaction with essential proteins (EP) or for modulation cc of EP activity e.g fungal gene transcription. The proteins tested in the cc invention include RPC34, PDP3, TRAZ, NAB2, MPT1, MTR2, BOS1, PDL30, RSA2, CC SQT1, MTW1, TFB1, SPC98, BFR2, RNAL, GCD7, SK16, KIP1, LCP5, NCE103, CC ECO1, ORC2, CNS1, YPD1, TIM10 and SRB4 from S. cerevislae, C. albicans CC and human homologues. The method involves contacting a culture with one CC or more test compounds and determining the effects on the growth or CC unibility of the culture of cells which preferably comprises fungal cells or yeast cells. Preferably the identified compounds interact with, or CC modulate (preferably inhibit) activity of C. albicans EP. The inhibitor CC inhibiting fungal, particularly C. albicans EP. The inhibitor CC inhibiting fungal agents interact with essential fungal elements CC that can be used to treat fungal infection by preventing the growth and CC preferantially killing the fungi, but does not inhibit the biological CC activity of mammalian homologues. This amino acid sequence represents a cc method of the invention.

XX Sequence 1023 AA;
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밁 Š 밁 δÃ В δÃ 멍 δ 밁 δÃ 뮹 Ş Query Match Best Local S Matches 132 989 465 626 572 169 519 116 414 284 228 13 PPKVSSG------PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM 61 62 MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----Q-----ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL 464 SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSV RTVPGATTTSSAATE-----TMENVKKCKNFLSTLIKLASSGKQSTETAANVKELVQNL NE-PNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS Similarity -TTIIKQV--Conservative -SQAQTTVQPSATLQRSPGVQPQLVLGGAAQTASLGTATAVQTGTPQ 27.7%; Score 491; DB 23; 38.4%; Pred. No. 1.1e-32; 52; Mismatches Length 1023; 722 327 Indels 64; Gaps 168 571 685 283 625 518 14;

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RESULT 8
AAR56487
ID AARE
XX AARE
XX AARE
XX AARE
XX TATP
CT 23-b
CX TATP
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     28-JAN-1993;
30-JUN-1993;
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93US-0087119
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(REGC) UNIV CALIFORNIA.

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RESULT 9
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Matches 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The TATA-binding protein associated factor dTAFIII10 (including specific antibodies and fusion products) are used in drug screening, diagnostics and therapeutics. They are used in the development of specific biochemical assays for screening compounds that agonise or antagonise selected transcription factors involved in regulating
                                 Drosophila; TATA-binding protein; TBP associated RNA polymerase II; transcription; messenger RNA; holoenzyme; lambda-gtll; expression library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATA-binding protein associated protein factors corresponding nucleotide sequence and deriv. ant in screening, diagnostics and therapeutics
          Drosophila
                                                                                     Drosophila
                                                                                                            27-JAN-1997
                                                                                                                                                                  AAW06077
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DB; AAQ70724.
                                                                                                                                                                                                                               QIP-SLQVPGQANIVQIR--GPQHA 482
                                                                                                                                                                                                                                                                                                                                                                                                  TMLENVK-KCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELK 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLML------VSPQQTVTRAETTS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression associated with human pathology.
                                                                                                                                                                                                                                                        LNPLAGPYGAKAGVYTLHSYGPTAA
                                                                                                                                                                                                                                                                                                                                ASPQPCLIGFLKKSLPLLRQALYTKELVIEGIKPPPQHVLGLAGLSQQLPKIQAQIRPIG
                                                                                                                                                                                                                                                                                                                                                         TOOGNTKEKCRKFLANLIEL -- STREPKPVEKNYRTLIQELVNANVEPEEFCDRLERLLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                        -QCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVS----VQT
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          melanogaster.
                                                                                   TATA-binding protein associated factor dTAFII110 protein
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, Weinzierl ROJ
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24.9%;
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Pred. No. 2.3e<sup>o</sup>
58; Mismatches
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?.3e-09;
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                                               nuclear fraction;
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(TBP) associated factor (TAR) designated TARTIIIO. The protein is a component of the TFIID fraction required for reconstituting RNA polymerase II in vitro transcription activity. The encoded protein has an estimated mol. wt. of 110 kD by SDS-PAGE, a calculated mol. wt. based on sequence of the gene of 99.4 kD and an estimated pl of 10.1. The invention relates to purified proteins involved in transcription by RNA polymerase II, the RNA polymerase which transcribes messenger RNA. RNA polymerase II transcription proceeds in vitro upon addition of several nuclear fractions designated TFIIA, B, D, E, F, H, I and J to RNA polymerase II holoenzyme. Fraction TFIID has been shown to contains a TBP and other TAFs. Purification of TFIID and separation of its components reveals 7 proteins ranging in size from 30-250 kD. Serum raised against the TFIID fraction allowed cloning of the corresp.
Query Match
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28-JAN-1993;
30-JUN-1993;
                                                                                                                                                                                                                                                                                                         This is the amino acid sequence of the Drosophila TATA-binding protein (TBP) associated factor (TAF) designated TAFTII110. The protein is a
                                                                                                                                                                                                                                                                                                                                                                                                            Screen for cpds. that bind human TATA-binding protein associated factor - by testing ability to bind to polypeptide fragments of tifactor, useful as (ant)agonists of transcription factors involved
                                                    Sequence
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93US-0013412.
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                                             PSQTTTTGQTQVRMI - -TPNALGTPRPTIGHTTISKQPPN - - - IRLPTAPRLVNTGGIRT
                                                                                                      ASPQPCLIGFLKKSLPLLRQALYTKELVIEGIKPPPQHVLGLAGLSQQLPKIQAQIRPIG
                                                                                                                                     SSPQPHLVPFLKKSVVALRQL-----
                                                                                                                                                                 TOOGNTKEKCRKFLANLIEL -- STREPKPVEKNVRTLIQELVNANVEPEEFCDRLERLLN
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                                                                                                                                                                                                                                                                                                                                               PQSPSITLSTLNTGQTPA-----LLVKTDNGFQLLRVGTTTGPPTVTQTITNTSNNS 184
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                                                             ----QCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVS----VQT
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Pred. No. 2.3e-09;
8; Mismatches 141
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28-JAN-1993;
30-JUN-1993;
09-MAY-1996;
                                                                                                                                                                                                                               AAW25028 represents TATA-binding protein associated factor (TAF) polypeptide, dTAFII10 (mol. weight 110kD). TAF peptides derived from dTAFII30 alpha, dTAFII30 beta, dTAFII40, dTAFII60, dTAFII80, dTAFII10, dTAFII50, and dTAFII250, their human equivalents and nucleic acids encoding them, are used to modulate transcription, including transcription initiation. TAFS are nuclear proteins involved in RNA polymerase I, I and III transcription. The peptides act by binding to a different TAF, an activator, or TBP (TATA-binding protein) or competitively inhibiting association of a TAF domain with another compound, typically a protein like TBP or another TAF, an activator,
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                                                                                                                                                                                                                                                                                                                                                                      Example 1; Column 35-40;
                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding human TATA-binding (TAF) peptide(s) - for production of recon
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                                                                       NITSRPAVPANPQTVKICTVPNSSSQ------LIKKVAVTPVKKLAQIGTTVVTTVP 127
                                                                                                                      PQIVAVKAPNTTIQFPANLQLPPGTVLIKSNSGPLML------VSPQQTVTRAETTS 76
APQLPQITQIQTIPAQQSQQQQVNNVSSAGGTATAVSSTTA---
                        KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSP 187
                                             NTTSTTNHPTTTQ-IRLQTVPAAASMTNTTATSNIIVNSVASSGYANSSQPPHLTQLNAQ 243
                                                                                              PQSPSITLSTLNTGQTPA------LLVKTDNGFQLLRVGTTTGPPTVTQTITNTSNNS 184
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24.9%;
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                                                                                                                                            Score 216; DB
Pred. No. 2.3e
58; Mismatches
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TAFS
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                                                                                                                                                          DB 18;
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                                                                                                                                                                     Length 921;
                                                                                                                                              Indels
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TBP;
                                                                                                                                             90;
                                                                                                                                             Gaps
                                                                                                                                              14;
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Query Match Best Local Matches

Similarity

12.2%;

Conservative

58;

Score 216; DB Pred. No. 2.3e 58; Mismatches

DB 22;

Length 921; Indels

90;

Gaps

14;

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RESULT 11
ABB61528
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                  sequences (ABL01840-ABL16175) and the encoded proceed process. (ABB57737-ABB72072).

The sequence data for this patent did not form specification, but was obtained in electronic is at ftp.wipo.int/pub/published_pct_sequences.
                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-rell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511).
                                                                                                                                                                                        New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                       WPI; 2001-656860/75
N-PSDB; ABL05631.
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11-JUL-2000;
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                                                                                                                                                                   Disclosure;
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2000US-0614150
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RESULT 12
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                          Disclosure; SEQ ID NO 24957; 21pp + Sequence Listing; English
                                                                                                                              New isolated nucleic a
                                                                                                                                                                 WPI; 2001-656860/75.
N-PSDB; ABL10158.
                                                                                                                                                                                                                                               23-MAR-2000;
11-JUL-2000;
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pharmaceutical.
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2000US-0614150.
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RESULT 13
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The sequence data for this patent did not fo specification, but was obtained in electroni at ftp.wipo.int/pub/published_pct_sequences.
  New isolated nucleic a
genes from Drosophila
                                 N-PSDB; ABL13909
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11-JUL-2000;
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                                                                                                                                                                                                      Drosophila melanogaster
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2000US-0614150
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 detection reagent for for elucidating cell s
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Pred. No. 2
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                                                                        Homo
                                                                                                                                                                        AAR57141;
                                                                                                                                                                                         AAR57141 standard; Protein;
                                                                                                                                                                                                                                              1018
    Active-site
                       Active-site
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                                                                                           transcription
                                                                                                  Herpes simplex virus; herpes virus; VP16; immediate early host cell factor; virus infection therapy; cellular protein
                                                                                                                                   Host cell
                                                                                                                                                     19-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence data for this patent did not form part of the printed cification, but was obtained in electronic format directly from
                                                                       sapiens
                                                                                                                                                                                                                                            VSTQNPTT--TTSKTSTVTITTPNPSPST
                                                                                                                                                                                                                                                       VQTLNPLAGPVGAKAGVVTLHSVGPTAAT
                                                                                                                                                                                                                                                                                                                           TQEATTSTQKVSTVTITTKKATESSPLTTLSTEEPNTTPKP------
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                                                                                                                                                                                                                                                                                                     SQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGA--TAPR--TVS 326
                                                                                                                                                                                                                                                                                                                                            SPEMGQNVKKLVEQLLDAK--IEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPN 270
                                                                                                                                                                                                                                                                                                                                                                                   VTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQ
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nilarity 22.1%;
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                                         Location/Qualifiers 21..31
    /note= "peptide R60"
168..186
/note= "peptide R37"
333..340
                                                                                                                                                   entry)
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Pred. No. 4.7e-06;
2; Mismatches 165
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  New Host Cell Factor polypeptide(s) and nucleic acid - a to develop agents for diagnosis or treatment of disease associated with expression of a HCF-modulated gene e.g.
                                                                                                                                        (COLD-)
                                                                                                                                                                      04-DEC-1992;
12-APR-1993;
                    Disclosure; Page 39;
                                                                                        N-PSDB;
                                                                                                  WPI; 1994-234207/28
                                                                                                                     Herr W,
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93US-0046585
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1158..1183
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1286..1311
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/note= "THE TNT
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611..623
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1853..1863
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1314..1339
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426..449
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 03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             viral genes, such as the immediate early herpes simplex virus-1 genes. Epitopes of the encoded protein can be used in defining functional domains of HCF, identifying compounds that associate with HCF or designing compounds capable of modifying HCF transcription. Such agents can be used to treat viral infections.
                                                                                   05-FEB-2001;
                                                                                                             09-AUG-2001
                                                                                                                                       WO200157190-A2
                                                                                                                                                                                                        Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                               AAM79978 standard;
                                                                                                                                                                  Homo sapiens
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2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
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Pred. No. 1.8e-
57; Mismatches
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Best Local Similarity
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20-OCT-2000;
30-NOV-2000;
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Zhao QA,
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N-PSDB; AAK53111.
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OVVYTTLPAPPAQAPLRGTVMQAPAVRQVNPQNSVTVRVPQTTTYVVNNGLTLGSTGP
                                                                                                                                 CKNFLAMLIKLACSGSQS-----PEMG--QNVKKLVEQLLDAKIEAEEFTRKLYV
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                       -VVTTTVSSSQSEKSI--IVSGATAPRTVSVQTLNPLAGPVGAKAGV---VTLHSVGP 351
                                                    IQPAPPLQPSGVPTSGPSQTTI-HLLPTAPT----TVNVTHRPVTQVTTRLPVPRAPANH
                                                                                                        CGK-----ATGSDSSGVIDLTMDDEESGASQDPKKLNHTPVSTMSSSQPVSRPLQP
                                                                                                                                                            SGLYSPSTNRGPIQMKIPISAFSTSSAAEQNSNTTPRIENQTNKTIDASVSKKAADSTSQ
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, Wang D,
Yang Y,
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D, Wang J, Zh, Wejhrman T,
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Search completed: February 16, 2003, 21:55:06 Job time: 34.5208 secs

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Gaps	801; 0;	Length Indels	ore 1773; DB 1; ed. No. 4.3e-155; Mismatches 0;
			CLASSIFICATION: . AATORNEY/AGENT INFORMATION: . NAME: OSMAN, RICHARD A REGISTRATION NUMBER: 36,627 REFERENCE/DOCKET NUMBER: B97-005 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 343-4341 TELEPHONE: (415) 343-4342 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 801 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein US-08-725-012-2
			COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/725,012 FILING DATE:
	•,	Factor	ESULT 1 S-08-725-012-2 Sequence 2, Application US/08725012 Sequence 2, Application US/08725012 Sequence 2, Application US/08725012 Sequence 2, Application US/08725012 Sequence 3, Application Rivks APPLICANT: Djlan, Robert TITLE OF INVENTION: B-Cell Specific Transcription NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA COUNTRY: USA ZID: 94104
			ALIGNMENTS
2, Appli 2, Appli 3, Appli 5, Appli 5, Appli 1, Appli 1, Appli 2, Appli 3, Appli 4, Appli 40, Appli 40, Appli 40, Appli 40, Appli 40, Appli 40, Appli 40, Appli 40, Appli	sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	28 142.5 8.0 750 4 US-09-165-239A-4 29 142.5 8.0 2476 2 US-08-276-967-2 30 141 8.0 2972 4 US-09-579-181-2 31 141 8.0 2972 4 US-09-579-181-1 31 131.5 7.8 1837 3 US-08-928-361B-5 33 137.5 7.8 907 3 US-08-783-774-2 34 137.5 7.8 907 5 PCT-US95-0461LA-19 35 137.5 7.8 907 5 PCT-US95-0461LA-19 36 135.5 7.6 878 4 US-09-556-706B-2 37 133 7.5 805 4 US-09-103-429A-4 38 132.5 7.5 805 4 US-09-103-429A-3 39 129 7.3 1481 2 US-08-616-844-40 41 129 7.3 1481 2 US-08-616-844-40 42 129 7.3 1481 3 US-08-944-868A-40 43 129 7.3 1481 3 US-08-944-868A-40 44 127.5 7.2 821 4 US-09-556-877-195 45 127.5 7.2 821 4 US-09-620-412C-195

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
NUMBER OF SEQUENCES: 36
                                                                                                                                                        MOLECULE TYPE:
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                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 28-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                         NAME: Osman, Richard A REGISTRATION NUMBER: 36,627
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VTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTT 359
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                                                                               Similarity
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                                                         Conservative
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                                                                           27.7%; Score 491; DB 1; 38.4%; Pred. No. 7.9e-37;
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                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                             NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 737 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS
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910 277299
TELEFAX: 910 277299
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                                    TOPOLOGY:
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0: FILING DATE: 28-JAN-1994
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 09-MAY CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
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                                                                     LENGTH:
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Tanese, Naoko
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                                                                                                                                                                  (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                       09-MAY-1996
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Best Local Similarity
                                            TELEFAX: (415) 398-324
TELEX: 910 27729
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 amino acid
                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                          APPLICATION NUMBER: US/00
FILING DATE: 28-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 Q-----ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP---- 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
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                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                         NAME: Osman, Richard A REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
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                                                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPKVSSG-----PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2, 553441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RTVPGATTTSSAATE-----TMENVKKCKNFLSTLIKLASSGKQSTETAANVKELVQNL
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Tanese, Naoko
                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dynlact, Brian D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang, Edith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Timothy
                                                                                                398-3249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robert
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                                                                                                                                                                         A-57650-2/AJT/RAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEST, ALBRITTON & HERBERT
er, Suite 3400
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-188-582-2
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Best Local (
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                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                       PRIOR APPLICATION DATA:
                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 POSPSITLSTLNTGQTPA------LLVKTDNGFQLLRVGTTTGPPTVTQTITNTSNNS 184
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: FLEHR, HOHBACH,
STREET: 4 Embarcadero Cente
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77
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                                                                   CLASSIFICATION:
                                                                                           APPLICATION NUMBER: FILING DATE: 09-MA
                                                                                                                                                                                                                                                                                                                   COUNTRY:
               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TQQGNTKEKCRKFLANLIEL -- STREPKPVEKNVRTLIQELVNANVEPEEFCDRLERLLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTTSTTNHPTTTQ-IRLQTVPAAASMTNTTATSNIIVNSVASSGYANSSQPPHLTQLNAQ
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Tanese, Naoko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hoey, Timothy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang,
                                                                                           09-MAY-1996
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                  SD
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                    08/188,582
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                   TEST, ALBRITTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354
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                                                                                                                                                                    Version
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ATTORNEY/AGENT INFORMATION: NAME: Osman, Richard A

REGISTRATION NUMBER:

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                                                                                                                                                                                                                                                                                                                                                                        US-08-046-585-5
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08046585 Patent No. 5453362 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 9
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                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT
                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   TITLE OF INVENTION: A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN: TITLE OF INVENTION: HOST CELL FACTOR NUMBER OF SEQUENCES: 15
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REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           461
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                                                                                               COUNTRY: USA
ZIP: 94111-4187
                                                                                                                                                  ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
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APPLICATION DATA:
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Herr, Winship
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              PatentIn Release #1.0,
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Pred. No. 2.6e-11;
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               Version #1.25
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                                                                                                                                                                                            Sequence 5, Application US/08393703
Patent No. 5585239
GENERAL INFORMATION:
APPLICANT: Lamarco, Kelly
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Best Local Similarity 24.2
Matches 108; Conservative
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                                                                                                                   APPLICANT: Wilson, Angus
APPLICANT: Herr, Winship
TITLE OF INVENTION: A NOVEL EKARYOTIC TRANSCRIPTION
TITLE OF INVENTION: HOST CELL FACTOR
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LENGTH: 2035 amino acids
                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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ADDREST:
STREET:
STREET:
CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 VSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLVSPQQTV 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Osman, Richard REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 12-APR-1993
                                                                                                                                                                                                                                                                                                                                                 TA--ITVSAAQTTL----TAAGGLTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKIATGHGQQGVTQVVLKGAPGQPGTILRTVP-----MGGVRLVTPVTVSAVKPAV----
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                       FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT Embarcadero Center, Suite 3400 Francisco
                                                                                                                                                                                          Lamarco, Kelly
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Pred. No. 4.3e-07;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

IBM PC compatible

RY: USA 94111-4187

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PCT-US93-11721-5
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              Sequence 5, Application PC/TUS9311721
GENERAL INFORMATION:
APPLICANT: Hamarco, Kelly
APPLICANT: Wilson, Angus
APPLICANT: Herr, Winship
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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TOPOLOGY: 1in
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REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 24-FEB-CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                    TIIKTIPMSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAP-----AKIITAV-- 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRAETTSNITSRPAVPANPQT-----VKICTVPNSSSQ----LIKKVAVTPVKKL 115
                                                                                                                                                                           TA--ITVSAAQTTL----TAAGGLTT 946
                                                                                                                                                                                                                                                                               SDMVIATCTTTVTTSPVVTTTVSSSQS-----EKSIIVSGATAPRTVSVQTLNP 332
                                                                                                                                                                                                                                                                                                                 PKIATGHGQQGVTQVVLKGAPGQPGTILRTVP-----MGGVRLVTPVTVSAVKPAV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQVVTTVVGGVTKTITLVKSPISVPGGSALISNLGKVMSVVQTKPVQTSAVTGQASTGPV 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGSSPQMSGMAALAAAAAATQKIPPSSA---PTVLSVPAGTTIVKT-----MAVTPGTTT 588
                                                                                                                                                                                                                                            -TTLVVKGTTGVTTLGTVTGTVSTSLAGAGGHSTSASLATPITTLGTIA--TLSSQVINP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
 INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2035 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----VVTVTPGKPLNTVTT------LKPSSLGASST------PSNE 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.9%; Score 176; DB 1; 24.2%; Pred. No. 4.3e-07;
A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 148; Indels 134;
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; MOLECULE TYPE:
PCT-US93-11721-5
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Best Local :
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2035 amino acids
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                  141
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                                  333 LAGPVGAKAGVVTLHSVGPTAATGGTT
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STRANDEDNESS: si
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TELEX: 910 277299
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
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                                                                                                                                                                                                                                                                                           TQIIQTKGPLPAGTILKLVTSADGKPTTIITTTQASGAGTKPTILGISSYSPSTTKPGTT
                                                                                             SDMVIATCTTTVTTSPVVTTTVSSSQS------EKSIIVSGATAPRTVSVQTLNP 332
                                                                                                                                           PKIATGHGQQGVTQVVLKGAPGQPGTILRTVP-----MGGVRLVTPVTVSAVKPAV----
                                                                                                                                                                                                                    TIIKTIPMSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAP-----AKIITAV--
                                                                                                                                                                                                                                                     PNLKAENSAAVQINLSPTMLENVKKCKNFLAML-IKLACSGSQSPEMGQNVKKLVEQLLD 229
                                                                                                                                                                                                                                                                                                                                                                                                          AQIGTTVV-----TTVPKP-----
TA--ITVSAAQTTL----TAAGGLTT
                                                                                                                                                                              AKIEAEEFTRKL-YVELKSSP-QP----HLVPFLKKSVVALRQLLPNSQSFIQQCVQQTS 283
                                                                                                                                                                                                                                                                                                                                                                    AQVVTTVVGGVTKTITLVKSPISVPGGSALISNLGKVMSVVQTKPVQTSAVTGQASTGPV 706
                                                                      -TTLVVKGTTGVTTLGTVTGTVSTSLAGAGGHSTSASLATPITTLGTIA--TLSSQVINP
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Osman, Richard A
36,627
NUMBER: 36,627
FP-57503-1/RAO
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Pred. No. 4.3e-07;
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946
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RESULT 10
US-08-700-651-5
; Sequence 5, Application US/08700651B
; Patent No. 6015882
; GENERAL INFORMATION:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 760
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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NAME: Murphy Jr., Gerald M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: No. 5580727el DNAs, Polypeptides Encoded Thereby
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                                                                                                                                                                                                                                                                                                                                                                                       61 MLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGT 120
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CLASSIFICATION: 435
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                                                                                                                                           TTTVTTSPVV 301
                                                                                                                                                                                                   EFTRKLYVELKSSPQPHLVPFLKKSVVAL-RQLLPNSQSFIQ---QCVQQTSSDMVIATC
                                                                                                                                                                                                                                  SSLANQ-QLPPACGARQLSKLKRFLTTLQQF--GNDISPEIGERVRTLVLGLVNSTLTIE
                                                                                                                                                                                                                                                                NSAAVQINLSPTM-LENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAE
                                                                                                                                                                                                                                                                                               ---PTMPPPPTTQG-APRTSSFTPT---TLTNGTSHSPTALNGAPSPPNGFSNGPSSSSS
                                                                                                                                                                                                                                                                                                                            TVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSL-GASSTP---SNEPNLKAE 176
                                                                                                             TSPVDSSELL
                                                                                                                                                                        EFHSKLQEATNFPLRPFVIPFLKANLPLLQRELLHCARLAKQNPAQYLAQHEQLLLDAST 371
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             752 amino acids
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(703) 205-8050
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Miyoshi, Hiroyuki
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                                                                                                             381
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28.8%; Pred. No. 1.1e-06;
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US-08-928-361B-6
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Best Local S
Matches 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver.
SEQ ID NO 5
LENGTH: 1721
TYPE: PRT
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APPLICANT: GIV, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DN
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CTYPTOSPORIDATION.

FILE REPERENCE: 480.19-4 (HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT APPLICATION NUMBER: 08-14
EARLIER APPLICATION NUMBER: 08-14
EARLIER FILING DATE: 1997-08-13
NUMBER OF SEQ ID NOS: 15
NUMBER OF SEQ ID NOS: 15
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APPLICANT: LEECH, JAMES
                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                  NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES 6
                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                            627 TKVPGKPPIATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     459 THVREREKVKDVGNTISVRCRKGAGKLEFP------DRSLDFTIPPVAGHNSCSII 508
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ZIP: 94306-1840
                                                                              STATE:
                                                                                                                    STREET:
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                                                                            Palo Alto
                                                                                                                    385 Sherman Avenue, Suite
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                                                                                                                                                                                                                                                                        Petersen, Carolyn
                       FORM:
                                                                                                                                                                                                             PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS, THEIR FUNCTIONAL MUTANTS, VARIANTS, AN FOR TREATMENT AND DETECTION/DIAGNOSIS
                                                                                                                                                                                               SPECIES INFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                            641
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                                                                                                                                                               Sequence 14, Application US/07757022B Patent No. 6433142
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Best Local Similarity
                                                                                                                                                 GENERAL INFORMATION:
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APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
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APPLICATION NUMBER: US
                                                                                 APPLICANT: Gesner, Thomas G. APPLICANT: Clark, Stephen C. APPLICANT: Turner, Katherine APPLICANT: Hewick, Rodney M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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                                CORRESPONDENCE ADDRESS:
                                                 TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                             APPLICANT:
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OPERATING
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                    ADDRESSEE:
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                                                                                                                                                                                                                                                               TKVPGKPPIATTTTT 641
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                                                                                                                                                                                                                                                                                              HSV--GPTAATGGTT 359
                                                                                                                                                                                                                                                                                                                                                          TC---TTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTL 346
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3: Genetics Institute,
87 CambridgePark Drive
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SYSTEM: PC-DOS/MS-DOS
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                                                  Megakaryocyte Stimulating Factors 143
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Pred. No. 0.00012;
1; Mismatches 183;
                  Inc
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-07-757-022B-14
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Best Local (
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INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
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APPLICATION NUMBER:
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APPLICATION NUMBER: US
FILING DATE: 19910910
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MEDIUM TYPE: Floppy disk
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                                       315 IVSGATAPR 323
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STATE: Massachu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
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FILING DATE: 18-JAN-1991
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TNSKATTPK 821
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                                                                                 PF-KITTLKTTTLAPK--
                                                                                                                       PFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSI 314
                                                                                                                                                                                                                                                                                                                                                                               KLA-----QIGTTVVTTVPKPSSVQSVA--VPTSVVTVTPGKPLNTVTTLKPSSLG 162
                                                                                                                                                                 KDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATT-----TQVTSTTTQDTT
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1 Similarity 20.3%;
75; Conservative 5
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08-AUG-1989
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Pred. No. 0.00012;
3; Mismatches 159;
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US-07-757-022B-84
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Best Local Similarity
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REFERENCE/DOCKET NUMBER: GI
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FILING DATE: 19910910
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                              ASSTP--SNEPNL--KAENSAAVQINLSPT--MLEN----VKKCKNFLAMLIKLACSG 210
                                                                                                                                                   KSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVK 113
                                                                                                                                                                                   APTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAPKELAPTT--- 619
                                                                                                                                                                                                            APVSAPPKVSSGPRLPAPQIVAVKAPNT------TTIQFPANLQLPPGTVLI 53
EVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTA 797
                                                           KPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTS
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(617)876-5851
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SYSTEM: PC-DOS/MS-DOS
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GENERAL INFORMATION:
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                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                             MOLECULE TYPE:
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                                                                                        TOPOLOGY:
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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               Score 144;
Pred. No. (
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
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REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
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                                                                                  APPLICATION NUMBER: US 0 FILING DATE: 08-AUG-1989 ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM:
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FILING DATE: 29-DEC-1989
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                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
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FILING DATE: 19910910
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                                              NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
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SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 20.3%;
Matches 75; Conservative 5
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INFORMATION FOR SEQ
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                                                                                                  PFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSI 314
                                                                                                                                  KDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATT-----TQVTSTTTQDTT 878
                                                                                                                                                                                                 EVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTA 824
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                                                                                                                                                                                                                                                                                           KLA-----QIGTTVVTTVPKPSSVQSVA--VPTSVVTVTPGKPLNTVTTLKPSSLG 162
                                                                   PF-KITTLKTTTLAPK---
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OR SEQ ID NO:
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Pred. No. 0.
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                                                                   -VTTTKKTITTTEIMNKPEETAKPKDRA 920
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Search completed: February 16, 2003, 22:02:57 Job time: 16.2248 secs

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/cgn2_6/ptodata/2/paa/US06_COMB.pep:*
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                    PCT-US01-08631-39827
1 US-09-763-909-2
PCT-US02-29964-410
PCT-US02-25829-25
7 US-60-243-468-1271
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  PCT-US94-01114-16
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                 Sequence 39827, A Sequence 2, Appli Sequence 410, Appl Sequence 25, Appl Sequence 1271, Ap
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Sequence 16, Appl
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-60-17627-149 -60-173-464-153 -10-219-999-625 -60-324-109-286 -60-3230-445-146 -10-210-08117-22 -10-221-625-22 -10-211-625-22 -09-488-725A-18 -09-791-537-189	09-270-767-459-6 09-270-767-450-6 09-270-767-450-7 09-629-4650-1 09-629-4650-1 09-629-639-19 09-134-000-67 09-134-000-18 60-191-681-14 60-167-217-18	-09-514-150-7944 -09-614-150-7944 -60-167-217-8067 -60-173-464-6463 -60-191-637-7965 -60-191-637-7965 -09-791-537-918	-US02-30474 -60-324-631 -US02-30474 -60-389-987 -60-412-418 -09-248-796 -60-096-409-131
1494, 62512, 28644, 1460, 1460, 22, App 22, Ap 22, Ap 22, Ap 1831, 1830, 1830,	45531 30469 15332 19, Ap 6703, 5061, 18689 14798		1660, 1665, 3271, 1773, 1773, 14351, 14351,

ALIGNMENTS

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                                                                                                                                               ; ORGANISM: Homo sapiens PCT-US01-08631-39827
                                                                                                                                                                               SOFTWARE: Custom
SEQ ID NO 39827
LENGTH: 801
TYPE: PRT
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                                                                       Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 110; Conservative 0
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                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/649,167 PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 60736
0;
                                                                     Score 562; DB 1;
Pred. No. 7.6e-53;
); Mismatches 0;
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CURRENT FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
SEQ ID NO 2
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local (
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                                                                         CURRENT APPLICATION NUMBER: PCT/US02/29964
CURRENT FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/323,739
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 809ACIP PCT
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                                              PRIOR APPLICATION NUMBER: PCT/US00/35017 PRIOR FILING DATE: 2000-12-22
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APPLICANT: Yamit-Hezi, Ayala
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                              APPLICATION NUMBER: US 09/491,404
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Zhao, Qing A.
Wang, Jian-Rui
Xue, Aidong J.
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Asundi, Vinod
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Pred. No. 8.3e-53;
; Mismatches 0;
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PCT-US02-25829-25
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; ORGANISM: Homo sapiens
PCT-US02-29964-410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Applica GENERAL INFORMATION:
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Best Local Similarity
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                                            APPLICANT:
                                                                         APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/515,126 PRIOR FILING DATE: 2000-02-28
                APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          545 VNTIIPTSQFPPASILKQITLPGNKILSLQASPTQKNRIKENVTSCFRDE 594
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APPLICATION NUMBER: US 09/496,914
FILING DATE: 2000-02-03
FILING DATE: 2000-02-03
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                                                                                      TANG, Y. TO
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                ΧŪ,
                             WALIA, Narinder K.
WARREN, Bridget A.
                                            TRAN, Uyen K.
WALIA, Narinder
                                                                        THORNTON, Michael
                                                                                                                SPRAGUE,
                                                                                                                                                  NGUYEN, Danniel
                                                                                                                                                            LEHR-MASON, Patricia M.
                                                                                                                                                                               <u>,</u>
                                                                                                                                                                                                                                                                                 KHAN, Farrah A.
                                                                                                                                                                                                                                                                                                                HONCHELL,
                                                                                                                                                                                                                                                                                                                            HAFALIA, April
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                                                                                                                                                                                                                                                                                                                                                                       GIETZEN,
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                                                                                                                                                                                                                                                                                                                                                                                        FORSYTHE, Ian J.
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DUGGAN, Brendan M.
ELLIOTT, Vicki S.
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BOROWSKY, Mark L.
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                  Yuming
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Monique G.
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                                                                                                     Tom
                                                                                                                   , Jayalaxmi
William W.
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Pred. No. 1.1e-49;
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CURRENT APPLICATION NUMBER: PCT/US02/25829
CURRENT FILING DATE: 2002-08-14

ITLE OF INVENTION: NUCLEIC ACID ASSOCIATED PROTEINS ILE REFERENCE: PF-1146 PCT

ZEBARJADIAN,

Yeganeh

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: LENGTH: 685
; TYPE: PRT
; ORGANISM: HUMAN
US-60-243-468-1271
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; Sequence 1271, Application US/60243468
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Best Local Similarity
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SEQ ID NO 1271
                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
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CURRENT FILING DATE: 2000-10-27
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TITLE OF INVENTION: ISOLA
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                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 4398735CD1
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61 VNTIIPTSQFPPASJLKQITLPGNKILSLQASPTQK 96
                                                                                                                                          Local Similarity
                                                                      1 AQPGPVLSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/316,751 FILING DATE: 2001-08-31 APPLICATION NUMBER: US 60/316,856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/328,185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100;
                                                    AQPGPVLSQPAGIPQAVQVKQL-----VVQQPSGGSEKQVTTISHSSTLTIQKCGQKTMP 527
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                                                                                                                                                                                                                                                                                                                                                                    AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                  ISOLATED HUMAN DRUG TARGET PROTEINS,
NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.8%;
90.9%;
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                                                                                                                      Score 302; DB 27;
Pred. No. 5.4e-24;
6; Mismatches 18
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Pred. No. 3.6
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PCT-US02-30474-1660
; Sequence 1660, Application
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
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                                                              RESULT 7
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Best Local
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                              483
                                                                                                                                            110 E 110
                                                                                                                                                                            423 PHNRIMLTTPQQIQLNPLQPVPVVKPAVLPGTKALSAVSAQAAAAQKNKLKEPGGGSFRD
                                                                                                                                                                                                                                      370 QP-PVLSLTQPTQVGVGKQGQPTPLVIQQPPKPGALIRPPQVTLTQTPMVALRQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                      60 PVNTIIPT-----SQFPPASILKQITLPGNKIL---SLQASPTQKNRIKENVTSCFRD 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                              483
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San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JAN-1994
                                                                                                                                                                                                                                                                                                                     16.5%;
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Pred. No. 1.3;
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PC/TUS0230474

APPLICANT:

Ren, Xue,

Feiyan Aidong J.

Jian-Rui Qing A.

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RESULT 8
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CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: US 60/324,631
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
                                    Sequence 1665, Application US/60324631
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhang, Jie
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SEQ ID NO 1660
LENGTH: 1051
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Best Local Similarity
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 810CIP PCT
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APPLICATION NUMBER: PCT/US01/03800
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FILING DATE: 2000-02-03
APPLICATION NUMBER: US 09/560,875
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                    Ren,
  Xue, Aidong
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Wehrman, Tom
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16.5%; Score 92.5; 27.3%; Pred. No. 2

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Length 1051; Indels

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; ORGANISM: HOMO US-60-324-631-1665
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CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
                                                 SOFTWARE: pt_FL_genes
SEQ ID NO 1665
LENGTH: 1051
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TITLE OF INVENTION: Novel Nucleic
TITLE OF INVENTION: Polypeptides
                                                                                                              NUMBER OF SEQ ID
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FILING DATE: 2000-02-03
APPLICATION NUMBER: US 09/560,875
FILING DATE: 2000-04-27
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FILING DATE: 2000-01-25
APPLICATION NUMBER: PCT/US01/02623
FILING DATE: 2001-01-25
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APPLICATION NUMBER: US 09/649,167
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Thad, Dunrui
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                                                           ; NAME/KEY: misc_feature ; LOCATION: (1)...(1083) ; LOCATION: (1)...(1083) ; OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set PCT-US02-30474-3271
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SEQ ID NO 3271
LENGTH: 1083
TYPE: PRT
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Query Match
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TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 810CIP PCT
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CURRENT FILING DATE: 2002-09-24
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FILING DATE: 2000-04-25
APPLICATION NUMBER: PCT/US00/35017
FILING DATE: 2000-12-22
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FILING DATE: 2000-01-25
APPLICATION NUMBER: PCT/US01/02623
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Asundi, Vinod
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Wang, Jian-Rui
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Xue, Aldong J
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  16.5%;
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Score 92.5; DB 1; Pred. No. 2.2;

    See File Wrapper or PALM

                  Length 1083;
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US-60-389-987-1773
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                                                                                                                                                                                                                                                                                                     US-60-412-418-1773
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                                                                                                                                                                                                                                                                                  Sequence 1773,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                               GENERAL INFORMATION:
              APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465P3
CURRENT APPLICATION NUMBER: US/60/412,418
CURRENT FILING DATE: 2002-09-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gibsón, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROJEILE REFERENCE: 660088.465P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/60/389,987
CURRENT FILING DATE: 2002-06-17
                                                                                                                                                                                                                  APPLICANT: Ghosh, Soumitra S. APPLICANT: Fahy, Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 3025
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TYPE: PRT
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NUMBER OF
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                                                                                                                                                                                                                                                                                                                                                                                                                         103 -VTSCFRD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                              353 GIPPNGSSP-SQLPPTS-CSQNPQPGD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 TMPVNTIIPTSQFPPASILKQITLPGNKILSLQASPTQKNRIKEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity les 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 PGPVLSQPAGIP----TGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQK 57
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SEQ ID NOS: 3025
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Fahy, Eoin D.
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28.9%;
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Pred. No. 7.9;
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DB 27; 41;

Indels Length 624;

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Gaps

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                                        ; ORGANISM: Candida albicans
US-60-096-409-14351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Candida albicans US-09-248-796-14351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-248-796-14351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14351, Application US/09
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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SEQ ID NO 1773
                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                         Sequence 14351, Application US/60096409A
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                                                                                                                                                                           APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.132
                                                                         LENGTH: 471
TYPE: PRT
                                                                                                                                    CURRENT APPLICATION NUMBER: US/60/096,409A CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/248,796
CURRENT FILING DATE: 1999-02-12
                                                                                                                                                                   FILE REFERENCE: GTC-016P
                                                                                                                      NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                            VQSQPTG---GFVPQTSFQQPQLVSQRTGPMQAQPT----GSLQAQPTGRPGEWGFVSM 427
                                                                                                                                                                                                                                                                                                                                                                                                        VLSQPAGIPTGSSSKQLESLEHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTII 65
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                                                                                                                                                                                                                                                                                                                  PTGGIPGLNAMQQHFLPNNQLPTSNLHSAMDNKLKENVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-614-150-18633
                                                                                                               CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILLING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18633, Application US/09614150 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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SEQ ID NO 6261
LENGTH: 1398
TYPE: PRT
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                                                                                                                                                                                                                                                                                              APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS
TITLE OF INVENTION: ARRAYS, FOR DETECTING
TITLE OF INVENTION: DROSOPHILA GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 2976-4031
CURRENT APPLICATION NUMBER: US/10/179,131
CURRENT FILING DATE: 2002-06-21
                                                                          PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/614,150 CURRENT FILING DATE: 2000-07-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: GREENE, JONATHAN R.
TITLE OF INVENTION: CANDIDA ALBICANS NUCLEIC ACIDS AND POLYPEPTIDES,
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                  APPLICATION NUMBER: 60/175,693
                                         FILING DATE: 1999-12-28
                                                       APPLICATION NUMBER: 60/173,383
  FILING DATE:
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PRIOR APPLICATION NUMBER: 60/191,637

PRIOR PRILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 18633

LENGTH: 3726

TYPE: PRT
ORGANISM: DROSOPHILA

US-09-614-150-18633

QUERY MATCH
BEST LOCAL SIMILARITY 18.2%: Pred. No. 3.4e+02;
MATCHES 30; CONSERVATIVE 24; Mismatches 50; Indels 61; Gaps 5;
MATCHES 30; CONSERVATIVE 24; Mismatches 50; Indels 61; Gaps 5;
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Sequence 87260, A	Sequence 87260, A	Sequence 87264, A	Sequence 87264, A	Sequence 87265, A	Sequence 87265, A	Sequence 1418, Ap	Sequence 48, Appl	Sequence 7803, Ap	Sequence 7803, Ap	Sequence 14, Appl	Sequence 3773, Ap	Sequence 555, App	Sequence 5061, Ap	Sequence 5061, Ap	Sequence 6703, Ap	Sequence 6703, Ap	Sequence 263, App	Sequence 263, App

ALIGNMENTS

RESULT 1

US-09-724-676-63928
US-09-724-676-63928
; Sequence 63928, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT APPLICATION NUMBER: US/09/724,676

NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 63928
LENGTH: 925

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                             SOFTWARE: PatentIn version 3.2
SEQ ID NO 63928
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                                                                           CURRENT APPLICATION NUMBER: US/O
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
ORGANISM: Homo sapiens
                TYPE: PRT
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                                                                                                                                                  SEQ ID NO 63931
LENGTH: 957
TYPE: PRT
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 63931
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                                                                                                                                                                                                                                                                                                                      APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen
                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
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US-09-724-676A-63922
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US-09-724-676-63922
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GENERAL INFORMATION
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 63922
LENGTH: 1021
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Best Local :
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CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 63922
LENGTH: 1021
TYPE: PRT
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CURRENT FILING DATE: 2000-11-28
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US-09-724-676-63925
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LENGTH: 1053
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILLING DATE: 2000-11-28
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TYPE: PRT
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Pred. No. 0.17
16; Mismatches
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US-09-724-676A-63929
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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
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SEQ ID NO 63929
LENGTH: 679
TYPE: PRT
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
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                               ENVISCFR 108
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RESULT 11

US-09-724-676-63920

Sequence 63920, Appl GENERAL INFORMATION:

Application

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RESULT 13
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                  Sequence 63923, Appli GENERAL INFORMATION: APPLICANT: Compugen
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Best Local
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
    TITLE OF INVENTION:
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TYPE: PRT
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1 Similarity 28.9%;
37; Conservation
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                                                 Application US/09724676
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LTD Variants of alternative splicing
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Pred. No. 0.63;
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Best Local Similarity
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 63923
LENGTH: 775
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CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILLING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
                                                                    APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen
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                                                                                                                                                                                                                                                                                                                                                                            647 QPPPPTSQATTALTAVVLSSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               758 EPGGGSFR 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 ENVISCER 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      647 QPPPPTSQATTALTAVVLSSS------VQRTAGKTAATVTSALQPPVLSLTQPTQVG 697
                                                                                                                                                                                                                                                                                                                             51 IQKCGQKTMPV-----NTIIPTSQFPPASILKQITLPGNKIL---SLQASPTQKNRIK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                           2 QPGPVLSQPAGIPTG---SSSKQLFSLFHVVQQPSGGNEKQVT-----TISHSSTLT 50
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                                                                                                                                                                                                                                                                                                       VGKQGQPTPLVIQQPPKPGALIQLNPLQPVPVVKPAVLPGTKALSAVSAQAAAAQKNKLK 757
                                                                                                                                                                                                                                                                     ENVISCER 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGKQGQPTPLVIQQPPKPGALIQLNPLQPVPVVKPAVLPGTKALSAVSAQAAAAQKNKLK 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
37; Conserv
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Pred. No. 0.69;
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Pred. No. 0.69;
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67
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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2: pir2:*
3: pir3:*
4: pir4:*
13.9
13.6
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T19690
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Compugen Ltd
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probable spermidin
1-phosphatidylinos
probable trancript
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drought-induced pr
hypothetical prote
DNA-directed DNA p
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trigger factor MG2
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T50075
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A;Reference number: Z25034
A;Accession: T50075
A;Status: preliminary; translated

from

GB/EMBL/DDBJ

A; Molecule type: DNA A; Residues: 1-410 <MCD>

A;Cross-references: EMBL:AL133357; PIDN:CAB62416.1; A;Experimental source: strain 972h(-); cosmid c1486

GSPDB:GN00066; SPDB:SPAC1486.06

C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 C:Accession: T50075

probable nicotinate phosphoribosyltransferase [imported] - fission yeast (Schizosacch C; Species: Schizosaccharomyces pombe

#text_change 21-Jul-2000
; Seeger, K.; Harris, D.

R;McDougall, R.C.; Rajandream, M.A.; Barrell, submitted to the EMBL Data Library, December 1

, в.с.; 1999

T124869 T1979 A46019 C86204
124869 119779 146019 186204
r24869 r19779
F96655 S71811
E96624
H84824
A90654 A85505
s73990
T42215

ALIGNMENTS

R;Mazo, A.M.; Huang, D.H.; Mozer, B.A.; Dawid, I.B. Proc. Natl. Acad. Sci. U.S.A. 87, 2112-2116, 1990 A;Title: The trithorax gene, a trans-acting regulator of the A;Reference number: A35085; MUID:90192757; PMID:2107543 A;Accession: A35085 RESULT 2 A35085 trithorax protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 20-Sep-1999 A;Status: nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-3759 <MAZ> submitted to GenBank, January 1990 A; Reference number: A38240 A; Accession: A38240 Βb γ 밁 δÃ A; Map position: 1 C; Superfamily: nicotinate phosphoribosyltransferase A; Molecule type: mRNA R; Mazo, A; Gene: SPDB:SPAC1486.06 Query Match Best Local S Matches 333 273 TANSADDLANVFHGVRQDSGCAEEYIEKVVKHYKSIGVDPSTKVIVHSDALNVDRCIELY 332 15 52 Local Similarity A.M. KYCEKCGIKSAFGIGTNL-TSDFQKVSNPSEVSKPMNIVIKLFSAEGTKAVKISDDI --- QKCGQKT-MPVNTIIPTSQFPPASILKQITLPGNKILSL-QASPTQKNRIKENV 103 29; Conservative 14.3%; 21; Score 80.5; Pred. No. 2. Mismatches DB 38; 2; Length Indels bithorax complex in 29; 388 Gaps 51 5 Dros

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A; Gene:
A; Map po
submitted to the Protein Su
A; Reference number: S63122
A; Accession: S63131
A; Molecule type: DNA
A; Residues: 1-636 <OBE>
                                                                                                        probable membrane protein YNL176c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N1661
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 19-Apr-2002
C;Accession: S63131
R;Obermaier, B.; Piravandi, E.; Rinke, M.; Domdey, H.
                                                                                                                                                                                                                                              RESULT 4
S63131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: FlyBase:trx
A;Cross-references: FlyBase:FBgn0003862
C;Superfamily: Drosophila trithorax protein
C;Keywords: DNA binding; transcription regulation; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-2361,'Y',2363-2397,'N',2399-2405,'N',2407-2411,'N',2413-3759
A;Cross-references: GB:M31617; NID:g158817; PID:g158818
C;Genetics:
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A; Cross-references: GB: AE001864;
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Best Local :
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                   175 RPSEVQATAPSRVLNQVTRVVTSPVDLDPGEEREAPLIALDSRGRVVEPVTLHPASVSVQ
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Deinococcus radiodurans
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                                                                                      Sequence Database,
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                                                                                      M.; Domdey, H.
base, April 1996
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С.; м
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probable nuclear pore protein - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-19
                                                                                      R;YOShloka, S.; Kato, K.; Nakai, K.; Okayama, H.;
DNA Res. 4, 363-369, 1997
A;Title: Identification of open reading frames in
A;Reference number: Z17323; MUID:98162722; PMID:99
A;Accession: T43197
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R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; submitted to the EMBL Data Library, February
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                   C;Species: Schizosaccharomyces pombe
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
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 A; Experimental
                     A; Cross-references:
                                   A; Molecule type: mRNA
A; Residues: 1-434 < YOS>
                                                                                                                                                                                        C; Accession: T43
                                                                                                                                                                                                                                              nucleoporin homolog -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Introns:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AL021839; PIDN:CAA17069.1; GSPDB:GN00067; SPDB:SPBC19G7.15
A;Experimental source: strain 972h-; cosmid c19G7
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                                                                      A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A; Accession: T39846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 14L
C; Keywords: transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-403 <LYN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                         110 WSTVNNPTKPVDETNATIPSSLLLSSGISPNATVSNAQYGPAQPPSVEEQV 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 ISVPTSSSVSSSSKVPS-----NRPSSSSSSDDTTSAYSSTYTFQSLQSTTS--SSIPP
                                                                                                                                                                                                                                                                                                                                                                                59
                                                                                                                                                                                                                                                                                                                                                                                                                   50
                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 AGIPTGSSSKQLF--SLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 LSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIP
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sces: EMBL:D89269; NID:g1749745; PIDN:BAA13930.1;
source: strain PR745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
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                                                                                                                                                                                                                                           fission yeast (Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.5%;
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                                                                        from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 76;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from GB/EMBL/DDBJ
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                                                                                                         frames in Schizosaccharomyces 22; PMID:9501991
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               PID: g1749746
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Query Match

Score

76; DB

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Length 434;

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A;Reference number: Z21513
A;Accession: T34369
A;Statur
                                                                                                                                                                                                                                                                                                       R;Favello, A. submitted to the EMBL Data Library, November 1995 submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: JC7576
R;Nishiyama, C.; Takahashi, K.; Nishiyama, M.; Okumura, K.; Ra, C
Blosci Biotechnol. Biochem. 64, 2601-2607, 2000
A;Title: Splice isoforms of transcription factor Elf-1 affecting
A;Reference number: JC7576; MUID: 21077473; PMID:11210123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transcription factor Elf-1, type 1 - rat
C;Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C;Accession: JC7576
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JC7576
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                                                                                                                                       A;Map position: 2
A;Introns: 36/1; 134/2; 180/1; 622/3; 691/2; 754/1; 1111/2; 1174/1;
                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-1777 <FAV>
A; Cross-references: EMBL
                                                                                                                                                                                                                                                                   A;Status:
                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein T19D12.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision.29-Oct-1999 #te
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C-Comment: This protein, as a key transcription
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A; Residues: 1-615 <NIS>
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                                                                                                                                                                                                      A; Experimental source:
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                                              AQPGPVLSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIRTIQASTQVP-----VVVSPGNQQLHTVTLQTVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVNTIIPTSQFPPASILKQITLPGNKIL---SLQASP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WSTVNNPTKPVDETNATIPSSLLLSSGISPNATVSNAQYGPAQPPSVEEQV
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                   AQPAQSSTSAATVTVSSS----
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30; Conservative
                                                                                               Similarity
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                                                                                                                                                                                                    EMBL:U41263; PIDN:AAC24428.1; GSPDB:GN00020; ce: strain Bristol N2; clone T19D12
                                                                                                                                                                                                                                                                                                                                                                         #sequence_revision.29-Oct-1999 #text_change
                                                                                             13.2%;
27.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 74;
Pred. No.
                                                                                             Score 74; DB Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 6.9;
4; Mismatches
                                                                             Mismatches
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                 -QSPTSSPAQQSSTPAGSSTVTVQQSSSFQSP 977
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17;
                                                                                                            DB 2;
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                                                                                                          Length 1777;
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A; Molecule type: DI
A: Residues: 1-1466
                                                                                                                                                                                       A36426
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A; Note: sequence extracted from NCBI backbone (NCBIP:88288) C; Genetics:
                                                                                             SPA2 protein yeast (Saccharomyces cerevisiae)
N;Alternate names: protein L1209; protein YLLO2
C;Species: Saccharomyces cerevisiae
C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1
C;Accession: A36426; S64769; S69386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A43361; MUID:92407982; A; Accession: A43361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Keywords: DNA binding; transcrip F; 210-290/Domain: ets DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GDB:131648
A;Map position: 1936-1936
C;Superfamily: ets DNA-binding domain homology
C;Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M82882
R;Thompson, C.B.; Wang, C.Y.; H
Mol. Cell. Biol. 12, 1043-1053,
                  A; Title: The SPA2 gene of Saccharomyces cerevisiae is in A; Reference number: A36426; MUID:91009481; PMID:2211820
                                                         R;Gehrung, S.; Snyder,
J. Cell Biol. 111, 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: cis-acting sequences required for A; Reference number: A42122; MUID:92186836; A; Accession: A42122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-619 <LEI>
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C;Date: 11-Feb-1993 #sequence_revision 11-Feb-1993 #text_change 07-May-1999
A; Reference number: A36426;
A; Accession: A36426
                                                                                                                                                                                                                       RESULT 10
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A; Residues: 204-282,'(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; not compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Leiden, J.M.; Wang, C.Y.; P
J. Virol. 66, 5890-5897, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: A43361; A42122
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                                                                                                                                                                                                                                                                                                                        -NRIKENV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204-282, 'G', 284-289
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                                                           1451-1464, 1990
                                                                                                                                                                                                                                                                                                                      103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 73; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 21;
l; Mismatches
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                                                                                                                                                           protein YLL021w
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                                                                                                                   12-Apr-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homology
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PMID:1545787
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                                                                                                                   #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 619
                                       important
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                                       for pheromone-induced
                                                                                                                     21-Jul-2000
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GEH>

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trigger factor MG238 [similarity] - Mycoplasma genitalium N;Contains: peptidylprolyl isomerase (EC 5.2.1.8), riboson C;Specites: Mycoplasma genitalium C;Specites: Mycoplasma Genitalium C;Specites: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_c
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                                  S
                                                                                                                                                                                                                                                                                                                     C.A.; Venter, J.C.
Science 270, 397-403, 1995
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: C64226
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A; Residues: 1-1466 <PUR>
A; Cross-references: EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, April 1996
A; Description: The sequence of 32 kb on the left arm of yeast chromosome XI:
mily and a new ABC transporter homologous to the human multidrug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the Protein Sequence Database, May 1996
A; Reference number: S64761
A; Accession: S64769
A; Molecule type: DNA
A; Residues: 1-1466 <GOF>
A; Cross-references: EMBL: Z73126; NID: g1360195; PID: e245456;
A; Note: experimental_source strain S288C
                                                                                                                                      F;170-214/Domain: BKBP-type peptidylprolyl isomerase homology <PPI>
                                                                                                                                                                                                   A; Genetic code:
                                                                                                                                                                                                                                       A; Experimental
                                                                                                                                                                                                                                                         A; Cross-references: GB:U39701;
                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-444 < TIGR>
                                                                                                                                                                                                                                                                                                              A; Status: preliminary; nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                      R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
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C; Keywords: coiled coil
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A; Cross-references:
A; Map position: 12L
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                                                                      Query Match
Best Local S
Matches 31
                                                                                                                                                               Superfamily: trigger factor; BKBP-type peptidylprolyl isomerase Keywords: cis-trans-isomerase
                                                                                                                                                                                                                      ;Genetics:
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                              PAGIPTGSSSKQLESLEHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQ 69
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PEQFQSFTSLKAFKSYFHKLME----NKKQETILQENN----QKIRQFLL-TNTKLP---
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                                                                                       12.9%; Score 72.5;
26.1%; Pred. No. 16;
                                                                                                                                                                                                                                       ; GB:L43967; NID:g1045915; PID:g1045927; TIGR:MG238 G-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 73; DB Pred. No. 58; 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NID:g1297003; PID:e238713;
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                                                                                                                                                                                                                                                                                                              sequence
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                                                                    39;
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, C.A.; Merrick,
314
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A; Introns: 171/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-545 < RUH>
                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: B53309
                                                                                                                                                                             Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Accession:
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Best Local :
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                              VQRVSTLPQASANKQAKEMESK ---
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23; Conserv
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-MSNSPTQKSKTEEN

574

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C; Accession: T39607
R; Lyne, M.; Wood, V.; Rajan
submitted to the EMBL Data
A; Reference number: Z21866
A; Accession: T39607
                                                                                                                                                                                                                                                                              A; Cross-references: EMBL:AL023554; P:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               fork head protein type transcription factor - fission yeast (Schizosaccharo C;Species: Schizosaccharomyces pombe C;Datc: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: prgZ
A;Genome: plasmid
C;Superfamily: dipeptide transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable pheromone binding protein prg2 - Enterococcus N,Alternate names: pheromone responsive gene Z protein
                                                                                                                                                                                                                                           A; Gene: SPDB:SPBC16G5.15c
                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Ruhfel, R.E.; Manias, D.A.; Dunny, G.M. J. Bacteriol. 175, 5253-5259, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB:L14285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Cloning and characterization of a A; Reference number: A53309; MUID:93352432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Enterococcus faecalis
Date: 13-Sep-1995 #sequence_revision 13-Sep-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 TVSPNVELFSAIKNAKEIASGKQAK------DTLAVKSIGEKTLEIELVEPTPYF----
64 IIPTSQFPPASILKQITLPGNKILSLQASPTQKNRIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 TGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPAS 74
                                                  SSPKKIDEOLHDLOGVDLVNGFEGISSWRESMVNKLRSSVSDSPTMNLANSNSKSSPV-A 538
                                                                                       SSSKQLFSLFHVVQQP-----
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                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               V.; Rajandream, M.
EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -TDLLSLTAYYPVQQKAIKE
                                                                                                                                              12.7%;
28.3%;
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Pred. No. 20;
15; Mismatches
                                                                                                                                                Score 71.5;
Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                          from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                PIDN:CAA19034.1;
                                                                                     -SGGNEKQV----TTISHSSTLTIQKCGQKTMPVNT 63
                                                                                                                                                                                                                                                                                                                                                                                                               . А.;
Мау
                                                                                                                              Mismatches
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1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIDN:AAA25554.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fission yeast (Schizosaccharomyces
                                                                                                                                                                 DB
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               102
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                                                                                                                                                                                                                                                                                                GSPDB:GN00067; SPDB:SPBC16G5.15c
                                                                                                                                                                 Length 642;
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                                                                                                                            Indels
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                                                                                                                              17;
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                                                                                                                                                                                                                                                                                                                       C; Superfamily: Synechocystis hypothetical protein s110350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ans
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein alr1278 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: A35913
R;Reith, W; Herrero-Sanchez, C.; Kobr, M.; Silacci, P.; Berte, C.; Barras, E.; Fey, S.; Genes Dev. 4, 1528-1540, 1990
Genes Dev. 4, 1528-1540, 1990
A;Title: MHC class II regulatory factor RFX has a novel DNA-binding domain and a functic A;Reference number: A35913; MUID:91071581; PMID:2253877
A;Accession: A35913
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                                                                                                                                                                                                                                                                                                                                                      A;Gene: alr1278
                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:BA000019; PIDN:BAB73235.1; PID:g17130625; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-979 <REI>
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C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ጓ; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;ACCESSION: AC1966
;ACCESSION: AC1966
;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Status: preliminary
                                                                                                                                                                                                                                       Query Match
Best Local 9
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 VQGTQQRLLVQTSVQAKPGHVSPLQL------TNIQVPQQALPTQRLVVQSAAPGSK 188
139 QSVQNNTSTNSPV----FPTAKILPDVSPP----TKLVASPLTKQEQKDEVT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 AVPAP---SQPTGAPTPSPAPQQYIVVTVSEGAMRASETVSEASPGSTASQTGVPTQVVQQ 137
                                                                                                 84 PVLSKPSTPETFTSE---FS--PLTPSSSAVNLGQTLAIGYSVQNNTSANSPVFPTATIP 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 PSGGNEKQVTTIS-----HSSTLTIQKCGQKTMPVNTIIPTSQFPPASILKQITLPGNK 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 12.7%;
Local Similarity 22.8%;
                                                                                                                                                   5 PVLSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHS------STLTIQ 52
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                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                         12.5%; Score 70.5; DB 2; Length 865; 29.5%; Pred. No. 55;
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Search completed: February 16, 2003, 22:00:55 Job time: 6.72163 secs

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Title:
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Maximum
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB DB
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562
1 AQPGPVLSQPAGIPTGSSSK.....
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Gapop 10.0 ,
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Listing first 45 s
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1 AQPGPVLSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLFIQKCGQKTMP 60

Query Match 100.0%; Best Local Similarity 100.0%; Matches 110; Conservative 0;

Score 562; DB 1; Pred. No. 3.5e-48;); Mismatches 0;

Length 801; Indels

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Gaps

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801 AA;

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	15-JUN	1-2002	(Rel. 4	1, Last	anr	annotation update)		
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¥ X X	Mammalia; NCBI_TaxID	ia; Eu	Eutheria; D=9606;	Primates	es;	Catarrhini;	i; Hominidae; Homo.	, čii +
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T2D3_HUMAN

1 000268; Q99721; Q9BX42; VJC...

1 15-JUL-1998 (Rel. 36, Created)

1 15-JUL-1998 (Rel. 36, Last sequence update)

1 15-JUN-2002 (Rel. 41, Last annotation update)

1 15-JUN-2002 (Rel. 41, Last annotation update)

1 15-JUN-2002 (Rel. 41, Last annotation 135 kDa sultation factor TFIID 135 kDa sultation factor TFIID 135 kDa sultation factor TRIID 135 kDa sultation factor TRIID 135 kDa sultation factor TAFIII35 (TAFIII35) (TAFIII35) (TAFIII35) (TAFIII35) OR TAF4 OR TAF4A OR TAF2C1 OR TAF2C OR TAFIII35 OR OS Homo sapiens (Human).

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       RESULT
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RA Doloukas P., Matthews L.H., Ashurst J., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Bailey J., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beusk D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Mine S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Millimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sins S.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sins S.,
RA Wiltehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wiltehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wiltehead S.L., Whittaker P., Willey D.L., Williams S.A.,
RA Milme G., Waray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
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                     MEDLINE-97098442; PubMed-8942982;

Tanese N., Saluja D., Vassallo M.F., Chen J.-L., Admon A.;

Tanese N., Saluja D., Vassallo M.F., Chen J.-L., Admon A.;

"Molecular cloning and analysis of two subunits of the human TFIID complex: hTAFII130 and hTAFII100.";

Proc. Natl. Acad. Sci. U.S.A. 93:13611-13616(1996).

-I- FUNCTION: MAKES PART OF TFIID IS A MULTIMERIC PROTEIN COMPLEX THAT PLAYS A CENTRAL ROLE IN MEDIATING PROMOTER RESPONSES TO VARIOUS ACTIVATORS AND REPRESSORS. POTENTIATES TRANSCRIPTIONAL ACTIVATION BY THE AF-2S OF THE RETINOIC ACID, VITAMIN D3 AND THYROID HORMONE.

-I- SUBUNIT: TFIID IS COMPOSED OF TATA BINDING PROTEIN (TBP) AND A NUMBER OF TBP-ASSOCIATED FACTORS (TAFS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97336072; PubMed-9192867;
Mengus G., May M., Carre L., Chambon P., David
"Human TAF(II)135 potentiates transcriptional
of the retinoic acid, vitamin D3, and thyroid
mammalian cells.";
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       SUBCELLULAR
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re 414:865-871(2001).
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       Nuclear
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15-JUN-2002
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CONFLICT
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CONFLICT
                                               Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                        Schizosaccharomyces
Eukaryota; Fungi; A:
MEDLINE=21848401; PubMed=11859360
                         SEQUENCE FROM
                                                                           Schizosaccharomycetales;
                                                                                                                    SPAC1486.06.
                                                                                                                                              Probable
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                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
33; Conserv
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185
233
293
1083
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(Rel. 41, Last annotation update)
cotinate phosphoribosyltransferase
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                         N.A.
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                                                                                        Ascomycota;
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185
264
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101
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                                                                           Schizosaccharomycetaceae
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Pred. No. 0
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MISSING (IN REF. 3).
P -> L (IN REF. 3).
W; A6453827572A0752 CRC64;
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                                                                                        Schizosaccharomycetes;
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OS DIOSO
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RA Brooks K., Barown D., Brown S., Chillingworth T., Churcher C. M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones M., Leather S., McDonald S., McLean J.,
RA James K., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Moodward J., Volckaert G., Aert R., Squares S., Stevens K.,
RA Faylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Weltjens I., Janger I., Berano S., Holzer E., Moestl D., Hilbert H.,
RA Gallbert F., Aves S., J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Gallbert F., Aves S., J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Gallbert F., Aves S., J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RI Mature 415:817-180(2002)
C. -- CATALYTIC ACTIVITY: Nicotinate D-ribose 1-diphosphate -
C. -- CATALYTIC ACTIVITY: Nicotinate D-ribose 1-diphosphate -
C. -- SIMILARITY: BELONGS TO THE NAPPTASE FAMILY.
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Best Loc
Matches
                                               Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                             P20659; Q27255; Q27327;
01-FEB-1991 (Rel. 17, Created)
16-OCT-2001 (Rel. 40, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
  SEQUENCE FROM N.A. MEDLINE=90192757;
                                                                                                                                                                           Trithorax protein.
                                                                                                                                                                                                                                                                              TRX_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                              273
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29; Conserv
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    PubMed=2107543
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No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 410;
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EMBL; M31617; AAA29025.1;
EMBL; Z50152; CAA90513.1;
EMBL; Z50152; CAA90513.1;
EMBL; Z31725; CAA83516.1;
EMBL; Z31725; CAA83515.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The trithorax in Drosophila,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95047388; PubMed=7958911; Kuzin B., Tillib S., Sedkov Y., Mizrokhi L., Maz Kuzin B., Tillib S., Sedkov Y., Mizrokhi L., Maz The Drosophila trithorax gene encodes a chromos directly regulates the region-specific homeotic Genes Dev. 8:2478-2490(1994).
                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -I- FUNCTION: FUNCTIONS IN SEGMENT DETERMINATION THROUGH INTERACTION WITH GENES OF BITHORAX (BX-C) AND ANTENNAPEDIA (ANT-X) COMPLEXES.
IT CAN BEHAVE AS AN ACTIVATOR OF BX-C.
-I- SUBCELLULAR LOCATION: Nuclear.
-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-I- MISCELLANEOUS: THIS PROTEIN HAS BEEN EXPERIMENTALLY SHOWN TO BINI
                                                                                                                                                                                                                 FlyBase; FBgn0003862; trx.
InterPro; IPR003889; FYrich_C.
InterPro; IPR003888; FYrich_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Conservation of structure and expression of the trithorax between Drosophila virilis and Drosophila melanogaster."; Mech. Dev. 53:113-122(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=Oregon-R; MEDLINE=96100387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sedkov Y., Tillib S., Mizrokhi L., Mazo A.;
"The bithorax complex is regulated by trithorax earlier during
Drosophila embryogenesis than is the Antennapedia complex, correlating
with a bithorax-like expression pattern of distinct early trithorax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND CHARACTERIZATION MEDLINE=95009521; PubMed=7924996;
                                                                                                                                                         InterPro;
                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                    TRANSFAC;
                                                                                                                                                                                                                                                                                  HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Development 120:1907-1917(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcripts.
                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                       InterPro;
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SIMILARITY: CONTAINS 5 PHD-TYPE ZINC FINGERS.
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IPR001965;
IPR001841;
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IPR001214;
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Znf_PHD.
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norax gene encodes a chromosomal
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L outstation -
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SMART; SM00542; FYRC; 1.
SMART; SM00541; FYRN; 1.
SMART; SM00249; PHD; 4.
SMART; SM00508; POSTSET; 1.
SMART; SM001084; RING; 3.
SMART; SM00317; SET; 1.

ZF_PHD_1; 4.

PF00628; PHD; 3. PF00856; SET; 1.

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Best Local S
Matches 30
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Q60775;
15-JUL-1998
15-JUL-1998
15-DEC-1998
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ZN_FING
ZN_FING
ZN_FING
ZN_FING
                                                                                                        "Cloning and expression of the murine Elf-1 cDNA.";

Gene 171:265-269(1996).

-1- FUNCTION: TRANSCRIPTION FACTOR THAT APPEARS TO BE REQUIRED FOR T

-1- CELL-RECEPTOR-MEDIATED TRANS ACTIVATION OF HIV-2 GENE

EXPRESSION. BINDS SPECIFICALLY TO TWO PURINE-RICH MOTIFS IN THE

HIV-2 ENHANCER. ELF-1 BINDS TO THE UNDERPHOSPHORYLATED FORM OF F

MAY INTERACT WITH OTHER TRANSCRIPTION FACTORS IN ORDER TO REGULA
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2953
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VARSPLIC
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                          TISSUE-Fibroblast;
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3012
                                                                                                                                                                                                                                                                 Davis
                                                                                                                                                                                                                                                                                    MEDLINE=96257231; PubMed=8666284;
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETS-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ω
                       SPECIFIC GENES (BY SIMILARITY).
SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: PREDOMINANTLY FOUND IN HEMATOPOIETIC
DETECTED IN OTHER CELL TYPES SUCH AS FIBROBLASTS.
             SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPMQQRQEPAPLSNECPVVSSPTPPKPVEQPIIHQMTSASVSKCY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVMEPQALEQQELANRVQHFSTSSSSSSSSSSSSSPTNVVNPMQQQAPSTTSSSTTRPTNRV
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                                                                                                                                                                                                                                                                 J.N.,
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ption regulation; zinc-finger; Metal-binding; DNA-binding;
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(Rel. 36,
(Rel. 37,
                                                                                                                                                                                                                                                                 Roussel M.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 36, Last sequence update)
(Rel. 37, Last annotation update)
transcription factor Elf-1 (E74-like factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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Rodentia;
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18.2%;
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POLY-GLU.
MISSING (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM).
P -> PWLTSPLKFLGLSTHGGLLLWLLLGVVVRLKQGG
(IN REF. 1).
R -> S (IN REF. 1).
G -> S (IN REF. 1).
G -> S (IN REF. 1).
          THE
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Pred. No. 17;
24; Mismatches
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PHD-TYPE 3.
PHD-TYPE 4 (ATYPICAL).
PHD-TYPE 5 (ATYPICAL).
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POLY-GLN.
GLN-RICH.
POLY-SER.
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                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
        ETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; Activator;
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> S (IN REF. 1).
D2756E50763D1CF5 CRC64;
          FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107
                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1).
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                                               CELLS
                                                                                                            REGULATE
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Best Local
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                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YNR6_YEAST P53882;
SGD; S0005120; YNL176C.
Hypothetical protein; Transmembrane.
DOMAIN 94 98 POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA_BIND SEQUENCE
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01-OCT-1996 (Rel. 34, C
01-OCT-1996 (Rel. 34, I
01-OCT-1996 (Rel. 34, I
Hypothetical 67.4 kDa p
YNL176C OR N1661.
                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not remove entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                      Obermaier B., Piravandi E., Rinke M., Domdey H.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS.
Pfam; PF00178; Ets; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nuclear protein; Transcription regulation; Activator; DNA-binding. DOMAIN 75 80 POLY-ASP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                           Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00413; ETS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00454;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSFAC; T05012; -. MGD; MGI:107180; Elf1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 QPGPVLS--QPAGIPTGSSSKQLFSLFHVVQ------
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een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
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Z71452; CAA96068.1;
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an email to license@lsb-sib.ch).
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612 AA;
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66221 MW;
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24.7%;
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Pred. No. 3.9;
22; Mismatches
                                                                                is not removed.
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cetaceae; Saccharomyces
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Best Local
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ELF1_HUMAN STANDARD; PH

P32519; Q9UDE1;

01-OCT-1993 (Rel. 27, Created)

01-OCT-1993 (Rel. 27, Last seque

16-OCT-2001 (Rel. 40, Last annot
                                                                                                                                     "Regulation of the retinoblastoma protein.";

to the retinoblastoma protein.";

Science 260:1330-1335(1993).

-1- FUNCTION: TRANSCRIPTION FACTOR THAT APPEARS TO BE REQUIRED FOR THE T-CELL-RECEPTOR-MEDIATED TRANS ACTIVATION OF HIV-2 GENE EXPRESSION. BINDS SPECIFICALLY TO TWO PURINE-RICH MOTIFS IN THE EXPRESSION. BINDS SPECIFICALLY TO THE UNDERPHOSPHORYLATED FORM OF RB.

HIV-2 ENHANCER, ELF-1 BINDS TO THE UNDERPHOSPHORYLATED FORM OF RB.
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TRANSMEM
                                                                                                                                                                                                                                                                                         MEDILINE-92186836; PubMed-1545787;
Thompson C.B., Wang C.Y., Ho I.C., Bohjanen P.R., Petryniak i June C.H., Miesfeldt S., Zhang L., Nabel G.J., Karpinski B.; "Cls-acting sequences required for inducible interleukin-2 en function bind a novel Ets-related protein, Elf-1.";
Mol. Cell. Biol. 12:1043-1053(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                  This
                                                                                                                                                                                                                              MEDLINE=93262492; PubMed=8493578;
Wang C.Y., Petryniak B., Thompson C.B.,
"Regulation of the Ets-related transcri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                        between
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for inducible trans activation in
J. Virol. 66:5890-5897(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Thompson
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                                                                                                         SIMILARITY: BELONGS TO THE
                                                                                                                    SUBCELLULAR LOCATION: Nuclear
                                                                                                                                 MAY INTERACT WITH OTHER SPECIFIC GENES.
                                                                   SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
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C.Y., Petryniak
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309
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stion factor Elf-1 (E74-like
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POLY-SER.
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Pred. No. 4
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Catarrhini;
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ption factor
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Elf-1 by
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RESULT 8
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                    This SWI
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CONFLICT
SEQUENCE
                                                       Purnelle B., Goffeau A.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: INVOLVED IN PHEROMONE-INDUCED MORPHOGENESIS AND
-I- SUBCELLULAR LOCATION: LOCALIZES A SHARP PATCH AT THE SHMOO TIP
(MATING PROJECTION) WHICH IS THE SITE OF POLARIZED CELL GROWTH.
-!- SIMILARITY: TO PROTEINS THAT FORM COILED-COIL STRUCTURES.
                                                                                                                                                                                "The SPA2 gene of Saccharomyces cerevisiae is pheromone-induced morphogenesis and efficient J. Cell Biol. 111:1451-1464(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSFAC; T01113; -. Genew; HGNC:3316; ELF1.
                                                                                                                                            STRAIN-S288c;
                                                                                                                                                                                                                     Gehrung S.,
                                                                                                                                                                                                                                 MEDLINE=91009481; PubMed=2211820
                                                                                                                                                                                                                                              STRAIN-S288c
                                                                                                                                                                                                                                                                               Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                              SPA2 protein.
SPA2 OR PEA1 OR YLL021W OR L1209.
                                                                                                                                                                                                                                                                                                                                                         01-NOV-1991
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nuclear protein; Transcription regulation; DOMAIN 75 80 POLY-ASP. DNA_BIND 208 290 ETS-DOMAIN. CONFLICT 283 283 Q -> G (IN REF SEQUENCE 619 AA; 67455 MW; ABOB41B2964/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
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PIR; A43361; /
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                   SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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39,
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28.9%;
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Pred. No. 8.9;
11; Mismatches
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                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequal to the control of the control o
                                               Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.NCBI_TaxID=2097;
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REPEAT
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EMBL; X97560; CAA66170.1;
EMBL; Z73126; CAA97469.1;
EMBL; Z73126; A36426.
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SEQUENCE FROM N.A.
STRAIN-ATCC 33530
                                                                                                      TIG OR MG238
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Pred. No. 24;
27; Mismatches
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LED COIL (POTENTIAL).
2EBB616152382C89 CRC64;
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TIGRRAMS; TIGRO0115; t1g; 1
PROSITE; PS00453; FKBP_PPIASE_1; FALSE_NEG.
PROSITE; PS00454; FKBP_PPIASE_2; FALSE_NEG.
PROSITE; PS00459; FKBP_PPIASE_3; 1.
Cell division; Chaperone; Isomerase; Rotamase; Complete
Cell division; Chaperone; PPIASE, FKBP-TYPE.
Cell division; Chaperone; PPIASE, FKBP-TYPE.
Tonath
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01-AUG-1991
16-OCT-2001
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                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
SEQUENCE FROM N.A. MEDLINE-91071581;
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STRAIN-ATCC 33530 / G-37;
MEDLINE-94075230; PubMed-8253680;
Peterson S.N., Hu P.-C., Bott K.F., Hut
"A survey of the Mycoplasma genitalium
sequencing.";
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                                                                                                                                                                                                                                                                                  P22670;
                                                                                                                                                                                                                                                                                                        RFX1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001179;
InterPro; IPR005215;
Pfam; PF00254; FKBP;
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                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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(Rel. 19, Last sequence up
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                                                                                                (Human).
Chordata;
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    PubMed-2253877
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26.1%;
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Pred. No. 6
                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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(RFX) (Enhancer
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C.A., Merricl
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                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             class II regulatory mutants concerns only complexes binding to the X boxes of class Mol. Cell. Biol. 12:4076-4083(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barras E., Mach B.;
"MHC class II regulatory factor RFX has a and a functionally independent dimerization
                                                                                                                                                                                                                                                                                                                                                    EMBL; X58964; CAA41730.1; -. EMBL; A20498; CAA01506.1; -. PIR; A35913; A35913.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHOWS THAT BLS IS NOT DUE TO RFX1.
MEDLINE-92375076; PubMed-1508204;
Sanchez-Herrero C., Reith W., Silacci P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BINDING TO RPL30 PROMOTER.
MEDLINE=94040774; PubMed=8
Safrany G., Perry R.P.;
                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                     DNA_BIND
                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                           Genew;
                                                                                                                                                                                                                                                                                                                           TRANSFAC; T00909; TRANSFAC; T01673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The DNA-binding defect observed in major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 132:279-283(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ribosomal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transactivator of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "RFX1 is identical to enhancer factor C transactivator of the hepatitis B virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Siegrist C.A., Durand B., Emery P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94019311; PubMed-8413236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reith W., Sanchez-Herrero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTITY BETWEEN RFX1 AND EF-C
                              32
                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: REGULATORY FACTÓR ESSENTIAL FOR MHC CLASS II GENE EXPRESSION. BINDS TO THE X BOXES OF MHC CLASS II GENES. ALSO BINDS TO AN INVERTED REPEAT (EMIL) REQUIRED FOR HEPATITIS B VIRUS GENES EXPRESSION AND TO THE MOST UPSTREAM ELEMENT (ALPHA) OF THE RPL30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE REX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: BINDS DNA AS AN HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                               600006;
VQGTQQRLLVQTSVQAKPGHVSPLQL-----TNIQVPQQALPTQRLVVQSAAPGSK
                           PSGGNEKQVTTIS-----HSSTLTIQKCGQKTMPVNTIIPTSQFPPASILKQITLPGNK 85
                                                                                      AQPGPVLSQPAGIPT----
                                                      AVPAP---SQPTGAPTPSPAPQQYIVVTVSEGAMRASETVSEASPGSTASQTGVPTQVVQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dev. 4:1528-1540(1990).
                                                                                                                                                                                                                                                                                                           HGNC: 9982;
                                                                                                                 Similarity 22.8
34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein-encoding
                                                                                                                                                                           979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. 13:6375-6384(1993).
                                                                                                                                                                                          438
920
744
                                                                                                                                                                                                                                    381
                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor RFX1 helps control the promoter of the mouse ein-encoding gene rpL30 by binding to its alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=8224874;
R.P.;
                                                                                                                                                                                                       411
528
936
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                                                                                                                                                                           104728
                                                                                                                                12.7%;
22.8%;
                                                                                                                %; Score 71.5; D
%; Pred. No. 21;
17; Mismatches
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                                                                                                                                                                           MW;
                                                                                                                                                                                        ASP/GLU-RICH (ACIDIC). NECESSARY FOR DIMERIZATION
                                                                                                                                                                                                                     EXPERIMENTALLY DEDUCED.
                                                                                                                                                                                                                                    GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kobr M., Silacci P.,
                                                                                                                                                                           556151F88C6AC9A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         David
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There are no restrictions
ong as its content is in
                                                                                                                                                                                                                                                  Activator;
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                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mach B.;
histocompatibility complex
one member of a family of
II promoters.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             novel DNA-binding
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                                                                                                                 43;
                                                                                                                                            1:
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                                                                                    -GSSSKQLFSLFHVVQQ
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188
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RESULT 11
PODX_HUMAN
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Matches 27
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CARBOHYD
CARBOHYD
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kershaw D.B., Beck S.G., Wharram B.L.,
Thomas P.E., Wiggins R.C.;
"Molecular cloning and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                         SEQUENCE
                                                                                                                VARIANT
                                                                                                                                       VARIANT
                                                                                                                                                 CARBOHYD
                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                              Glycoprotein;
                                                                                                                                                                                                                                                                                          MIM;
                                                                                                                                                                                                                                                                                                     Genew;
                                                                                                                                                                                                                                                                                                               EMBL; U97519;
                                                                                                                                                                                                                                                                                                                                      or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              podocalyxin.";
J. Biol. Chem. 272:15708-15714(1997).
-!- FUNCTION: Functions as an antiadhesin that maintains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Podocalyxin-like protein 1 precursor.
PODDXL OR PCLP1 OR PCLP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          000592;
15-JUN-2002
                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PODX_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kershaw D.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97332652; PubMed=9188463;
 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86
                      G
                                                                                                                                                                                                                                                                                                                                                                                                                          podocyte by charge repulsion.
SUBCELLULAR LOCATION: Type I membrane protein
TISSUE SPECIFICITY: Glomerular epithelium cell
PM: Sialoglycoprotein.
SIMILARITY: BELONGS TO THE PODOCALYXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     filtration pathway between
                     PVLSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQV-----TTISHSSTLTIQKCGQKT- 58
                                                                                                                                                                                                                                                                                          602632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGQVSLTVHGTQQVHSPPEQSPVQANSSS
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                                             l Similarity
27; Conser
                                                                                                                                                                                                                                                                                                HGNC: 9171;
                                                                                                                                                                                                                                                                                                                                    requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Orthologous
                                                                                         528
                                                                                                                196
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171; PODXL.
                                                                                                                                                                                                                                                                            Signal;
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                                                                                                                                      528
431
452
528
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146
330
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                                                                                         55595
                                                       12.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 relationship
                                                                                                                                                                                                                                                                            Transmembrane; Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              characterization of helationship to rabbit
                                                                                         MW;
-HLMKISSSSTVAIPGYTFTSPGMTTTLPSSVISQRTQ
                                             18;
                                            Score 71; DB Pred. No. 12; B; Mismatches
                                                                                                                                      N-LINKED
N-LINKED
T -> R.
                                                                                                                                                                       N-LINKED
                                                                Score 71;
                                                                                                                                                                                              N-LINKED
                                                                                                                                                                                                         SER/THR-RICH.
                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                        /FTId=VAR_012237.
23A32B291F008D56
                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                      PODOCALYXIN-LIKE PROTEIN 1.
                                                                                                                           /FTId=VAR_012236
                                                                                                                                                                                                                                                                  POTENTIAL.
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l and rat
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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59

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094916; 095693; Q9UN18;

16-CCT-2001 (Rel. 40, Created)

16-CCT-2001 (Rel. 40, Last sequence update)

16-CCT-2001 (Rel. 40, Last annotation update)

Nuclear factor of activated T cells 5 (T cell transcription factor NFAT5) (NF-AT5) (Tonicity-responsive enhancer-binding protein) (Tone-binding protein) (Tone-binding protein) or TONEBP) (ToneBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes The complete sequences of 100 new cDNA clones from brain which for large proteins in vitro.";
                                                                                                                                                                                           "Isolation and characterization expressed in human brain.";
                                                                                                                                                                                                                                                                                                                         Lopez-Rodriguez C., Aramburu J., Rakeman A.S., Cope. Gilbert D.J., Thomas S., Disteche C., Jenkins N.A., "NAATS: The NF-AT family of transcription factors expressed in the control of transcription factors expressed in the control of transcription."
                                                                                                                                                                                                                                                                                                                                       In I., Thomas
                                                                                                                                                                                                                                                                                                                                                                                                               Miyakawa H., Woo S.K., Dahl S.C., Handler J.S., Kwon H.M.; "Tonicity responsive enhancer binding protein, a rel-like stimulates transcription in response to hypertonicity."; Proc. Natl. Acad. Sci. U.S.A. 96:2538-2542(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                        Zuehlke C., Kiehl
                                                                                                                                                                                                                                    MEDLINE=20029268; PubMed=10565538;
                                                                                                                                                                                                                                                                     SEQUENCE OF
                                                                                                                                                                                                                                                                                                              direction."
                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99162641; PubMed-10051678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lopez-Rodriguez C., Aramburu J., "NFAT5, a constitutively nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99307389; PubMed=10377394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Brain;
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          1- SUBUNIT: DOES NOT BIND WITH FOS AND JUN 1
MIGHT BE CAPABLE OF FORMING STABLE DIMERS
1- SUBCELLULAR LOCATION: NUClear
1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A, B AN
PRODUCED BY ALTERNATIVE SPLICING.
1- TISSUE SPECIFICITY: HIGHEST LEVELS IN SKI
HEART AND PERIFHERAL BLOOD LEUKOCYTES. AI
LUNG, LIVER, KIDNEY, PANCREAS, SPLEEN, TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSUE-Brain
                                                                                                                                    OSMOLYTES
                                                                                                                                                                 FUNCTION: PLAYS
                                                                                                                                                  REGULATES HYPERTONICITY-INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fos and Jun.'.
. Natl. Acad.
                                                                                                                                                                                                                                                                                                Spring
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5:355-364(1998).
                                                                                                                                                                                10:1-6(1999).
                                                                                                                                                                                                                                                                                                Harb.
                                                                                                                                                                                                                                                                     675-1531 FROM
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 INTESTINE
                                                                                                                                                                                                                                                                                             Symp. Quant.
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                                                                                                                                                                                                                                                                                                                                                                                     (ISOFORM
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Primates;
                                                                                                                                             A ROLE IN THE INDUCIBLE EXPRESSION OF TONICITY-INDUCED CELLULAR ACCUMULATION
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cerization of
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 COLON
                                                                                                                                                                                                                                                                                                Biol.
                                                                                                     STABLE DIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rakeman
NFAT pro
                                                                                                                                                                                                       A., Grzeschik K.H., Schwinger E.; novel CAG repeat containing genes
                                                                                                                                                                                                                                                                                             64:517-526(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nan A.S., Rao
protein that
                                                                                                                      JUN
            SKELETAL MUSCLE, BRAIN,
ALSO EXPRESSED IN PLACENTA,
THYMUS, PROSTATE, TESTIS,
                                                                                                                                                                                                                                                                                                                           factors expands
                                                                        AND C
                                                                                                                   TRANSCRIPTION FACTORS.
                                                                                                     HTIW
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N.A., Rao A.
                                                                        (SHOWN HERE);
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does
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01-NOV-1995
15-JUN-2002
      STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White (
Kerlavage A.R., Bult C.J., Tomb J.-F
McKenney K., Sutton G., Fitzhugh W.,
                                                                                                                                                                                                                                                                                                                                                                                                    VARSPLIC
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CONFLICT
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TOC 51907;
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Parteria; Proteobacteria;
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InterPro; IPR000451;
Pfam; PF01833; TIG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF163836; AAD48441.1;
HSSP; Q00653; 1A3Q.
TRANSFAC; T04940; -.
Genew; HGNC:7774; NFAT5.
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                                                                                     NCBI_TaxID=727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 franscription
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                                                                                                                                                                                                                                                                             53 KCGQKTMPVNTIIPTSQFPPASILKQITLPGNKILSLQA
                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                       1 AQPGPVLSQPA----GIPTGSSSKQL-FSLFH--VVQQPSGGNEKQVTTISHS-STLTIQ 52
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Z97016; CI
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                                                                                                                                       (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 41, Last annotation updatage III subunit gamma/tau (EC 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulation;
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                                                                                                                                                                                                   STANDARD;
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                                                                                                           gamma subdivision;
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                                                                                                                                                                                                                                                                                                                                              18;
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POLY-GLN.
POLY-GLN.
MISSING (
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     Le O., Clayton R.A., Kirkness
.-F., Dougherty B.A., Merrick
w., Fields C.A., Gocayne J.D.
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(EC 2.7.7.
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THAT SHOWN FROM
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                                                                                                           Pasteurellaceae;
                                                                                                                                                                                                                                                                             91
                                                                                                                                                                                                                                                                                                                                              28;
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lyne J.D.,
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in no way
commercial
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MEDLINE-97311184; PubMed-9166592;

Anna C.H., Devereux T.R.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ς,
                                                                                                     Venter J.C.; "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                      CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE CORE DIMERIZATION TO FORM THE POLIII' COMPLEX. POLIII' ASSOCIATES WITH THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', PSI, AND WITH THE BETA CHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 ISHSSTLTIQKCGQKTMPVNTIIPTSQF--PPASILKQITLPGNKILSLQASPTQKNRIK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | | | : | : | : | | | | 448 LHIQELDEEKSHKKM----TALPVREWTEPKPKHIEKPTLPSNAAQAPQKNSTEENSSD 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PVLSQ-------PAGIPTGSSSKQLFSLFHVVQQPSGGNEKQ------VTT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMA4_MOUSE STANDARD; PRT; 551 AA.
P97471; 09CW56;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Mothers against decapentaplegic homolog 4 (SMAD 4) (Mothers against DPP homolog 4) (Deletion target in pancreatic carcinoma 4 homolog)
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Sprigss T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                            Science 269:496-512(1995).
-!- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA. THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONICLEASE ACTIVITY
                                                                                                                                                                                                                                                                                       CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam, PF00004; AAA; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
ATP-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 52 ATP (POTENTIAL).
688 AA; 77042 MW; DD3401A54C6C9A6F CRC64;
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InterPro; IPR000862; RFCdomain.
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Matches 31
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SMA4_MOUSE
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STRAIN-A/J; TISSUE-Lung;

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Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Redischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyono P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Winshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytokine Growth Factor Rev. 11:49-58(2000).
-!- FUNCTION: COMMON MEDIATOR OF SIGNAL TRANSDUCTION BY TGF-BETA
(TRANSFORMING GROWTH FACTOR) SUPERFAMILY; SMAD4 IS THE COMMON
SMAD (CO-SMAD) (BY SIMILARITY). REQUIRED FOR GASTRULATION. MAY ACT
AS A TUMOR SUPPRESSOR.
                                          'Sequence and chromosomal mapping of the mouse homolog (Madh4) of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: MAY FORM TRIMERS WITH RECEPTOR-REGULATED SMAD (R-SMAD).
INTERACTS WITH C-SKI, MSG1 AND AFT2 (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: IN THE CYTOPLASM IN THE ABSENCE OF LIGAND, MIGRATION TO THE NUCLEUS WHEN COMPLEXED WITH R-SMAD (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weinstein M., Yang X., Deng C.-X.;
"Functions of mammalian Smad genes as revealed by targeted gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
--- TISSUE SPECIFICITY: UBIQUITOUR.
--- SIMILARITY: BELONGS TO THE DWARFIN/SMAD FAMILY.
--- SIMILARITY: CONTAINS 1 DWA/MH1 DOMAIN.
--- SIMILARITY: CONTAINS 1 DWB/MH2 DOMAIN.
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DOMAIN 31 140 DWA.

DOMAIN 274 319 SAD.
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                                                                                                                                                                    MEDLINE-21085660; PubMed-11217851;
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InterPro; IPR003619; Dwarfin_A.
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                                                          DPC4/MADH4 gene.";
Genome 8:443-444(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 409:685-690(2001).
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Pfam; PF03166; MH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disruption in mice."
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TRANSFAC; T05067; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVIEW.
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Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Azawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojboori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Kadota K., Matsuda H., Kashurner M., Batalov S., Casavant T.,
Kadota K., Matsuda T., Gissi C., King B., Kochiwa H.,
Korimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Kushi M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Kusonseti M.J., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Nordone P., Rung B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Winnshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIVITY OF G PROTEIN ALPHA SUBDNITS THEREBY DRIVING THEM INTO THEIR INACTIVE GDP-BOUND FORM. BINDS SELECTIELY TO G(Z)-ALPHA AND IS INHIBITED BY THE PHOSPHORYLATION AND PALMITOYLATION OF THE G-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN (BY SIMILARITY).
SUBCELULAR LOCATION: Membrane-bound (Potential).
PROTEINTY ACYLARD. HEAVILY PALMITOYLATED IN THE CYSTEINE STRING MOTIF (BY SIMILARITY).
SIMILARITY: CONTAINS I RGS DOMAIN.
                                                                                                                                                                                                                                                                                                            222 SQPASILAGSHSEGLLQIASGPQPGQQNGFTAQPSTYHHNSTTT--WTGSRTAPYTPNL 279
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                          8 SQPAGIPTGSSSKQLFSLFHVVQ--QPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTII 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIGSK_MOUSE STANDARD; PRT; 239 AA.
0902B1; 0902B2; 09CUV8;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
Regulator of G-protein signaling 20 (RGS20) (Regulator of G-protein RGS20 OR RGS21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                   Score 69; DB 1; Length 551,
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND VARIANT ARG-32.
STRAIN-129/B6, and BALB/C;
Barker S.A., Wang J., ROSS E.M.;
A mouse ortholog of RGS21.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                   S -> A (IN REF. 2).
R -> P (IN REF. 2).
0835EF88D9C1C980 CRC64;
                                                                                                                                                                                                                      31;
                                                                                                                                                                                             Pred. No. 19;
6; Mismatches
                               POLY-ALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C57BL/6J; TISSUE-H1ppocampus;
MEDLINE-21085660; Pubmed-11217851;
                                                                                                          60417 MW;
                                                                                                                                                                   12.3%;
35.9%;
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                                                                                                                                                                                       Best Local Similaring
Matches 23; Conservative
320
450
257
292
551 AA;
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"Functional anno
                                                                                                                                                                                                                                                                                                                                                                                                                                          280 PHHQ 283
                                                                                                                                                                                                                                                                                                                                                                                    66 PTSQ 69
                                                   CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                   Query Match
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                         and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 ----STLTI-----QKCGQKTMPVNTIIPTSQFPPASILKQITLPGNKILSLQASPTQKN 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal transduction inhibitor; Membrane; Lipoprotein; Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AQPGPVLSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHS----
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229 RGS.
32 M -> R (IN BALB/C).
26986 MW; F383923163344D18 CRC64;
                                                                  between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as 1
                                                                                                                                                                                                                                               modified and this statement is not removed.
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ne : 6.11991 secs
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InterPro; IPR000342; Regl_Gprotein.
Pfam; PF00615; RGS; 1.
PRINTS; PR01301; RGSPROTEIN.
ProDom; PD001580; Reg_of_prG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF191554; AAF05757.1; -. EMBL; AF191552; AAF05756.1; -. EMBL; AK013773; BAB28987.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00315; RGS; 1
PROSITE; PS50132; RGS;
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113
32
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SEQUENCE
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Run on:

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051643 enterococcu

09h663 homo sapien

09d611 homo sapien

096rk0 homo sapien

096rk0 homo sapien

096rk0 homo sapien

095189 bos taurus

060139 schizosacch

09131 cercopithic

096q13 cercopithic
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094199 arabidopsis
095xyl arabidopsis
095xyl arabidopsis
087xd5 anabaena sp
043395 brassica na
095056 homo sapien
09914 homo sapien
                  Q9eqyl rattus norv
Q9eqy2 rattus norv
Q9eqy3 rattus norv
Q22579 caenorhabdi
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O9ddc0 pleurodeles
O9y497 homo sapien
P70098 cricetulus
                                                                                                                                                                                                                                                                                                                                                                                                099cx6 bovine herp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BALBYC; TISSUE-PO BRAIN;
Metsis M., Brunkhorst A., Neuman T.;
Exp. Cell Res. 0:0-0(2001).
Exp. Cell Res. 0:0-0(2001).
EMBL; AY038601; AAK94779.1; -.
EMBL; AY038601; AAK94779.1; -.
MGD; MGI:2152346; Taf4a.
NON_TER 1 1
SEQUENCE 662 AA; 71398 MW; 91A75F38CB0D0DA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 QP-PVISLTQPTQVGVG---KQAPPTPLVIQQPPKPGALIRPPQVTLTQTPMVALRQ--- 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 KTMPVNTIIPT-----SQFPPASILKQITLPGNKIL---SLQASPTQKNRIKENVTSC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Sukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 17.5%; Score 98.5; DB 11; Length 662; Best Local Similarity 30.6%; Pred. No. 0.03; Matches 38; Conservative 18; Mismatches 43; Indels 25.
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
TATA-binding protein associated factor TAFII135 (Fragment).
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Q99CX6
Q9XUS2
Q9DDC0
Q9Y4G7
P70098
QBTZG3
QBEQY1
QBEQY1
QBEQY3
QBEQY3
QBEGY3
QBEGY3
QBERKO
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11608
2296
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584
642
783
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1157
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QQ.
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O94233 kluyvercmyc
O94t83 schizosacch
O94t11 drosophila
O8408 drosophila
Q9446 drosophila
Q9446 drosophila
Q5193 enterococcu
Q52193 enterococcu
Q567 gallus gall
O42963 schizosacch
Q9867 schizosacch
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                                                                                                                             (without alignments)
2933.659 Million cell updates/sec
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                                                                                                            February 16, 2003, 21:31:01; Search time 7.72591 Seconds
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1 AOPGPVLSQPAGIPTGSSSK.....ASPTQKNRIKENVTSCFRDE 110
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               GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                         of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                         US-09-763-909-2_COPY_443_552
                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                              - protein search, using sw model
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Q9RYE1
Q52188
Q52193
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Q8XTG8
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Q8WQ86
Q8T0A8
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O94233
Q9UTK3
                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4: sp_human:*
5: sp_invertebrate:*
6: Sp_mammal:*
7: sn_mho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_vertebrate:*
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sp_organelle:*
sp_phage:*
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sp_bacteria:*
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length: 2000000000
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3726
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Match Length
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114.5
114.0
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Maximum DB seq
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Perfect score:
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                                                                              OM protein
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Result

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RESULT 2

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Trx proce....
TRX OR CG861...
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Bukaryota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Frandroidea; Drosophilidae; Drosophila.
                                                                                        |:|| ||| || | : | | : | | | : |:|:
142 GVPTASSSSSSSSTIPLINCKSTNAKSKAIQVEQTTSITHTQPKPIRAKIAPAACKKQV 201
                                                                                                                                                                                           202 MPIPTLKPSAKMESAKVKPQVKMEQLDVTLDHIQSAQPVEPKKKPGSKTALKKEIKILKM 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 TANSADDLANVFHGVRQDSGCAEEYIEKVVKHYKSIGVDPSTKVIVHSDALNVDRCIELY 332
                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-972H-;
McDougall R.C., Rajandream M.A., Barrell B.G., Seeger K., Harris D.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AL133357; CABG416.1; -
Glycosyltransferase; Transferase.
SEQUENCE 410 AA; 46694 MW; E4230ADD9ABA6077 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                           37; Gaps
                                                                12 GIPTGSSSKQLFSLFHVVQQPSGGNEK-----QVTTISHSSTLTIQ-----KCGQKT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 TGSSSKQLFSLFHVVQQPSG------51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 KYCEKCGIKSAFGIGTNL-TSDFQKVSNPSEVSKPMNIVIKLFSAEGTKAVKISDDI 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 --- QKCGQKT-MPVNTIIPTSQFPPASILKQITLPGNKILSL-QASPTQKNRIKENV 103
                                                                                                                                                  59 MPVNTIIPTSQFPPASILKQITL----SLQASPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.3%; Score 80.5; DB 3; Length 410; 24.8%; Pred. No. 1.6; ive 21; Mismatches 38; Indels 2
                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                           42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative nicotinate phosphoribosyltransferase. SPAC1486.06.
                                                                                                                                                                                                                                                                                                                                                                                    410 AA.
        Pred. No. 2.1;
                         24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                PRT;
    20.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -MAY-2000 (TrEMBLrel. 13,
L.MAR-2001 (TrEMBLrel. 16,
L-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 24.88 Matches 29; Conservative
                         27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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01-JUN-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                    95 QKNRIKENVT 104
                                                                                                                                                                                                                                                           : |::|::|
262 ENNKLKKELT 271
      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                              Q9UTK3
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                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 PGPASCQPGRQPLSPSATGDT-----RGVPQPSWGPEAQAASASSSPLEALEAC-LK 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 TMPVNTIIPTSQFPPASILKQITLPGNKILSLQASPTQKNRIKEN------- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353 GIPPNGSSP-SQLPPTS-CSQNPQPGD-----SRSQKPELQPHRSHSEEATREPVLPL 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 PGPVLSQPAGIP----TGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQK 57
                                                                                                                                                                                                                                                                                                                                                                                                                Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XX. The complete sequences of 100 new cDNA clones from brain which code for large Proteins in vitro."; DNA Res. 8:85-95(2001).

EMBL: AB058765; BAB47491.1; -.
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bourgarel D., Nguyen C.C., Bolotin-Fukuhara M.; "HAP4, the gluocse-repressed regulated subunit of the HAP transcriptional complex involved in the fermentation-respiration shift, has a functional homologue in the respiratory yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyceties;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kluyveromyces lactis.";
Mol. Microbiol. 31:1205-1215(1999).
EMBL; AF072675; AAD20134.1; -
SEQUENCE 643 AA; 70841 MW; AFC8FDEC2FFCE3B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              624 AA; 64576 MW; 82D1B996B9EFB53B CRC64;
                                                                                                                                                                     Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 84.5; DB Pred. No. 0.93;
                                                                                                       624 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.5%; Score 81.5;
                                                                                                                                                Created)
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                                                                                                       PRT;
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MEDLINE-99195821; PubMed-10096087;
                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21245130; PubMed-11347906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.0%;
28.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                          KIAA1862 protein (Fragment)
KIAA1862.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37; Conservative
                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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404 GLQSCVRD 411
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403 FRDD 406
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SEQUENCE

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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

Ballaw R.M., Basu A. M. H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Beeson K.Y., Basu D.A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ra Beeson K.Y., Bench P.V., Berman B.P., Bhandari D., Bulshakov S.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawleylista C.C., Ferraz C., Ferriera S., Fleischman W.,

RA Dodson K.J., Browlean R., Gary N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J. H., Cawley M., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Rotck J.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Alali M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,

Liu X., Mattei B., McIntosh T.C., McIeod M.P., McDhrerson D.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

Raison D. R., Nation K.A., Nusakern D.R., Pacieb J.M.,

Raison D.R., Nation K.J., Nusakern D.R., Pacieb J.M.,

Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Ray Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen E.,

RA Williams S.M., Woodage T., Worler E., Wang A.H., Wang X.,

Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Ray Rainer E., Spradling A.C., Standertow K., Mu Y., Strong R., Supski M.P.,

Ray Shriskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Walliams S.M., Woodage T., Worley W., Zhu W., Zhon Q., Zhu X., Smith H.O.,

Ray Sequence 287 J. Wassarman D.A., Weinsten B., Wang R., Shu K.,

Ray Sequence Sequence of Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3012 FVMEPQALEQQELANRVQHFSTSSSSSSNCSLPTNVVNPMQQQAPSTTSSSTTRPTNRV 3071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASILKQITLPGNKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              400095 MW; E3DDB8F062BD7796 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGPVLSQPAGIPTGSSSKQL--FSLFHVVQQPSGGNEKQV------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.1%; Score 79.5; D. 18.2%; Pred. No. 26; ive 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0003862; trx.
InterPro; IPR003889; FYrich_C.
InterPro; IPR003888; FYrich_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001214; SET.
InterPro; IPR001965; Znf_PHD.
InterPro; IPR001841; Znf_ring
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Pfam; PF00856; SET; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SET;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3726 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P20393; 1A6Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS50280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          499 PLKINVLGGSQGNSNKMRAIFNSASSIQHENG-----VTTIVPASSLA---ASNQTAAMN 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AQPGP-VLSQPAGIPTGSS----SKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKC 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PVLSQPAGIPTGSSSKQ--LFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chavez C., Dorsett V., Farfan D., Frise B., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., C., Lewis S.E., Rubin G.M., Celniker S., Submitted (DEC-2001) to He. EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                            'DdEB1 is a permanent centrosomal resident in Dictyostelium and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 506;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          56983 MW; F20BC182BAAA639C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65734 MW; E64C523CA2EA0623 CRC64;
                                                                                                                                                    Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum
NCBL_TaxID-44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21, Created)21, Last sequence update)21, Last annotation update)
                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 GOKTMPVNTIIPTSQFPPASILKQITLPGNKILSLQASPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 PSTPKPTNTPIPSTTGKPT----LTOPTFKPTPKSVSPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.0%; Score 78.5; 32.0%; Pred. No. 3.
206
                                                                                                                                                                                                                                                                                             required for proper spindle formation.";
Mol. Biol. Cell 12s:309a-309a(2001).
Mell; AJ26053; CAD19801.1; -.
InterPro; IPR001715; Calponin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 78.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                  Dictyostelium discoideum (Slime mold).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
                                       Created)
                                                                                             Microtubule-associated protein EB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.0%; 27.5%;
                                   (TrEMBLrel. 20, TrEMBLrel. 20, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00307; CH; 1.
Pfam; PF03271; EB1; 1.
PROSITE; PS50021; CH;
                                                                                                                                                                                                                                                        Rehberg M., Graef R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          506 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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Best Local Similarity
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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01-JUN-2002 (
LD15062p.
                                                     01-MAR-2002
01-JUN-2002
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                                   01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
                                                                                                                                                                                                                                       STRAIN-AX2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Q8TOA8;
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08W086
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RESULT 9
Q9RYE1
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                                                                                                                                                                                                                                                                                                                                                                                RA Addms N.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
B. Standon R.C., Rogers Y.-H.C., Blazej R.G., Chang O., Chen L.X.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Henderson S.N.,
RA Brandon R.C., Bater E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
Ballew R.M., Bau A., Asaendala J., Baytaktaroglu L., Beasley E.M.,
RA Ballew R.M., Bau A., Bakendala J., Baytaktaroglu L., Beasley E.M.,
RA Ballew R.M., Bau M., Rauch F., Bhandari D., Blolabakov S.,
RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,
RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Burtis R.C., Busam D.A., Dahlke C., Perraz C., Ferraz C., Ferra
                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.0%; Score 78.5; DB 5; Length 622; 27.5%; Pred. No. 4.2; .ive 19; Mismatches 40; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66817 MW; F6089D08F1D8D81A CRC64;
                 Last sequence update)
Last annotation update)
63 TIIP-TSQFPPASILKQITLPGNKILSLQ----ASPTQKNRI
                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                         STRAIN-BERKELEY;
MEDLINE-20196006; Pubmed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              797.1; -.
CG4068.
                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, CG4068 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28; Conservative
                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0029738;
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Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      Ephydroidea; Dro
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                                                                                                                   09W4F6
                                                                                                                                                                                                                     CG4068
                                                                                  RESULT 8
Q9W4F6
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5 PVLSQPAGIPTGSSSKQ--LFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVN 62

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"Cloning and characterization of a region of enterococcus faecalis plasmid pPD1 encoding pheromone inhibitor (ipd), pheromone sensitivity (traC), and pheromone shutdown (traB) genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 13.9%; Score 78; DB 16; Length 346;
Best Local Similarity 22.0%; Pred. No. 2.4;
Matches 24; Conservative 24; Mismatches 45; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 RPSEVQATAPSRVLNQVTRVVTSPVDLDPGEEREAPLIALDSRGRVVEPVTLHPASVSVQ 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 QPAGIPTGSSSKQLFSLFHVVQQP---SGGNEKQVTTIS-------HSSTLTIQ 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-RI;
MEDLINE-20036896; PubMed-10567266;
White O., Elsen J.A., Heldelberg J.F., Hickey E.K., Peterson J.D.,
White O., Elsen J.A., Heldelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                         Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales; Deinococcaceae; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakayama J., Yoshida K., Kobayashi H., Isogai A., Clewell D., Suzuki A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 KCGOKTMPVNTIIPTSQFPPASILKQITLPGNKILSLQASPTQKNRIKE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1E348C53CC4D2BA8 CRC64;
                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
63 TIIP-TSQFPPASILKQITLPGNKILSLQ----ASPTQKNRI 99
                         Enterococcus faecalis (Streptococcus faecalis).
                                                                                                                                                             346 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 protein; Complete proteome 346 AA; 37095 MW; 1E348C53
                                                                                                                                                      PRT;
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MEDLINE-96032393; PubMed-7559344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus
Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 286:1571-1577(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001864; AAF09603.1;
TIGR; DR0008; -
                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                      Deinococcus radiodurans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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SEQUENCE 34
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                                                                                                                                                                                  Q9RYE1;
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Q52188;
                                                                                                                                                                                                                                                                                              DR0008
                                                                                                                                                           Q9RYE1
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Q52188
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Similarity
                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                   STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FISSUE=TESTIS;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Matches 2
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    RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96032394; PubMed-7559345; Fulimoto K., Ike Y.; Fulimoto S., Tomita H., Wakamatsu E., Tanimoto K., Ike Y.; Physical Mapping of the Conjagative Bacteriocin Plasmid ppD1 of Enterococcus faecalls and Identification of the Determinant Related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and characterization of a region of enterococcus faecalis plasmid pPD1 encoding pheromone inhibitor (ipd), pheromone sensitivity (traC), and pheromone shutdown (traB) genes."; J. Bacteriol. 177:5567-5571(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 TASPNVELFSAIKNAKEIASG--KQV----KDTLAVKSIGEKTLEIELVEPTPYF---- 183
                                                                                                                                                 Gaps
                                                                                                                                                                         TGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPAS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 TGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPAS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-96032393; PubMed-7559344;
Nakayama J., Yoshida K., Kobayashi H., Isogai A., Clewell D.,
                                                                                                                    'Match 13.8%; Score 77.5; DB 2; Length 545; Local Similarity 29.5%; Pred. No. 4.6; les 26; Conservative 13; Mismatches 28; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.8%; Score 77.5; DB 2; Length 545; 29.5%; Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28; Indels
                                                                               POTENTIAL.
0338A2D15E091C73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         545 AA; 60747 MW; 2277F1287C9D8291 CRC64;
                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus faecalis (Streptococcus faecalis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the Pheromone Response.";
J. Bacteriol. 177:5574-5581(1995).
EMBL; D78016; BAA11195.1;
Interpro; IPR000914; SBP_bac_5.
Pfam; PF00496; SBP_bac_5; 2.
PROSITE; PS01040; SBP_BACTERIAL_5; UNKNOWN_1.
J. Bacteriol. 177:5567-5573(1995).
EMBL; D28859; BAA06007.1; -.
InterPro: IPPROJU4; SBP_bac_5.
PROSITE; PSO1040; SBP_BACTERIAL_5; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Mismatches
                                                                                                                                                                                                                            75 ILKQITLPGNKILSLQA-SPTQKNRIKE 101
                                                                                                                                                                                                                                                     -----TDLLSLTAYYPVQQKAIKE 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 ILKQITLPGNKILSLQA-SPTOKNRIKE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TDLLSLTAYYPVQQKAIKE 202
                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                           SEQUENCE 545 AA; 60780 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
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                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                 Plasmid; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pPD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suzuki A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                       Query Match
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                                                                                SIGNAL
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Bukaryota; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Mostera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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"Rad54b, a Rad54-related gene product, is involved in recombinational
DNA repair.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 VQQPSGGNEKQVTT-ISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASILKQITLPGNKIL 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :| | ::: | | | | ::| | 38 VMEPQALEQQELANRVQHFSTSSSSSSSSSCHTVVLPWQQAPSTISSSTIRPINRVL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Champe M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
Yu C., Lewis S.E., Rubin G.M., Celniker S., Phouanenavong S., Wan K.,
Submitted (Auc-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY051904; AAK93281.;
FlyBase; FBgn0003862; trx.
InterPro; IPR001214; SET.
Premp. PR00155; SET.
Prem. PR00155; SET. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (40G-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF178529; AAG09308.1; -.
InterPro; IPR001410; DEAD.
InterPro; IPR0001410; DEAD.
InterPro; IPR000330; SNF2.N.
Pfam; PF00271; helicase_C; 1.
Pfam; PF00176; SNF2.N; 1.
SMART; SM00499; DEXDC; 1.
SMART; SM00490; HELICC; 1.
ATP-binding; Helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             751 AA; 83669 MW; C9E299C65A623C57 CRC64;
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                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
LD39445p.
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Last annotation update)
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19.2%; Pred. No. 6.7;
ive 22; Mismatches 37;
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PRELIMINARY;
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Search completed: February 16, 2003, 21:59:18 Job time: 12.7259 secs
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                        NCBI_TaxID=9606;
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    DDT BERNA BE
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                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- 58
                                                                                                                                         12 GIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98162722; PubMed-9501991;
Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
"Identification of open reading frames in Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lyne M., Rajandream M.A., Barrell B.G., Devlin K., Churcher C.M.; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 -----MPVNTIIPTSQFPPASILKQITL-PGNKILSLQASPTQKNRIKENV 103
                                              DB 13; Length 918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.5%; Score 76; DB 3; Length 403; 27.0%; Pred. No. 4.7;
                                                                                             49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Indels
918 AA; 102878 MW; B4DB2AEA45006685 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungl; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetes; Schizosaccharomycetaceae; Schizosaccharomyces.
NCBI_TaxID=4896;
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5, Last annotation update)
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(TrEMBLrel. 16, Last sequence update)
                                                                                                                                                                                                                                                                 228 PQTTMKQFCKP----IKSACQPSTKENILLNPQSC 258
                                                                                                                                                                                                                                    72 PASILKQITLPGNKILSLQASPTQKNRIKENVTSC 106
                                            ; Score 77; DB 1; Pred. No. 9.6; 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           403 AA
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01-70N-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequ
01-OCT-2000 (TrEMBLrel. 15, Last and
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                                            Query Match
Best Local Similarity 27.4%;
Matches 26; Conservative 1.
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09H8R3;
01-MAR-2001
01-MAR-2001
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SEQUENCE
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042963
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Q9H8R3
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RA ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

RA ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

RA Nibalikawa T., Nagala K., Sugano S., Shiratori A., Sudo H.,

RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Takiguchi S.,

RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

RA Ninomiya K., Iwayanagi T.;

RED human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

REMBL, AKO23360; BAB14543.1;

RITERPRO; IPRO0109; HLH_Dasic.

R Pfam, PF00010; HLH; 1.

R SMART; SMO353; HLH; 1.

R SMART; SMO353; HLH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 ISHSSTLTIQ------KCGQKT------MPVNT--IIPTS-----QFP--- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 PGSVMGIRLPAPSKPSETPPSSTSSSAFSVMNPVIQAVGSSSAVNVITQAPSLLSSGASF
                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         696 AA; 77150 MW; 9FA72151A4EA6A9E CRC64;
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 -- PASILKQITLPGNKILSLQASPTQKNRIKENVTSCFRDE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 PVPSSILQHVA-----SLQMKRESQNPDQKDETNSIKRE 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 PGPVL-----SQPAGIPTGSSSKQLFSLFHVVQQPSGGN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 13.5%; Score 76; DB 4 Best Local Similarity 23.0%; Pred. No. 8.9; Matches 37; Conservative 23; Mismatches
                                 OVARC1001306 protein (Fragment).
Homo sapiens (Human).
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Sequence 48, Appl Sequence 52, Appl Sequence 52, Appl Sequence 62, Appl Sequence 110, Appl Sequence 110, Appl Sequence 15, Appl Sequence 15, Appl Sequence 179, Appl Sequence 10, Appl Sequence 10, Appl Sequence 11, Appl Sequence

Sequence Sequence Sequence Sequence Sequence Sequence

us-09-763-909-2_copy_1_359.rapb

Sequence:

Run on:

Searched:

Database

Result

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APPLICANT: SANDERSON, Karen
APPLICANT: SANDERSON, Karen
APPLICANT: HAQ, Tariq
APPLICANT: LUG, Shuhao
APPLICANT: LUG, Shuhao
APPLICANT: LUG, Pugene
TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND METHODS OF USE
FILE REPERENCE: 0342/16548-US2
CURRENT APPLICATION NUMBER: US/09/893,519A
FRIOR APPLICATION NUMBER: US 60/215,164
PRIOR APPLICATION NUMBER: US 60/215,164
PRIOR APPLICATION NUMBER: US 60/224,457
PRIOR APPLICATION NUMBER: US 60/224,457
NUMBER OF SEQ ID NOS: 146
SOFTWARE: Patentin version 3.1
| US-10-124-557-48
| US-10-124-557-40
| US-10-124-557-52
| US-10-124-557-52
| US-10-124-557-52
| US-10-124-557-62
| US-09-801-368-110
| US-09-924-417-60
| US-09-941-132-195
| US-09-841-132-195
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| US-09-841-132-195
| US-09-841-132-195
| US-09-841-132-140
| US-09-801-368-114
| US-09-801-368-104
| US-09-901-368-104
| US-09-901-630-11
| US-09-901-630-11
| US-09-901-630-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
OTHER INFORMATION: Corresponds to SEQ ID NO: 87
DUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Human Genbank/CAA72189
DATABASE ENTRY DATE: 1997-06-25
RELEVANT RESIDUES: (1)..(1023)
                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ANADYS PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-09-803-519A-14
Sequence 14, Application US/09893519A
Sequence 14, No. US20030027243A1
CENERAL INFORMATION:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: THOMESON, CTAIG
APPLICANT: MOORE, Joffrey
APPLICANT: BUURMAN, Ed T.
APPLICANT: BRADLEY, John
APPLICANT: HARRIS, Sandra
APPLICANT: HARRIS, Sandra
APPLICANT: MENDILLO, MATC
APPLICANT: MOORE, DAILEI
APPLICANT: MCOCY, MALISSA
APPLICANT: SANDERSON, KATEN
  1537
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                           125
124
123.5
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118.5
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127.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
 Sequence 1068, Ap
Sequence 1068, Ap
Sequence 1068, Ap
Sequence 1069, Ap
Sequence 35720, Ap
Sequence 34748, A
Sequence 34748, A
Sequence 14, Appl
Sequence 14, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Appl
                                                                                                   (without alignments)
1296.883 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, A Sequence 84, A Sequence 74, A Sequence 104, Sequence 104, Sequence 44, A Sequence 42, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                    February 16, 2003, 21:56:34; Search time 7.07238 Seconds
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Sequence
Sequence
Sequence
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1773
1 GTLVTKVAPVSAPPKVSSGP.......KAGVVTLHSVGPTAATGGTT
                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_WWW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCT_WWW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
           GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-025-380-1068
US-09-922-217-1068
US-09-823-263-1068
US-09-803-263-1068
US-09-801-368-108
US-09-801-368-106
US-09-801-368-106
US-09-801-368-106
US-09-801-368-106
US-09-801-368-106
US-09-801-368-106
US-10-124-557-14
US-10-124-557-14
                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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US-10-124-557-60
                                                                                                                                                                                                                             140259 seqs, 25548876 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
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                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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167.5
167.5
162.5
152.5
151
149.5
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1822 -SCRATMYPDVPIGQLGQTVVCDVSVGLICKNEDQ----------KPG 1858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1607 TTTTPPPTTTPSPPTTTPITP-PTSTTTLPPTTTPSPPTTTTPPPT----TTPSPPT 1661
                                                                                        104 IKKVAVTPVKKLAQIGTTVVTTVPKPSSVQSVAVP----TSVVTVTPGKPLNTVTLKPS 159
                                                                                                                                                                       SLGASSTP----SNEPNLKAENSAAVQIN--LSPTMLENVKKCKNFLAMLIK 205
                                                                                                                                                                                                                                                           206 LACSGSQSP----EMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKS 260
      62 LVSPQQTVTRAET-----TSNITSRPAVPANPQT------VKICTVPNSSSQL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 IKKVAVTPVKKLAQIGTTVVTTVPKPSSVQSVAVP----TSVVTVTPGKPLNTVTTLKPS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 LVSPQQTVTRAET-----TSNITSRPAVPANPQT------VKICTVPNSSSQL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 SLGASSTP----SNEPNLKAENSAAVQIN--LSPTMLENVKKCKNFLAMLIK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 TLVTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM 61
                                                                                                                                                                                                                                                                                                                                            261 VVALRQLLPNSQSF1QQCVQQTSSDMVIATCT---TTVTTSPVVTTVSSSQSEKSIIVS
                                                                                                                                                                                                  1774 STTTPTTPCVPLCNWTGWLDSGKPNFHKPGGDTELIGDVCGPGWAANI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1068
LENGTH: 5179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.4%; Score 167.5; DB 10; Length Best Local Similarity 22.0%; Pred. No. 0.00096; Matches 89; Conservative 39; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 GATAPRIVSVQTLNPLAGPVGAK----AGVVTLHSVGPTAATGGT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1068, Application US/0992217
Patent No. US20020076414A1
GENERAL INFORMATION:
APPLICANT: W. Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk John A.
APPLICANT: Stolk John A.
APPLICANT: Stolk John A.
APPLICANT: Wang, Tongtong
APPLICANT: Sinith, Carole Lynn
APPLICANT: Smith, Carole Lynn
APPLICANT: Wang, Alloner.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-922-217-1068
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                                                                                                                                                                                                                                       169 NE-PNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSOSPEMGONVKKLVEQL 227
                                                                                                                                                                                                                                                                                                                                                                                                        414 PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL 464
                                                                                                                                                                                                                                                                                                116 AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS 168
                                                                                                                                                                                                                                                                                                                           519 ----TIIIKQV---SQAQTTVQPSATLQRSPGVQPQLVLGGAAQTASLGTATAVQTGTPQ 571
                                                                                     Gaps
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                                                                                                                             13 PPKVSSG-----PRLPAPQIVAVKAPNTTIQFPANLQLPPGTVLIKSNSGPLM 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228 LDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ----TS
                                                                                     64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE FILE REFERENCE: 210121.471C14
CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FASTSEQ for Windows Version 4.0
                                         Length 1023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                     96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 686 Q-----ATTALTAVVLSSSVORTAGKTAATVTSALOPPVLSL 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSV 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.4%; Score 167.5; DB 9; Best Local Similarity 22.0%; Pred. No. 0.00096; Matches 89; Conservative 39; Mismatches 180;
                                         27.7%; Score 491; DB 9;
38.4%; Pred. No. 6.5e-29;
ilve 52; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1068, Application US/10025380 Publication No. US20020182191A1 GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun APPLICANT: Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Secrist, Heather
Benson, Darin R.
Mangher, Madeleine Joy
Stolk, John A.
Wang, Tongtong
Jiang, Yuqiu
Smith, Carole L.
King, Gordon E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fanger, Gary R.
Vedvick Thomas S.
                                                               Best Local Similarity 38.49
Matches 132; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-10-025-380-1068
US-09-893-519A-14
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LENGTH: 5179
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APPLICANT:
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                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNSGPLMLVSPQQT---VTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAV-- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      738 PTPSSSSTTESSSAPVTSSTTESSSAPVPTPSSSTTESSSAPVPTPSSSTTESSSAPVPTP 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------VTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSPTMLENVKKCKNFLA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  518 TTESSSAPVTSSTTESSSAPVPTPSSSTTESSSAPVPTPSSSSTTESSSAPVPTPSSSTTE 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 TLVTKVAPVSAPPKVSSGPRLPAP-----QIVAVKAPNTTTIQFPANLQLPPGTVLIK 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --APVSSSTTESSVAPVPTPSSSSNITESAPSSIPFSSTTESFSTGTTVTPSSSK.----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 -TPVKKLAQIGTTVVTT-----VPKPSSVQS-----VAVPTSVVTVTPGKPLNT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          798 SSSTTESSVAPVPTPSSSSNITSSAPSSTPFSSSTESSSVPV---PTPSSSTTESSS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 MLIKLACSGSQS-----PEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      950 SACETISGCSPKTVTTTVPTTTTTTSVTTSSTTTTTTTVCSTGTNSAGETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.1%; Score 162; DB 10; Best Local Similarity 21.2%; Pred. No. 0.0004; Matches 87; Conservative 62; Mismatches 181;
                                                                                                                                                                                                                                                                                                PAPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Sec.
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR PILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
                                                                                                                                                    Milne, Todá
No. US20020128250Alman, Thea
Royer, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Saccharomyces cerevisiae US-09-801-368-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
SEQ ID NO 108
                                       APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Hottzman, Doug
APPLICANT: Madden, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K. APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                         Salama, Sofie
                                                                                                                                                                                                                                                               Sherman, Amir
Silva, Jeff
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                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Aljun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C12
CURRENT APPLICATION NUMBER: USV/09/833,263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1068
LENGTH: 5179
                                                                                                                                                    ----KPG 1858
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 LACSGSQSP----EMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKS 260
                                          LACSGSQSP-----EMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKS 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 SLGASSTP-----SNEPNLKAENSAAVQIN--LSPTMLENVKKCKNFLAMLIK 205
                                                                                                                            VVALRQLLPNSQSFIQQCVQQTSSDMVIATCT---TTVTTSPVVTTTVSSSQSEKSIIVS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 IKKVAVTPVKKLAQIGTTVVTTVPKPSSVQSVAVP----TSVVTVTPGKPLNTVTTLKPS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVALRQLLPNSQSFIQQCVQQTSSDMVIATCT --- TTVTTSPVVTTTVSSSQSEKSIIVS 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLVTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM 61
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9.4%; Score 167.5; DB 10; Length
Best Local Similarity 22.0%; Pred. No. 0.00096;
Matches 89; Conservative 39; Mismatches 180; Indels
                                                                                                                                                                                                                                           1919 PTTTPITTTT-TVTPTPTPTGTQTPTTTPITTTTTTTTTTGT 1962
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                                                                                                                                                                                                                GATAPRIVSVQTLNPLAGPVGAK----AGVVTLHSVGPTAATGGT 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1822 -SCRATMYPDVPIGQLGQTVVCDVSVGLICKNEDQ-----
                                                                                                                                                                                                                                                                                                                                                          Sequence 1068, Application US/09833263
Patent No. US20020110547A1
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; ORGANISM: Homo sapiens
US-09-833-263-1068
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                                                                                                                                                                                                                                                                                                                                          US-09-833-263-1068
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APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR REPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
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                                                                                                                                                                          155 TASKTATT--STITSLPTTVFTTTSK----ITAGSEIPTASTTDSATTAISTKASGTT 206
                                                                                                                                                                                                                                                                 217 GQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQ 276
          105 --KKVAVTPVKKLAQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLG 162
                                                                                                                                                                                                                                                                                                                                                                                                277 QCV --- QQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPL 333
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                                                                                                                                         163 ASSTPSNEPNLKAE-NSAAVQINLSPIMLEN----VKKCKNFLAMLIKLACSGSQSPEM
                                                                                                                                                                                                                                                                                                                                 ------TAVVSTKAPVTTAMTTAMTGSE------TAVVSTKAPVTTTQSGFS
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No. US20020128250Alman, Thea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 AGPVGAKAGVVTLHSVGPTAATGGTT 359
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; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-106
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SOFTWARE: Patentin version 3.0
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Madden, Kevin
Maxon, Mary
Milne, Todd
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Salama, Sofie
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Silva, Jeff
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APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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N: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3

N: EXPRESSED IN PLACENTA, SIGNAL = 1.7

N: EXPRESSED IN BRAIN, SIGNAL = 2.4

N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8

N: EXPRESSED IN HEAT, SIGNAL = 2.1

N: EXPRESSED IN HELA, SIGNAL = 1.5

N: EXPRESSED IN BELIOO, SIGNAL = 1.5

N: EXPRESSED IN BONE MARROW, SIGNAL = 2.7

N: SWISSPROT HIT: P28968, EVALUE 2.00e-05
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 35720
LENCTH: 386
                                              TITLE OF INVENTION: GENE EXPRESSION ANALISAL
CURRENT APPLICATION NUMBER: US/09/664,761
CURRENT FILING DATE: 2001-05-23
PRIOR PPLING DATE: 2001-05-23
PRIOR PILING DATE: 2000-02-04
PRIOR PLING DATE: 2000-03-26
PRIOR PLING DATE: 2000-06-26
PRIOR PLING DATE: 2000-06-36
PRIOR PLING DATE: 2000-06-36
PRIOR PLING DATE: 2000-09-37
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PPLING DATE: 2000-09-21
PRIOR PPLING DATE: 2000-09-21
PRIOR PPLING DATE: 2000-09-21
PRIOR PPLING DATE: 2000-09-21
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OTHER INFORMATION: EXPRESSED IN BT474,
OTHER INFORMATION: EXPRESSED IN DADULT I
OTHER INFORMATION: EXPRESSED IN PLACEN
OTHER INFORMATION: EXPRESSED IN BRAIN,
OTHER INFORMATION: EXPRESSED IN HEARIN,
OTHER INFORMATION: EXPRESSED IN HEART,
OTHER INFORMATION: EXPRESSED IN HEARY,
OTHER INFORMATION: EXPRESSED IN HELLO,
OTHER INFORMATION: EXPRESSED IN HELLO,
OTHER INFORMATION: EXPRESSED IN BOINE MA
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Best Local Similarity 22.09
Matches 85; Conservative
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1940 AIAEPVSAAPCLHEAPPPVDSKKPLEEKTA--PPVTNNSEIQASEVLVAADKEKVAPV- 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 TVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQIN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSP--VVT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 LSPIMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVE 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2092 TPVNAT -----VGTVNAAPGTVNAAASAVNATASAVTVTAGAVTAASGGVTATTGTVT 2144
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 TIVSSSQSEKSIIVSGATAPRIV -- SVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                             9 PVSAPPKVSSGPRLPAPQIVAVKAPNTTIQFPANLQLPPGTVLIKSNSGPLMLVS--PQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 67 QTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTP--VKKLAQIGTTVVT
N: EXPRESSED IN BONE MARROW, SIGNAL = 10
N: EXPRESSED IN FETAL LIVER, SIGNAL = 8.9
N: EXPRESSED IN ADULT LIVER, SIGNAL = 4.8
N: EXPRESSED IN PLACENTA, SIGNAL = 1.4
N: EXPRESSED IN HEART, SIGNAL = 7.2
N: EXPRESSED IN HEART, SIGNAL = 7.2
N: EXPRESSED IN HELA, SIGNAL = 7.1
N: EXPRESSED IN HELA, SIGNAL = 7.1
N: EXPRESSED IN HELAO, SIGNAL = 7.7
N: EXPRESSED IN HALLOO, SIGNAL = 7.7
N: EXPRESSED IN HA170, SIGNAL = 7.7
N: EXPRESSED IN HT.00 SIGNAL = 7.7
N: EXPRESSED IN HT.00 SIGNAL = 7.7
N: EXPRESSED IN HT.00 SIGNAL = 1.2
N: EST_HUMAN HIT: AU117052.1, EVALUE 3.00e+10
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                                                                                                                                                                                                                                                                                                                                                 Length 2665;
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Patent No. US20020137894A1

GENERAL INFORMATION:

Clark, Stephen C.
Jacobs, Renneth
Hewick, Rodney W.
Gesner, Thomas G.

TITLE OF INVENTION: Magakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                            8.4%; Score 149.5; DB 10; Length 23.7%; Pred. No. 0.0086; Live 50; Mismatches 161; Indels.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
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APPLICATION NUMBER: US 07/643,502
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RAPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
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                                             OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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Best Local S
Matches 85
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                                                                                                                                                                                          937 TILITVSSCESNSCS-----NTVSSAVVSTATITINGITTEYTTWCPLSATELTTVSK 989
     893
                                                                            LACSGSQSPEMGQNVKKLVEQLLDAKIEAEE----FTR---KLYVELKSSPQPHLVPFLK 258
                                                                                                                                                 ---SPVVTTTVSS 307
                                                                                                                                                                                                                                                                       SQS-EKSIIVSGATAPRTVSVQTLNP--LAGPVGAKAGVVTLHSVGPTAAT 355
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LENGTH: 2665
                                                                                                                                               259 KSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTV-
  ISTVA - - - PRSTGLNSQTESTNSSKETMSSENSASV -
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FILING DATE: 2001-01-30
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
APPLICATION NUMBER: PCT/US01/00665
APPLICATION NUMBER: PCT/US01/00665
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCI/US01/00670
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NG DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 09/632,366 FILING DATE: 2000-08-03 APPLICATION NUMBER: GB 24263.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ICATION NUMBER: US 60/236,359
NG DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/207,456
FILING DATE: 2000-05-26
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FILING DATE: 2000-09-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34248, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: MAP TO AL034555.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LE REFERENCE: Aeomica-X-1
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                                                                                           MPSSSATSPKTG---
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54 KSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVK 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     738 EVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTTKTPAATKPEMTTTA 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------SQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLV 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             798 KDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATT-----TQVTSTTTQDTT 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 APVSAPPKVSSGPRLPAPQIVAVKAPNT------TTIQFPANLQLPPGTVLI 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                620 --TKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 ASSTP--SNEPNL--KAENSAAVQINLSPT--MLEN-----VKKCKNFLAMLIKLACSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1022;
                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.1%; Score 144; DB 12; 20.3%; Pred. No. 0.006; ive 53; Mismatches 159;
                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-10-124-557-84
                                                                                            COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617)876-1170
TELEPRA: (617)876-5651
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 74, Application US/10124557 Patent No. US20020137894A1
                               ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                || | : : | | |
PF-KITTLKTTTLAPK----
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Best Local Similarity 20.3%
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315 IVSGATAPR 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | || |:
894 TNSKATTPK 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-10-124-557-74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 KLA-----QIGTTVVTTVPKPSSVQSVA--VPTSVVTVTPGKPLNTVTTLKPSSLG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 ASSTP--SNEPNL--KAENSAAVQINLSPT--MLEN-----VKKCKNFLAMLIKLACSG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 KSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --TKEPTSTISDKPAPTIPKGIAPTIPKEPAPTIPKEPAPTIPKGIAPTILKEPAPTIPK 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 APVSAPPKVSSGPRLPAPQIVAVKAPNT------TTIQFPANLQLPPGTVLI 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       717 KDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATT-----TQVTSTTTQDTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFLKKSVVALRQLL.PNSQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodiney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
CORRESPONDENCE: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.1%; Score 144; DB 12; Length 9. Best Local Similarity 20.3%; Pred. No. 0.0053; Matches 75; Conservative 53; Mismatches 159; Indels
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1889
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                               NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 11near

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-124-557-14
                                                                                                                                                                                                                                                                 TELEPHONE: (617)876-1170
TELEPRA: (617)876-5851
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 84, Application US/10124557
Patent No. US20020137894A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         LENGTH: 941 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           771 PF-KITTLKTTTLAPK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      315 IVSGATAPR 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              813 TNSKATTPK 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
US-10-124-557-84
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255 PFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSI 314
                                                         --VTTTKKTITTTEIMNKPEETAKPKDRA 877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 KSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --TKEPTSTISDKPAPTIPKGTAPTIPKEPAPTIPKEPAPTIPKGTAPTILKEPAPTIPK 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- TTIQFPANLQLPPGTVLI 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1049;
                                                                                                                                                                                                                                                                                                                                                                                             Jacobs, Kenneth
Hewlok, Rodney M.
Gesner, Thomas G.
IIILE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.1%; Score 144; DB 12;
20.3%; Pred. No. 0.0062;
tive 53; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/124,557 FILING DATE: 16-Apr-2002 CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/390,901 FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: GI 5190 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-124-557-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 APVSAPPKVSSGPRLPAPQIVAVKAPNT-
                                                                                                                                                                                                                                                                     Sequence 58, Application US/10124557; Patent No. US20020137894A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Turner, Katherine Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELEFAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Cambridge
                                       Query Match
Best Local Similarity
Matches 75; Conserv
                                                                                                      315 IVSGATAPR 323
                                                                                                                                                     878 TNSKATIPK 886
                                                                                                                                                                                                                                                 US-10-124-557-58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                604 --TKEPTSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPK 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 KLA------QIGTIVVTIVPKPSSVQSVA--VPTSVVIVIPGKPLNIVTILKPSSLG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               662 КРАРКЕТАРТТИКОРТЅТТЅОКРАРТТРКЕТАРТТРКЕРАРТТРККРАРТТРЕТРРРТТЅ 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 ASSTP--SNEPNL--KAENSAAVQINLSPT--MLEN-----VKKCKNFLAMLIKLACSG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----SQSPEMGONVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLV 254
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EVSTPTTTKEPTTIHKSPDESTPELSAEPTPKALENSPKEPGVPTKTPAATKPEMTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1038;
                                                                                                                                           TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
RADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.1%; Score 144; DB 12; Length 1
Best Local Similarity 20.3%; Pred. No. 0.0061;
Matches 75; Conservative 53; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/124,557
FILLING DATE: 16-Apr-2002
CLASSIFICATION APPR: US/10/124,557
PRIOR APPLICATION DATE: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/457,196
FILING DATE: 08-AUG-1889
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: CSET, LUANN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FELEPHONE: (617)876-1170
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
                                                                          Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
                                                                                                                                                                                                                                                                                            STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                     CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-124-557-74
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54 KSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVK 113
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                                                                                                                                                                                                                                                                738 --ТКЕРТSTTSDKPAPTTPKGTAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPK 795
                                                                                                                                                                                                                                                                                                          114 KLA------QIGTTVVTTVPKPSSVQSVA--VPTSVVTVTPGKPLNTVTTLKPSSLG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----SQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLV 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSI 314
                                                                                                                                8 APVSAPPKVSSGPRLPAPQIVAVKAPNT------TTIQFPANLQLPPGTVLI 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : : | : | | | : : | | | 316 KDKTTERDLRTTPETTAAPKMTKETATTTESKITATT-----TQVTSTTTQDTT
                                                   Length 1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                               Query Match

8.1%; Score 144; DB 12;
Best Local Similarity 20.3%; Pred. No. 0.0069;
Matches 75; Conservative 53; Mismatches 159;
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-0AN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inc.
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FILING DATE: 16-Apr-2002
CLASSIFICATION: <URNOWN>
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 44, Application US/10124557
Patent No. US20020137894A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
COUNTRY: U.S.A.
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US-10-124-557-104
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                      KLA------QIGTTVVTTVPKPSSVQSVA--VPTSVVTVTPGKPLNTVTTLKPSSLG 162
                                               210
                                                                                                                                           EVSTPITIKEPTIHKSPDESIPELSAEPIPKALENSPKEPGVPTIKIPAAIKPEMIITA 824
                                                                                                                                                                                                                                     825 KDKTTERDLRTTPETTTAAPKMTKETATTTEKTTESKITATT-----TQVTSTTTQDTT 878
                                                                                                                                                                                                                                                                                                                          ------VTTTKKTITTTEIMNKPEETAKPKDRA 920
                                                                                                                                                                                                                                                                                  PFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSI 314
                                                                                                         ASSTP--SNEPNL--KAENSAAVQINLSPT--MLEN-----VKKCKNFLAMLIKLACSG
                                                                                                                                                                                            ------SQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONTUTER NEADMILE FORM MEDIUM TYPE: Floppy disk COMPUTER: IDM PC COMPATIBLE CONTUTER: IDM PC COMPATIBLE CONTUTER: IDM PC COMPATIBLE CONTUTER: DATE: PC-DOS/MS-DOS COFFWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

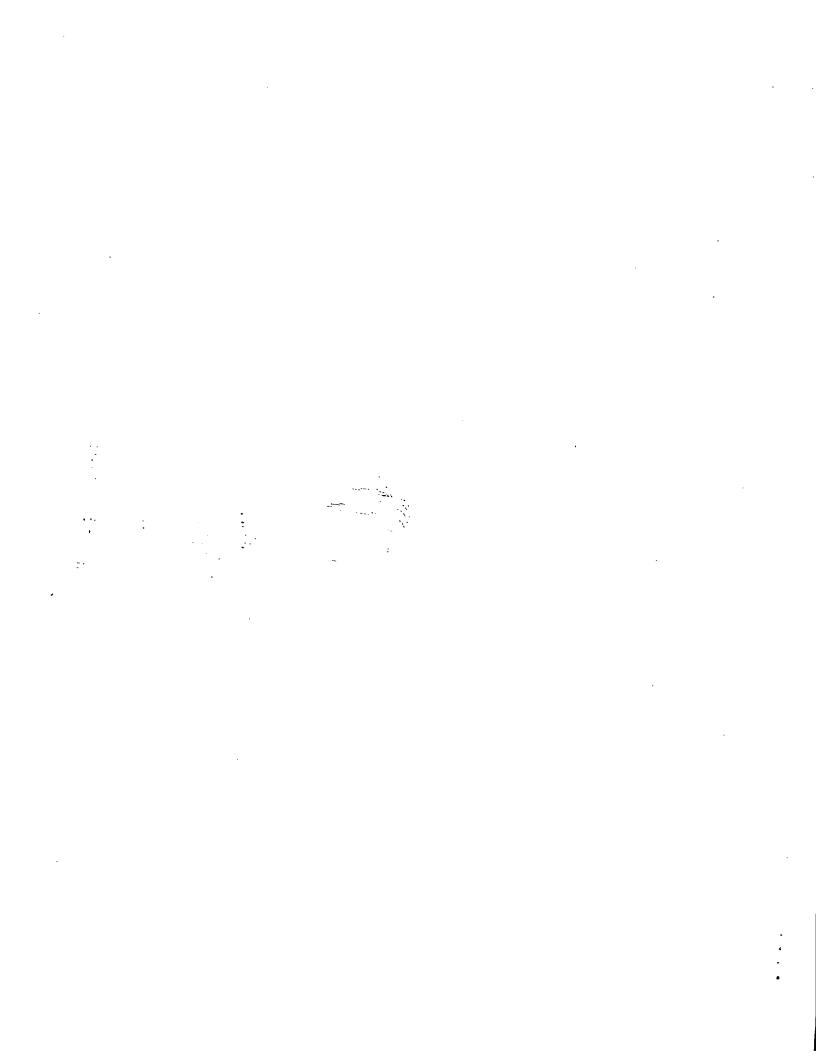
PRIOR APPLICATION NUMBER: US/10/124,557
FILING DATE: 18-Apr-2002
CLASSIFICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-GC-1999
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-GC-1999
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-GC-1999
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-GC-1999
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Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
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STREET: 87 CambridgePark Drive
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 104, Application US/10124557 Patent No. US20020137894A1 GENERAL INFORMATION:
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LENGTH: 1140 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Turner, Katherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clark, Stephen C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                          PF-KITTLKTTTLAPK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 KLA------QIGTTVVTTVPKPSSVQSVA--VPTSVVTVTPGKPLNTVTTLKPSSLG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 703 KPAPKELAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTS 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           877 PF-KITTLKTTTLAPK--------VTTTKKTITTTEIMNKPEETAKPKDRA 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       588 APTIPKEPAPTIPKEPAPTIPKETAPTIPKGTAPTILKEPAPTIPKKPAPKELAPIT--- 644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1311;
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8.1%; Score 144; DB 12;
Best Local Similarity 20.3%; Pred. No. 0.0084;
Matches 75; Conservative 53; Mismatches 159;
                                                                                                                   FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
FILING DATE: 08-AUG-1989
                                                                                               APPLICATION NUMBER: US 07/643,502
                                                                                                                                                                                                                                                                                                          REGISTRATION UNMBER: 31,822
REGISTRATION UNMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: February 16, 2003, 22:02:32 Job time : 18.0724 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-124-557-42
                                                CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1311 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617)876-5851 INFORMATION FOR SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                         PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : | : | | | 604 --TKEPTSTISDKPAPTTPKGTAPTIPKEPAPTIPKEPAPTIFKGTAPTIFK 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    662 КРАРКЕLAPTTTKGPTSTTSDKPAPTTPKETAPTTPKEPAPTTPKKPAPTTPETPPPTTS 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 PFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSI 314
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                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 APVSAPPKVSSGPRLPAPQIVAVKAPNT------TTIQFPANLQLPPGTVLI 53
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                                                                                                                                                                                                                                                                                                                                                         Length 1270;
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Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                    Query Match 8.1%; Score 144; DB 12; Length 1
Best Local Similarity 20.3%; Pred. No. 0.008;
Matches 75; Conservative 53; Mismatches 159; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                         REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-5851
INFORMATION FOR EGO ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 1270 amino acids
                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
05-10-124-557-44
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 42, Application US/10124557 Patent No. US20020137894A1 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                           TYPE: amino acid
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Sequence 1660, Ap Sequence 1665, Ap Sequence 1311, Ap Sequence 2011, Ap Sequence 2011, Ap Sequence 2, Appl Sequence 3610, Ap Sequence 3624, Ap Sequence 3624, Ap Sequence 11876, Ap Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 697, Appl Sequence 686, Appl Sequence 686, Appl Sequence 687, Appl Sequence 1349, Appl Sequence 1349, Appl Sequence 1249, Appl Sequence 2184, Appl Sequence 687, Appl Sequence 687, Appl Sequence 687, Appl Sequence 2184, Appl Sequen
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/540,167
PRIOR FILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
1 PCT-USO1-20592-14
1 PCT-USO1-20592A-14
2 PCT-USO2-30474-1660
2 US-60-324-631-1665
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ilarity 100.0%; Pred. No. 4.6e-139;
Conservative 0; Mismatches 0;
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PCT-US01-08631-39827
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1827.005 Million cell updates/sec
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                         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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PCT-US02-25829-25
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PCT-US02-29964-410
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Listing first 45 summaries
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MLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGT
                         MLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGT
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Goodrich, Ryle W.
Weng, Gezhi
Haley-Vicente, Dana
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Ghosh, Malabika
Asundi, Vinod
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Zhao, Oing A.
Wang, Jian-Rui
Xue, Aidong J.
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Ren, Felyan
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PCT-US02-29964-410
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PCT-US02-29964-410
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GENERAL INFORMATION:
GRAFIEIN, Rivka
APPLICANT: Dikstein, Rivka
APPLICANT: Vamit-Hezi, Ayala
TITLE OF INVENTION: A TRANSCRIPTION FACTOR TFIID SUBUNIT,
TITLE OF INVENTION: PAFFIIIOS, POLYPEPTIES, DNA ENCODING THEREFOR AND
TITLE OF INVENTION: PHARMACUTICAL COMPOSITIONS
FILE REFERENCE: 13005/002001
                                      Gaps
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Score 1773; DB 1;
Pred. No. 5e-139;
Mismatches 0;
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CURRENT FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
Query Match 100.0%; S
Best Local Similarity 100.0%; P.
Matches 359; Conservative 0;
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  VITIVSSSQSEKSIIVSGATAPRIVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTT 359
                         APPLICANT: YUE, Huibin
APPLICANT: ZEBARABIAN, YEGANEN
TITLE OF INVENTION NUCLEIC ACID ASSOCIATED PROTEINS
FILE REFERENCE: PF-1146 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILLING NORER: PCT/0502/25029

CURRENT FILLING DATE: 2002-08-14

PRIOR APPLICATION NUMBER: US 60/313,111

PRIOR FILLING DATE: 2001-08-14

PRIOR FILLING DATE: 2001-08-24

PRIOR FILLING DATE: 2001-08-24

PRIOR FILLING DATE: 2001-08-24

PRIOR PAPLICATION NUMBER: US 60/314,756

PRIOR PAPLICATION NUMBER: US 60/315,105

PRIOR PAPLICATION NUMBER: US 60/316,751

PRIOR PILLING DATE: 2001-08-31

PRIOR FILLING DATE: 2001-08-31

PRIOR FILLING DATE: 2001-08-31

PRIOR FILLING DATE: 2001-08-31

PRIOR FILLING DATE: 2001-08-31

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PRIOR PILLING DATE: 2001-08-31
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CURRENT FILING DATE: 2002-08-14
                                                                                                                                                    Sequence 25, Application PC/TUS0225829 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEHR-MASON, Patricia M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRIFFIN, Jennifer A. HAFALIA, April J.A. HONCHELL, Cynthia D. ISON, Craig H.
                                                                                                                                                                                                                                                                                                                                                                       ELLIOTT, Vicki S.
EMERLING, Brooke M.
FORSYTHE, Ian J.
GIETZEN, Kimberly J.
                                                                                                                                                                                                                BAROSSO, Ines
BAUGHN, Mariah R.
BECHA, Shanya D.
BLAKE, Julie J.
BOROWSKY, Mark L.
BURFORD, Neil
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                                                                                                                                                                                             APPLICANT: INCYTE GENOMICS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAMKUMAR, Jayalaxmi
SPRAGUE, William W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEE, Sally
LEE, Soo Yeun
LI, Joana X.
LU, Dyung Aina M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRAN, Uyen K.
WALIA, Narinder K.
WARREN, Bridget A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Danniel B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ernestine A.
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YAO, Monique G.
YUE, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Farrah A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GORVAD, Ann E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAL, Preeti G.
LEE, Ernestine
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Sequence 1271, Application US/60243468
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: CLOO0929
CURRENT APPLICATION NUMBER: US/60/243,468
CURRENT APPLICATION NUMBER: US/60/243,468
SOFTWARE: FILING DATE: 2000-10-27
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----SVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAA 210
                                                                                                                                                                                                                                                                                                                                         IGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAEN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                       1 GTLVTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPP---GTVLIKSNS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GTLVTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPL 60
                                                                                                                                                                                                                                                                                                                                                                                                                    SAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
                                                                                                                  DB 1; Length 865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 685;
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                                                                                                            Score 1761.5; DB 1
Pred. No. 4.8e-138;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.5e-122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                 ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 4398735CD1
PCT-US02-25829-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.8%; Score 1575; 90.0%; Pred. No. 1.
                                                                                                              99.48;
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23; Conservative
                                                                                                                                                   Conservative
ORGANISM: Homo sapiens
FEATURE:
                                                                                                            Query Match
Best Local Similarity
Matches 359; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-60-243-468-1271
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TT 428
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Best Local Simi
Matches 323;
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116 AQIGTIVVITVPKPSSVQSVAVPISVVIVIPGKPLNIVT--TLKPSSLGASS----IPS 168
                                    ----TILIKOV----SQAQTTVQPSATLQRSPGVQPQLVLGGAAQTASLGTATAVQTGTPQ 225
                                                                         169 NE-PNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL 227
                                                                                                                                                         LDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ----TS 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 PPKVSSG------PRLPAPQIVAVKAPNTTIQFPANLQLPPGTVLIKSNSGPLM 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LONG, Fan
APPLICANT: DAVIDOV, Eugene
TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND METHODS OF USE
FILE REFERENCE: 0342/16548-US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
CTHER INFORMATION: human genbank accession #: CAA72189
NAME/KEY: misc_feature
CTHER INFORMATION: Corresponds to SEQ ID NO: 87
PCT-US01-20592-14
                                                                                                                                                                                                                                    284 SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSV 327
                                                                                                                                                                                                                                                                         O-----ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.7%; Score 491; DB 1;
38.4%; Pred. No. 2.3e-31;
tive 52; Mismatches 96,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: PCT/USO1/20592
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,164
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/224,457
PRIOR FILING DATE: 2000-08-10
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ANADYS PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application PC/TUS0120592 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESILVA, Thamara
HARRIS, Sandra
KOMARNITSKY, Svetlana
MENDILLO, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 146
SORTWARE: Patentin version 3.1
SEQ ID NO 14
LENGTH: 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                THOMPSON, Craig
MOORE, Jeffrey
BUURMAN, Ed T.
BRADLEY, JOhn
DESILVA, Thamara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SANDERSON, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 27.74
Best Local Similarity 38.44
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOORE, Daniel
MCCOY, Melissa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAQ, Tariq
ZHU, Shuhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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APPLICANT:
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                                211 VQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGONVKKLVEQLLDAKIEAEEFTRK 270
                                                                                         LYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPV 300
                                                                                                                  62 LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 PIATTSGIRATLIPIVLAPRLPQP-----PQNPINIQ---NFQLPPGMVLVRSENGQLL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                           301 VTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTT 359
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dynlact, Brian D.
APPLICANT: Hoey, Timothy
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Nacko
APPLICANT: Tanese, Nacko
APPLICANT: Wang, Edith
APPLICANT: Wang, Edith
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 PPKVSSG------PRLPAPQIVAVKAPNTTIQFPANLQLPPGTVLIKSNSGPLM 61
            VQINLSPIMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/01114 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36.627
REFERENCE/DOCKET NUMBER: 36.627
REFERENCE/DOCKET NUMBER: FP-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
TELERAX: (415) 781-1989
TELERAX: (415) 398-3249
TELERX: (415) 398-3249
TELERX: 910 277299
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 737 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                        Sequence 16, Application PC/TUS9401114
GENERAL INFORMATION:
APPLICANT: Tjian, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/WS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                Tjian, Robert
Comai, Lucio
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STATE: California
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STREET: 4
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PCT-US94-01114-16
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228 LDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ----TS 283
                                                                                                                                                      Sequence 14, Application US/09893519A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                            HARRIS, Sandra
KOMARNITSKY, Svetlana
MENDILLO, Marc
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                              THOMPSON, Craig
MOORE, Jeffrey
BUURMAN, Ed.T.
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DESILVA, Thamara
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SANDERSON, Karen
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                                                                                                                                                                                                                                                                                                                            MOORE, Daniel
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ZHU, Shuhao
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                                                                                                                                        US-09-893-519A-14
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                                                                          LDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ----TS 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NE-PNLKAENSAAVQINLSPIMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND METHODS OF USE FILE REFERENCE: 0342/16548-US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96; Indels
                                                                                                                                          Q-----ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL 7:2
                                                                                                                       284 SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSV 327
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38.4%; Pred. No. 2.3e-31;
ive 52; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Corresponds to SEQ ID NO: 87
PCT-US01-20592A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: PCT/US01/20592A CURRENT FILING DATE: 2001-06-28 PRIOR APPLICATION NUMBER: US 60/215,164 PRIOR FILING DATE: 2000-06-29 PRIOR APPLICATION NUMBER: US 60/224,457 PRIOR FILING DATE: 2000-08-10
                                                                                                                                                                                                                              Sequence 14, Application PC/TUS0120592A GENERAL INFORMATION:
APPLICANT: ANADYS PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                          THOMPSON, Craig
MONE, Jeffrey
BUDRAN, Ed T.
BRADLEY, John
DESILVA, Thamara
HARRIS, Sandra
KOMARNITSKY, Svetlana
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NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                 SANDERSON, Karen
                                                                                                                                                                                                                                                                                                                                                                                  MENDILLO, Marc
MOORE, Daniel
MCCOY, Melissa
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Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                HAO, Tariq
ZHU, Shuhao
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                 -US01-20592A-14
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LENGTH: 1023
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND METHODS OF USE
                                                                                                                                         686 Q-----ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL 722
                                                                                                     284 SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSV 327
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DATABASE RWIRY DATE: 1997-06-25;
RELEVANT RESIDUES: (1)..(1023)
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38.4%; Pred. No. 2.3e-31;
ive 52; Mismatches 96;
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OTHER INFORMATION: Corresponds to SEQ ID NO: 87
PUBLICATION INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/893,519A
CURRENT FILING DATE: 2001-06-28
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PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/224,457
PRIOR FILING DATE: 2000-08-10
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228 LDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ----TS 283
                                                                                                                                                             540 RIVPGATITSSAAIE-----TMENVKKCKNFLSILIKLASSGKQSTETAANVKELVONL 593
                                                                                                                                                                                                                                                           116 AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS----TPS 168
                                                              169 NE-PNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL
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CURRENT APPLICATION NUMBER: US/60/324,631
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR PLICATION NUMBER: US 09/552,317
PRIOR PLICATION NUMBER: PCT/US00/35017
PRIOR PLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR PLING DATE: 2000-01-25
PRIOR PLING DATE: 2000-01-25
PRIOR PLING DATE: 2000-01-25
PRIOR PLING DATE: 2000-02-03
PRIOR PLING DATE: 2000-02-03
PRIOR PLING DATE: 2000-02-05
PRIOR PLING DATE: 2000-02-05
PRIOR PLING DATE: 2000-02-05
PRIOR PLING DATE: 2000-02-05
PRIOR PLING DATE: 2000-02-26
PRIOR PLING DATE: 2000-05-18
PRIOR PLING DATE: 2000-05-19
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IITLE OF INVENTION: Novel Nucleic Acids and
IITLE OF INVENTION: Polypeptides
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Ghosh, Malabika
Wang, Dunrui
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Wang, Jian-Rui
Wehrman, Tom
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Xue, Aldong J
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Weng, Gezhi
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Asundi, Vind
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62 LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
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                                                                                                            686 Q-----ATTALIAVVLSSSVQRTAGKTAATVTSALQPPVLSL 722
                                                                        284 SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSV 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Haley, Vicente, Dana APPLICANT: Haley, Vicente, Dana APPLICANT: Drmanac, Radoje T TITLE OF INVENTION: Novel Nucleic Acids and TITLE OF INVENTION: Polypeptides CURRENT APPLICATION NUMBER: PCT/USO2/30474 CURRENT APPLICATION NUMBER: PCT/USO2/30474 CURRENT FLING DATE: 2000-09-24 PRIOR APPLICATION NUMBER: US 60/324,631 PRIOR APPLICATION NUMBER: US 09/486,725 PRIOR PILING DATE: 2000-01-21 PRIOR PELING DATE: 2000-01-21 PRIOR PELING DATE: 2000-01-25 PRIOR PELING DATE: 2000-125 PRIOR PELING DATE: 2000-125 PRIOR PPLICATION NUMBER: US 09/491,404 PRIOR FILING DATE: 2000-125 PRIOR PPLICATION NUMBER: US 09/491,404 PRIOR FILING DATE: 2001-01-25 PRIOR PPLICATION NUMBER: US 09/496,914 PRIOR FILING DATE: 2001-01-25 PRIOR PPLICATION NUMBER: US 09/560,875 PRIOR PRILING DATE: 2000-02-03 PRIOR PILING DATE: 2000-04-27 PRIOR PLING DATE: 2000-04-27 PRIOR PLING DATE: 2000-04-27 PRIOR APPLICATION NUMBER: US 09/560,875 PRIOR APPLICATION NUMBER: US 09/555,126 PRIOR APPLICATION NUMBER: US 09/515,126 PRIOR PELING DATE: 2000-02-28
                                                                                                                                                                                                                                                Sequence 1660, Application PC/TUS0230474 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                Ren, Felyan
Xue, Aldong J.
Zhao, Oing A.
Wang, Jian-Rui
Wehrman, Tom
Zhou, Ping
Ghosh, Malabika
Wang, Dunrui
Ma, Yunging
Asundi, Vinod
Wang, Zhiwei
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Matches 132, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
PCT-US02-30474-1660
                                                                                                                                                                                                                                                                                                                           Zhang, Jle
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; LOCATION: (1)...(1083)
; OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as
PCT-US02-30474-3271
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TITLE OF INVENTION: ISOLATED DROSOPHILA PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLEUCLES ENCODING DROSOPHILA PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 AQIGTTVVTTVP-----KPSSVQSVAVPTSVVTVTP----GKPLNTVTTLKPSSL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GASSIPSNEPNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 PPKVSSG-----PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 3476
SOFTWARE: PL_genes Version 6.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         523 SRVSQAQTTVQPSATLKRSPGSQPQLVLGCAAKTAXLGTAPAVQTGTPQRTVP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.0%; Score 479; DB 1;
36.3%; Pred. No. 2.6e-30;
tive 50; Mismatches 97
                 CURRENT APPLICATION NUMBER: PCT/US02/30474
CURRENT FILING DATE: 2002-09-24
PRIOR FILING DATE: 2002-09-24
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2000-01-21
PRIOR PILING DATE: 2000-01-21
PRIOR PILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-01-25
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR PILING DATE: 2000-11-25
PRIOR PPLICATION NUMBER: US 09/491,404
PRIOR PILING DATE: 2001-01-25
PRIOR PPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR PILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR PELING DATE: 2000-04-27
PRIOR PELING DATE: 2000-04-27
PRIOR FILING DATE: 2000-02-05
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Best Local Similarity 36.3%
Matches 127; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              487 ----TIIIKQV---SQAQTTVQPSATLQRSPGVQPQLVLGGAAQTASLGTATAVQTGTPQ 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 PPKVSSG-----PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 NE-PNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 27.7%; Score 491; DB 27; Length 1051; Best Local Similarity 38.4%; Pred. No. 2.4e-31; Matches 132; Conservative 52; Mismatches 96; Indels 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284 SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSV 327
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APPLICANT: Drmance, Radole T
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
                                     PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: PCT/CS01/08631
PRIOR APPLICATION NUMBER: US 09/52,929
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: PCT/US01/08656
PRIOR APPLICATION NUMBER: PCT/US01/08656
PRIOR APPLICATION NUMBER: PCT/US01/14827
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
STORMARE: PCT/US01/14827
SOFTWARE: PL-EL-Genes Version 6.0
SEQ ID NO 1665
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GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Xue, Aidong J.
APPLICANT: And Aidong J.
APPLICANT: And Aidong J.
APPLICANT: Wang, Jian-Rui
APPLICATION NUMBER: US 09/649,167
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Zhou, Ping
Ghosh, Malabika
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Asundi, Vinod
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US-60-324-631-1665
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Sequence 20611, Application US/60173464
GENERAL INFORMATION:
APPLICANT: Li, PECET W.D.
TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES
TITLE OF INVENTION: MUSERED G-PROTEIN COUPLED REPERBACE: CLOO0173
CURRENT FILING DATE: 1999-12-29
NUMBER OF SED ID NOS: 30269
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                      288 TQQGNTKEKCRKFLANLIEL--STREPKPVEKNVRTLIQELVNANVEPEEFCDRLERLLN 345
                                                                                                                                                                                                                                     :|||| |: |||||: ||| 346 ASPQPCLIGFLKKSLPLLRQALYTKELVIEGIKPPPQHVLGLAGLSQQLPKIQAQIRPIG 405
                                                                                                                                                                                                                                                                                                                        PSQTTTIGQTQVRMI--TPNALGTPRPTIGHTTISKQPPN---IRLPTAPRLVNTGGIRT 460
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ASPQPCLIGFLKKSLPLLRQALYTKELVIEGIKPPPQHVLGLAGLSQQLPKIQAQIRPIG 405
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                                                KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 POSPSITLSTLNTGQTPA-----LLVKTDNGFQLLRVGTTTGPTTVTQTITNTSNNS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 NITSRPAVPANPQTVKICTVPNSSSQ-----LIKKVAVTPVKKLAQIGTTVVTTVP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 PQIVAVKAPNTTTIQEPANLQLPPGTVLIKSNSGPLML-----VSPQQTVTRAETTS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TMLENVK-KCKNFLAMLIKLACSGSOSPEMGONVKKLVEQLLDAKIEAEEFTRKLYVELK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 APQLPQITQIQTIPAQQSQQQVNNVSSAGGTATAVSSTTA------ATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 921;
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                                                                                       244 APQLPQITQIQTIPAQQSQQQONNVSSAGGTATAVSSTTA---
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                                                                                                                                                                                                                                                                                                                                                                                                    LNPLAGPVGAKAGVVTLHSVGPTAA 354
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                                                                                                                                                                                                           SSPQPHLVPFLKKSVVALRQL-----
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Best Local Similarity
Matches 96; Conserv
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LENGTH: 921
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      185
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GENERAL INFORMATION:
APPLICANT: L1, PECET W.D.
TITLE OF INVENTION: ISSOLATED G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: UCCLEIC ACID MOLECULES ENCODING GPCR PROTEINS AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLO00173
CURRENT APPLICATION NUMBER: US/60/173,464
CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 30269
SOFTWARE: PastSEQ for Windows Version 4.0
ENGTH: 921
                                                                                                                                                                                                                                                                                                                                                   111 POSPSITLSTLNTGGTPA-----LLVKTDNGFQLLRVGTTTGPTTVTQTITNTSNNS 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 ASPOPCLIGFLKKSLPLLRQALYTKELVIEGIKPPPQHVLGLAGLSQQLPKIQAQIRPIG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384 PSQTTTIGQTQVRMI--TPNALGTPRPTIGHTTISKQPPN---IRLPTAPRLVNTGGIRT 438
                                                                                                                                                                                                                                                                                                                                                                                            NITSRPAVPANPQTVKICTVPNSSSQ-----LIKKVAVTPVKKLAQIGTTVVTTVP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                    163 NTTSTTNHPTTTQ-IRLQTVPAAASMTNTTATSNIIVNSVASSGYANSSQPPHLTQLNAQ 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277 ----QCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVS---VQT
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FILE REFERENCE: CL000152
CURRENT APPLICATION NUMBER: US/60/167,217
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 23195
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11401
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Search completed: February 16, 2003, 22:18:31 Job time : 133.688 secs

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RESULT 2
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GTVLIKSN : : GMVLVRSE LIKKVAVT IIAR-QVT : : : :	ngth 679;	Seque Seque Seque Seque B Seque O Seque Seque Seque Seque Seque Seque Seque Seque Seque Seque Seque Seque Seque Seque Seque Seque Seque Seque Seque
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US-09-724-676A-63929
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SEQ ID NO 63927
LENGTH: 709
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APPLICANT: Compugen LTD
APPLICANT: INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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116 AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS
                                 337 MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPI1AR-QVTP----
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                                                                                                   PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL 336
                                                                  LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNS;SQLIKKVAVTPVKKL 115
                                                                                                                                      PPKVSSG------PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDGKIEAEDFTSRLYRELNSSPQPYLVPFLKRSLPALRQLTPDSAAFIQQSQQQPPPPTS 557
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                                                                                                                                                                                         27.7%; Score 491; DB 5 38.4%; Pred. No. 5e-21;
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Pred. No. 4.8e-21;
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CURRENT APPLICATION NUMBER: U.
CURRENT FILING DATE: 2000-11
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.:
SEQ ID NO 63927
LENGTH: 709
TYPE: PRT
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US-09-724-676-63920
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Sequence 63927, Application US/09724676A

GENERAL INFORMATION:
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                                                                                                                                 Sequence 63920, Appl GENERAL INFORMATION:
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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative FILE REFERENCE: 129181.4 Compugen
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Pred. No. 5e-21;
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RESULT 15

US-09-724-676-63924

Sequence 63924, Application US/09724676

GENERAL INFORMATION:

APPLICANT: Compugen LTD

TITLE OF INVENTION: Variants of alternative splicing

FILE REFERENCE: 129181.4 Compugen

CURRENT APPLICATION NUMBER: US/09/724,676

CURRENT PRILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 97222

SOFTWARE: Patentin version 3.2

SEQ ID NO 63924

LENGTH: 837

TYPE: PRT
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Search completed: February 16, 2003, 22:04:25 Job time: 17.606 secs
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Best Local Similarity
Matches 132; Conserv
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                                                      Q-----ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL 722
                                                                                                                                                                      RTVPGATTTSSAATE-----TMENVKKCKNFLSTLIKLASSGKQSTETAANVKELVQNL 625
                                                                                                                                                                                          NE-PNIKAENSAAVQINISPTMIENVKKCKNFLAMIIKLACSGSQSPEMGQNVKKIVEQI 227
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                                                                                                                                                                                                                                                     AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS 168
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RESULT 13
US-09-724-676-63926
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US-09-724-676A-63921
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  Sequence 63926, Application US/09724676
GENERAL INFORMATION:
APPLICANT: COmpugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
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CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 63921
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Best Local Similarity
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
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TYPE: PRT
ORGANISM: Homo sapiens
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; Pred. No. 5.7e-21
52; Mismatches 9
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US-09-724-676A-63926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 63926
LENGTH: 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 63926, Application US/09724676A GENERAL INFORMATION:
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SEQ ID NO 63926
LENGTH: 807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
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les 132; Conserv
NE-PNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL
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                                                             ----TTIIKQV----SQAQTTVQPSATLQRSPGVQPQLVLGGAAQTASLGTATAVQTGTPQ 571
                                                                                                      AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS
                                                                                                                                                                                    LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
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Pred. No. 5.7e-21
2; Mismatches 9
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US-09-724-676-63923
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Best Local S
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CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 63923
LENGTH: 775
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 63923, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INCENTION: Variants of alternative
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                  SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSV
                                                             LDGKIEAEDFTSRLYRELNSSPQPYLVPFLKRSLPALRQLTPDSAAFIQQSQQQPPPPTS
                                                                             LDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ----TS 283
                                                                                                                           RTVPGATTTSSAATE-----TMENVKKCKNFLSTLIKLASSGKQSTETAANVKELVQNL
                                                                                                                                                          NE-PNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL 227
                                                                                                                                                                                                                        AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS-----TPS 168
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-ATTALTAVVLSSVQRTAGKTAATVTSALQPPVLSL 690
                                                                                                                                                                                                                                                                                                                                                                                                         27.7%; Score 491; DB 5; 38.4%; Pred. No. 5.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM 61
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US-09-724-676-63921
Sequence 63921, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative
FILE REFERENCE: 129181.4 Compugen
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US-09-724-676A-63923
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 12981.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEO ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 63921
LENGTH: 805
TYPE: PRT
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LENGTH: 775
                                                                                                                                              Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 654 Q-----ATTALTAVVLSSSVQRTAGKTAATVTSALQPPVLSL
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                                                                                            13 PPKVSSG----
                                                                                                                                              Local Similarity
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   LVSPQQTVTR-----
                                                    PTATTSGIRATLTPTVLAPRLPQP------PQNPTNIQ---NFQLPPGMVLVRSENGQLL 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTVPGATTTSSAATE----TMENVKKCKNFLSTLIKLASSGKQSTETAANVKELVQNL
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38.48;
                                                                             ----PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM 61
                                                                                                                                            27.7%;
-AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
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                                                                                                                          Score 491; DB 5;
Pred. No. 5.7e-21;
2; Mismatches 96
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Pred. No. 5.
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US-09-724-676A-63920
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LENGTH: 711
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
FILE REFERENCE: 129181.5 Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version
SEQ ID NO 63920
LENGTH: 711
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                                                                                                          423
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                                                                                                                                                                          369 MI-PQQALAQMQAQAHAQPQTTMAPRPATPTSAPPVQISTVQAPGTPIIAR-QVTP----
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                                                                                                                                                                                                                                                                                 13 PPKVSSG-------PRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLM 61
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LDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ----TS
                                                                                                                                         AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS----TPS
                                    RTVPGATTTSSAATE-----TMENVKKCKNFLSTLIKLASSGKQSTETAANVKELVQNL
                                                                    NE-PNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL
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                                                                                                     ----TTIIKQV----SQAQTTVQPSATLQRSPGVQPQLVLGGAAQTASLGTATAVQTGTPQ
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                                                    ; ORGANISM: Homo sapiens US-09-724-676A-63930
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US-09-724-676A-63930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
                                                                                                         SOFTWARE: Patentin
SEQ ID NO 63930
LENGTH: 741
Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
                                                                                                                                                                                                                    APPLICANT: Compugen LTD TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen
                                                                                                                                                           NUMBER OF SEQ ID NOS: 97222
                                                                                            TYPE: PRT
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38.4%;
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Pred.
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Pred. No. 5.2e-21;
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 491; DB
No. 5.2e-
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                                                                                                This cDNA sequence encodes a human tata-binding protein associated factor, hTAFILIO5, isolated from Daudi cell nuclear extracts. Tightly associated subunits (TAF's) are components of the transcription factor FFIID and are thought to mediate transcription a ctivation. This encoded protein may be produced recombinantly from transformed host cells or purified from human cells. hTAFILIOS specific binding agents such as specific antibodies could be used for diagnosis (e.g. genetic hybridisation screens for hTAFILIOS transcripts), therapy (e.g. genetic bropharmaceutical industry (e.g. as immunogens, reagents for isolating B cell specific activators or other transcriptional regulators).
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                                                        for
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                                                        associated
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Pred. No. 0;
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                                                        protein
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                                                     human tata-binding
                                                               protein
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ilarity 99.9%;
Conservative
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tches 2556;
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1199 1440 1200 TCCAGCAGTAACTTTTGGAGAACTTCAGGTGCAGCTATTTGTCTTCCATCTGTGAAACC CGTGGTTGCCTTACGACAACTTCTGCCTAACTCCCAGAGCTTCATCCAGCAATGTGTTCA 1020 AGCTGGAGTTGTGACACTTCATTCTGTGGGCCCAACTGCTGCAACAGGAGGAAGAACAGC GCAGACTTCTAGTGACATGGTCATTGCTACCTGTACTACAACAGTAACAACTTCTCCTGT GGTGACAACTACAGTGTCCTCAAGCCAGTCTGAAAAGTCAATTATTGTTTCTGGAGCAAC **AGCACCCAGAACTGTGTCAGTGCAAACTTTGAACCCACTTGCTGGTCCAGTGGGAGCAAA** AGCTGGAGTTGTGACACTTCATTCTGTGGGCCCAACTGCTGCAACAGGAGGAACAACAGC TGTTGTTTCCTTCTGCTGGACCACATCTGCAAGCCTGTTATTGGGACTCCAGTTCAAAT TCCAGCAGTAACTTTTGGAGAAACTTCAGGTGCAGCTATTTGTCTTCCATCTGTGAAACC CAAACTTGCCCAGCCGGGCCCTGTCCTTTCACAACCAGCTGGGATTCCAACAGGCAGTTC **AAGCAAGCAACTATTCTCATTGTTTCACGTAGTTCAGCAGCCTTCAGGAGGCAATGAAAA** ACAAGTGACCACAATTTCACATTCCTCAACATTGACCATTCAGAAATGTGGACAGAAGAC 1440 ACAAGTGACCACAATTCACATTCCTCAACATTGACCATTCAGAAATGTGGACAGAAGAG GATGCCAGTGAACACCATAATACCTACTAGTCAGTTTCCTCCAGCTTCCATTCTAAAGCA GATGCCAGTGAACACCATAATACCTACTAGTCAGTTTCCTCCCAGCTTCCATTCTAAAGCA AATTACCȚCTGCCTGGAAATAAAATTCTGTCACTTCAAGCATCTCCTACTCAGAAAATA GAATAAAAGAGAATGTAACATCATGCTTCCGAGATGAGGATGACATGATGATGACTT CTATGGCAGGGGTCAACCTTAATGAAGAAAATGCCTGCATCTTAGCAACAACTCTGAAT TGGTTGGCACACTCATTCAGTCATGTAAAGATGAACCATTTCTTTTATTGGAGCTCTAC 720 661 781 841 901 900 961 1021 1201 1261 1260 1321 1320 1381 1380 1441 1501 1500 1561 1560 1621 1681 1679 1741 721

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    Drosophila TATA-b
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ABL32588
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ABK83575
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  Transcription fact
DNA encoding novel
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TATA-binding prote
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Drosophila melanog
TATA-binding prote
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(without alignments)
11229.263 Million cell updates/sec
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1. /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

2. /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

3. /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

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Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Best Local Similarity 99.9%;
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                                  AAGCATTGTTGCACTGTCCTGAAATTTCAATTTCTGGAAAATAACACCAACATGAAAGAG
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                          AAAAGAGAATCTTAGACATTGGTAAAAAGCATGACATTACAGAACTTAACTCTGATGCTG
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TATA box-binding protein associated factor II 105; TAFII1105; catranscription factor; apoptosis; cytostatic; immunosuppressive; antiinflammatory; virucide; antiibacterial; ds.
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This DNA encodes a polypeptide comprising a (modified) fragment (I) of a TATA box-binding protein associated factor II 105 (TAFII105). A pharmaceutical composition comprising (I) or the polynucleotide or an inhibitor or antagonist of (I) is useful for treating cancers and inducing apoptosis in pathological cells. The composition is also useful for treating autoimmune diseases, inflammatory processes and viral or
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptide encoding TATA box binding protein associated factor II 105 useful for treating e.g. cancers and inducing apoptosis has a dominant negative effect on the normal biological activity of the binding
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RESULT 3 AAS73655 ID AAS73655 standard; cDNA; 3468 XX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chair reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and lits binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. Assoldly-Assysfet represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed security in the printed of the contraction of the printed of the contraction 
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medical imaging; diagnostic; genetic disorder; ss.
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                                                        novel human diagnostic protein #9459.
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Matches 2552; Conservative
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P-PSDB; ABG09468.
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This is the nucleotide sequence encoding the human TATA-binding protein (TBP) associated factor (TAF) designated TAFII130. The protein is a component of the TRID fraction required for reconstituting RNA polymerase II in vitro transcription activity. The encoded protein has an estimated mol. wt. of 130 kD by SDS-PAGE.

The invention relates to purified proteins involved in transcription by RNA polymerase which transcribes messenger RNA. RNA polymerase which transcribes messenger RNA. RNA polymerase TEILA by SDS-PAGE.

FNA. RNA polymerase II transcription proceeds in vitro upon addition of several nuclear fractions designated TEILA, B, D, E, F, H, I and J to RNA polymerase II holoenzyme. Fraction TFIID has been shown to contains a TBP and other TAFs. Purification of TFIID and separation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, TATA-binding protein; TBP associated factor; TFIID; holoenzyme;
RNA polymerase II; transcription; messenger RNA; nuclear fraction;
lambda-gtil; expression library; ds.
                                                                                                                                                                                                                                                         Screen for cpds, that bind human TATA-binding protein associated factor - by testing ability to bind to polypeptide fragments of the factor, useful as (ant)agonists of transcription factors involved
                                                                                                                          CAAAGCATTGTTGCACTGTCCTGAAATTTCAATTTCTGGAAAATAA-CACCAACATGAAA
                                                                                             TCTGAAGTGACCACTCCTCCTTCCACATCCTTGCTATTTACTGCCAAAGAAGACA
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Wang E, Weinzierl ROJ;
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                                                                                                     1377 TGTCTCGGCACAAGCAGCTGCTGCACAGAAAATAAACTCAAGGAGCCTGGGGGAGGTTC 1436
                                                                                                                      1646 CTTCCGAGATGAGGATGACATCAATGATGTGACTTCTATGGCAGGGGTCAACCTTAATGA 1705
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 from 30-250 kD
its components reveals 7 proteins ranging in size from 30-250 k
Serum raised against the TFIID fraction allowed cloning of the
genes from lambda-gtll expression libraries.
                                                    Length 3603;
                                                                     15;
                                                                     288; Indels
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                                   Sequence 3603 BP; 969 A; 961 C; 830 G; 843 T; 0 other;
                                                    DB 17;
                                                   Score 338.2; DB 17
Pred. No. 1.6e-84;
0; Mismatches 288
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63.9%;
                                                                     Conservative
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polypeptide, hTAFII130 (mol. weight 130kD). TAF peptides derived from hTAFII30 alpha, hTAFII30 beta, hTAFII40, hTAFII30, hTAFII100, https://doi.org/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.100/10.
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                                  TATA-binding protein associated factor; TAF; nuclear protein; RNA polymerase transcription; TATA-binding protein; TBP; initiation; ds.
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Pred. No. 1.6e-84;
0; Mismatches 288; Indels
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FATA-binding protein associated factor, hTAFII130 cDNA
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Wang E, Weinzierl ROJ;
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Matches 536; Conservative
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               1617 AAAACATGGTATAACGGAATTACATCCAGATGTAGTTATGTATCACATGCCACGCA
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                                                                           TATA-binding protein associated protein factors - and corresponding nucleotide sequence and deriv. antibodies,
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                                                                                                                                                                                                                                                                                                                                                                                gene expression associated with human pathology
                                                                                                                                 screening, diagnostics and therapeutics
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WPI; 1994-264019/32.
P-PSDB; AAR56494.
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1833 GACATTACAGAACTTAACTCTGATGCTGTGAACTTGATCTCCCAAGCAACACAGGAACGA 1892
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01810-ABL30511), expressed DNA sequences (ABL01810-ABL30511), expressed DNA
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2097 CAGACAGTTCACGCGACAAGAATCACGCGGGTCAACCTCAGGGACCTCATATTTTGTTT 2156
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                          2351 GGAACAGGAACGGGAGATGAAGTATTCTCGAGCTCTATACCTGGCCCTTCTGAAGTGA 2408
                                         2157 AGAAAATGAACGTGAGGCATTCACTGCTGCTCTACAAGCATTCCTTAAGTGA 2214
                                                                                                                                                                                               Drosophila melanogaster expressed polynucleotide SEQ ID NO 22751.
                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
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0; Mismatches 377; Indels
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11-JUL-2000; 2000US-0614150.
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GCCAAGAGTCGTTCTAATAAAGAAGATCCAGAACAGCTGAGATTAAAGCAGAAAGCCAAA 2132
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pharmaceutical; gene;
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GATGAGGATGACATCAATGATGTGACTTCTATGGCAGGGGTCAACCTTAATGAAGAAAT 1712
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     3247 TGTCGCAGTTCCATGCTGTTCAAGACATACCTCAAGTGATCGCTGCTGTTGCCCCATCAA 3305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The TATA-binding protein associated factor dTAFIIIIO (including specific antibodies and fusion products) are used in drug screening, diagnostics and therapeutics. They are used in the development of specific biochemical assays for screening compounds that agonise or antagonise selected transcription factors involved in regulating
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                                                                                                                                                                                                                               therapeutic; gene transcription regulation
                                                                                                                                                                                          TATA-binding protein-associated factor dTAFIII10 cDNA
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Weinzierl ROJ;
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Wang E,
                                                                                                                                                                                                                        TATA-binding
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                                                                                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
Drosophila and for elucidating cell signalling and cell-cell
                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Prosophila. The invention useful in developmental biology and in elucidating cell signalling and insectiods. Theractions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL0150-ABL30511), expressed DNA sequences (ABL016176-ABL30511), expressed DNA
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                                                                                                                                                                                                                                                                                                                         5.6%; Score 143.8; DB 23; Length 4559;
50.8%; Pred. No. 1.4e-29;
Live 0; Mismatches 377; Indels 6;
                                                 Claim 1; SEQ ID NO 6904; 21pp + Sequence Listing; English
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       CTACGAGGCCTTCTAGAAAACTGACTGCAATTGCTCAGCATCGAATGACTACTTACAAG 1952
                AACCTTCTTGCTTCTGG---GACATCCAGCCTGACAGCCACAAACAGTTGCATCGTCCA 2309
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                                                                                         CIGGACAAGGCCGAGCAGAAGCGACACGAGGAACIGGAGCGIGAGAIGCIGCIGCGGGCA 2964
                                                                                                                           GCCAAGTCACGGTCGAGGGTGGAAGATCCCGAGCCAGGCCAAGATGAAGGCGAGGCCAAG 3024
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nuclear fraction;
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93US-0013412.
93US-0087119.
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This is the nucleotide sequence encoding the Drosophila TATA-binding protein (TDP) associated factor (TAF) designated TAFIIIO. The protein is a component of the TFIID fraction required for reconstituting RNA polymerase II in vitro transcription activity. The encoded protein has an estimated mol. wt. of 110 kD by SDS-PAGE, a calculated mol. wt. based on sequence of the gene of 99.4 kD and an estimated protein. The invention relates to purified proteins involved in transcription by RNA polymerase II, the RNA polymerase which transcribes messenger RNA. RNA polymerase II transcription proceeds in vitro upon addition of several nuclear fractions designated TFIIA, B, D, E, F, H, I and J to RNA polymerase II holoenzyme. Fraction TFIID has been shown to contains a TBP and other TAFs. Purification of TFIID and separation of its components reveals 7 proteins ranging in size from 30-250 kD. Serum raised against the TFIID fraction allowed cloning of the corresp. genes from lambda-gtil expression libraries.
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                                                                        Screen for cpds. that bind human TATA-binding protein associated factor - by testing ability to bind to polypeptide fragments of th factor, useful as (ant)agonists of transcription factors involved
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50.7%; Pred. No. 4.1e-29;
+ive 0; Mismatches 378; Indels
                                                                                                                                                                                                               Examples; Column 27-36; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 50.7
Matches 395; Conservative
WPI; 1996-333245/33.
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AAT79604 encodes Drosophila TATA-binding protein associated factor (TAF) polypeptide, dTAFIIIO (mol. weight 110kD). TAF peptides derived from dTAFII30 alpha, dTAFII30 beta, dTAFII140, dTAFII60, dTAFII180, dTAFIII10, dTAFII150, their human equivalents and nucleic acids encoding them, are used to modulate transcription, including transcription initiation. TAFS are nuclear proteins involved in RNA polymerase I, II and III transcription. The peptides act by binding to a different TAF, an activator, or TBP (TATA-binding protein) or competitively inhibiting association of a TAF domain with another compound, typically a protein like TBP or another TAF, an activator, or DNA.
2253 AACCTTCTTGCTTCTGG---GACATCCAGCCTGACAGCCACCAAACAGTTGCATCGTCCA 2309
                               3204
                                                           2369
                                                                        2428
                                                                                                                                         3265 rereceaerrecargererreaacararecreaagrearecrecrecrecearcaa 3323
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used
                                                        2310 AGAATCACGAGAATCTGCCTCAGGGACTTGATATTTTGTATGGAACAGGAACGGGAGATG
                            3145 GGTTCAAGTGGCGGCGGAGTGCTAAGCAGCTCGGGATCTGCGCCGACGACGTTACGGCCT
                                                                                                               TATA-binding protein associated factor; TAF; nuclear protein; RNA polymerase transcription; TATA-binding protein; TBP; initiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding human TATA-binding protein associated (TAF) peptide(s) – for production of recombinant peptide(s), for modulating transcription of TAFs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4615 BP; 1394 A; 1199 C; 1091 G; 931 T; 0 other;
                                                                                                                                                                                                                                                                                                  TATA-binding protein associated factor, dTAFII110 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Column 35-40; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
538..3303
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dynlact BD, Hoey T, Wang E, Weinzlerl ROJ;
                                                                                                                                                                                                                AAT79604 standard; cDNA; 4615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-0188582.
93US-0013412.
93US-0087119.
96US-0646715.
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                                                                                                                                                                                                                                                                         (first entry)
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P-PSDB; AAW25028.
                                                                                                                                                                                                                                                                                                                                                                                      Drosophila sp.
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30-JUN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JAN-1994;
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Tjian R,
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DB 18; Length 4615;

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5.6%;

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2965 GCCAAGTCACGGTCGAGGGTGAAGATCCCGAGCAGGCCAAGATGAAGGCGAGGCCAAG 3024
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                                                GATGAGGATGACATCAATGATGTGACTTCTATGGCAGGGGTCAACCTTAATGAAGAAAT 1712
                                                                   2548 GGTGACGATGATATCAACGATGTTGCCGCCATGGGAGGTGTTAACTTGGCGGAGGGTCG 2607
                                                                                                                 1713 GCCTGCATCTTAGCAACAAACTCTGAATTGGTTGGCACACTCATTCAGTCATGTAAAGAT 1772
                                                                                                                                                                                                                                                                                                                  CTACGAGGCCTTCTAGAAAACTGACTGCAATTGCTCAGCATCGAATGACTACTTACAAG 1952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGATGCAACGCGCCGAAATGGAGGAGTTGCGTCAACGAGATGCCAATCTGACGGCGCTG 3084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACCTTCTTGCTTCTGG---GACATCCAGCCTGACAGCCACCAAACAGTTGCATCGTCCA 2309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2310 AGAATCACGAGAATCTGCCTCAGGGACTTGATATTTGTATGGAACAGGAACGGGAGGTG 2369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antifungal; fungal gene transcription; RPC34; POP3; TFA2; NAB2; MPT1; MTR2; BOS1; BOS1; POL30; RSA2; SQT1; MTW1; TFB1; SPC98; BFR2; RNA1; GCD7; SK16; NIP1; LCP5; NCE103; ECO1; ORC2; CNS1; YPD1; TIM10; SRB4; yeast; fungus; d8; gene.
                                                                                                                                       CAGCGAATTCTCGGCTGTA---CCGAAACATCGGCACGCAGATTCGATCCTGCAAGAT
                                                                                                                                                                                                     1953 GCAAGTGAAAATTACATCCTGTGTAGTGATACCAGGTCACAGCTCAAATTTCTTGAAAAG
2845 TTGGATCCACGCTATGAGCCCGCCAAGGATGTGCGCGGTCAGATTTCTCGAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACATTACAGAACTTAACTCTGATGCTGTGAACTTGATCTCCCAAGCAACACAGGAACGA
                                                                                                                                                                                                                                                                                   GGACTGGATGAGCCGTCGCAGGATGTGGCCGTTCTGATATCGCACGCCTGTCAGGAGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCAAGAGTCGTTCTAATAAAGAAGATCCAGAACAGCTGAGATTAAAAGCAGAAAGCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2133 GAGTTACAGCAATTGGAACTTGCACAGATACAGCATAGAGACGCTAAATCTCACAGCTCTT
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                  Indels
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 Pred. No. 4.1e-29;
0; Mismatches 378;
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50.7%;
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               Matches 395; Conservative
Best Local Similarity
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ABK32842
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ABN33770 standard; DNA; 60 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes a method of screening a candidate antifungal compound for interaction with essential proteins (EP) or for modulation of EP activity e.g fungal gene transcribtion. The proteins tested in the invention include RPC34, POP3, TFE2, NAB2, MPT1, MPT2, BOS1, POL30, RSA2, SQT1, MTW1, TFB1, SPC98, BFR2, RNA1, GCD7, SKI6, NIP1, LCP5, NCE103, ECC1, ONC2, CMS1, YPD1, TIM10 and SRB4 from S. cerevisiae, C. albicans and human homologues. The method involves contacting a culture with one or more test compounds and determining the effects on the growth or viability of the culture of cells which preferably comprises fungal cells or yeast cells. Preferably the identified compounds interact with, or modulate (preferably inhbit) activity of C. albicans EP. The inhibitor compounds identified by the method are useful for preventing or inhibiting fungal, particularly C. albicans growth in culture or in a mammal. The antifungal agents interact with essential fungal elements that can be used to treat fungal infection by preventing the growth and preferentially killing the fungal infection by preventing the growth and preferentially killing the fungal infection by preventing the protein cativity of mammallan homologues. This sequence encodes a target protein inced to test the antifungal compounds, described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                    Screening candidate antifungal compound for interaction with essential protein, modulation of essential protein activity, binding to essential protein, by contacting protein with test compound and determining effects
                                                                                                                                                                                                                                          Long F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1836 ACTGGCTTCATCTGGCAAGCAGTCTACAGAGACAGCAGCTAATGTGAAAGAGCTCGTGCA 1895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           556 TICICCGACAATGCTAGAAAATGTGAAGAAATGCAAGAACTTCCTTGCAATGTTAATAAA 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        616 ACTAGCATGTAGTGGATCACAGTCCCCTGAAATGGGGCCAAAATGTGAAGGAGCTGGTGGA 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       676 ACAACTITIGGAIGCAAAAAICGAAGCAGAAGAAITIACIAGGAAACIGIAIGIIGAACI 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAGTCTTCACCTCAGCCTCACCTGGTTCCTTTAAGAAAAGCGTGGTTGCCTTACG 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 24; Length 2307;
                                                                                                                                                                                                                     Komarnitsky S;
Haq T, Zhu S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAACTICIGCCIAACTCCCAGAGCTICATCCAGCAATGIGTICAGCAGAC 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 65.7%; Score 135.8; DB 24; Length Similarity 66.7%; Pred. No. 1.8e-27; Osservative 0; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2307 BP; 359 A; 969 C; 724 G; 255 T; 0 other;
                                                                                                                                                                                                                     Harris S,
Sanderson K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Figure 80; 522pp; English.
                                                                                                                                                                                                                   Desilva T,
Mccoy M, Sa
                                                                            28-JUN-2001; 2001WO-US20592.
                                                                                                                  29-JUN-2000; 2000US-215164P.
                                                                                                                                                                              (ANAD-) ANADYS PHARM INC.
                                                                                                                                                                                                                                    Mendillo M, Moore D, M
Davidov E, Thompson CM;
                                                                                                                                                                                                                   Moore J, Buurman ET,
                                                                                                                                                                                                                                                                                                  WPI; 2002-147962/19.
                                                                                                                                                                                                                                                                                                                     P-PSDB; AAU82954.
WO200202055-A2.
                                       10-JAN-2002
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massenger RNAs that populate a (sub-)transcriptome, where the canonic present into present into present into present into present into present into propulate a (sub-)transcriptom units that populate a genome. The library comprises several oligonuclectides, each capable of hybridising selectively to a set of messenger RNAs transcribted from a given transcription unit of the genome. Which encodes one or more messenger RNA splice variants. The oligonuclectide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised minical libraries to detect transcripts of a sub-transcriptome under a particular biological or pathology specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a patient suffering from a particular disorder. ABN27253 to ABN259589 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New oligonucleotide libraries comprising oligonucleotides which selectively Mybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-specific genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes oligonucleotide libraries for detecting
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Human spliced transcript detection oligonucleotide SEQ ID NO:6518.
                                                                              Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.
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Local Similarity 100.0%; Pred. No. 6.6e-07;
Les 60; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 60 BP; 17 A; 17 C; 11 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wasserman A, Mintz E, Mintz L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUL-2001; 2001WO-IB01903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-2000; 2000US-221607P.
02-MAY-2001; 2001US-287724P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-257383/30.
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                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                  developmental biology; cell signalling; insecticide;
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Pred. No. 2.5e-05
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                    BP
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ABL09422 standard; cDNA; 9525
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11-JUL-2000; 2000US-0614150
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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51.4%; Pred. No. 2.5e-05;
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0; Mismatches 149;
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3066 GGACTGGATGAGCCGTCGCAGGATGTGGCCGTTCTGATATCGCACGCCTGTCAGGAGCGC 3007
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Search completed: February 16, 2003, 22:28:41 Job time : 631 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

February 16, 2003, 20:54:50; Search time 16.4197 Seconds (without alignments) 2152.161 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-763-909-2 4264 1 GTLVTKVAPVSAPPKVSSGP......KZHQHERALFTIRTLITLTY 852

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched: Total number of hits satisfying chosen parameters:

112892

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt_40:* Database :

SUMMARIES

	Description	092750 homo sapien	homod	P47825 droso	P51610 homo sapien	_	P08640 saccharomyc	. Q02817 homo sapien	O88799 mus musculu	· Q02910 drosophila		 P39712 saccharomyc 	P32323 saccharomyc	Q9y493 homo sapien	P47033 saccharomyc			P46590 candida alb	P28968 equine herp	_	Q09624 caenorhabd1	P32768 saccharomyc	P38894 saccharomyc	P55200 mus musculu	Q05049 xenopus lae		P54674 dictyosteli	Q04893 saccharomyc	рошо	homo	homod	sacch	7	Q07284 epstein-bar
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38	PROMOTER RESPONSES TO VARIOUS ACTIVATORS AND REPRESSORS	S TO VARI	OUS ACT	TVAT	A CENTE	REPRESSORS	MEDI	WIT INC	
ဗ္ဗ	-1- SUBUNIT: TFIID IS COMPOSED OF TATA BINDING PROTEIN (TBP) AND	COMPOSEI	OF TAT	rA BIN	NDING PR	OTEIN (TBP) ANE	A C	
႘	NUMBER OF TBP-ASSOCIATED FACTORS (TAFS). TAFII105 MAY FORM	CIATED E	ACTORS	(TAF	3). TAFI	I105 MAY F	ORM		
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ខ្លួ	This SWISS-PROT entry is copyright. It is produced through a collaboration	is copyr	right. It is produ	it is	produce	ced through a collaboratic	a col	laborat	ion
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000268; 099721; 09Bx42; 09Bx40;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transcription intiation factor TFIID 135 kDa subunit (TAFII-135)
TAF4 OR TAF4A OR TAF2C1 OR TAF2C OR TAFII135 OR TAFII130.
Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
GTLVTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTIQFPANLQLPPGTVLIKSNSGPL
                MLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGT
                        TVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAA
                                                                            VQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGONVKKLVEQLLDAKIEAEEFTRK
                                                                                                                                       VTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTA
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Mengus G., May M., Carre L., Chambon P., Davidson I.;
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G -> GPG (IN REF. 2).
MISSING (IN REF. 3).
P -> L (IN REF. 3).
                                                                                                                                                                                                                                                                                                        30.7%; Score 1307.5; DB :
llarity 40.0%; Pred. No. 2.8e-60;
Conservative 103; Mismatches 200
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POLY-ASP.
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Matches 330;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Radron G.G., Worthan J.R., Yandell M.D., Zhang O., Chen L.X., Bratch G.G., Morthe M.D., Evander B.C., Chang O., Chen L.X., Bratch G.G., Change M. P., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Miklos G.L.G., Randon R.C., Baxter E.G., Helt G., Nolson C.R., Miklos G.L.G., Rallew R.M., Basu A., Baxnendale J., Baytaktarollu L., Beasley B.M., Beson K.Y., Bencos P.V., Berman B.P., Bhandari D., Bolahako S., Borkova D., Botchan M.R., Boule C., Davenport L.B., Davies P., Botchan M.R., Boule C., Davenport L.B., Davies P., Acherry J.M., Cawley S., Dallike C., Davenport L.B., Davies P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman W., Rabell B., Delcher A., Dangen P., Gabriellan A.E., Gaary N.S., Gabbatt W.M., Glasser K., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K., Alodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K., Jalali M., Kalush F., Karpen G. H., Wei M.-H., Ibeywan C., Jalali M., Kalush F., Karpen G. H., Ke Z., Kunison J.A., Kerchum K.A., Jalali M., Kalush F., Karpen G. H., Karits N.L., Liang Y., Lin X., Mattei B., McIntosh T.C., McLeod M.P., Drit V., Merchun K.A., Moy M., Wurphy B., Murphy L., Muzny D.M., Nelson D.L., Ablasco D., Mattei B., McIntosh T.C., McLeod M.P., Puri V., Reese M.G., Shore C., Siden Klamos I., Simpson M., Stupski M.P., Shu B., Ranger B., Spier E., Spradling A.C., Stapleron M., Stupski M.P., Shu B., Wallen S., Woldoge T., Worley K.C., Wu D., Yang S., Yao Q.A., Wallen S.W., Woldoge T., Worley K., Col. W., Wallen S., Wull D., Yang S., Zhon G., Zhan R., Hang X.H., Whore R., Worley K., Zhan M., Zhang G., Zhan G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kokubo T., Gong D. W., Roeder R.G., Horikoshi M., Nakatani Y.;
"The Drosophila 110-kDa transcription factor TFIID subunit directly
interacts with the N-terminal region of the 230-kDa subunit.";
proc. Natl. Acad. Sci. 0.S.A. 90:8896-5900(1993).
                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Wakaryota, Metazoca; Arthropda; Mandibulata; Pancrustacea; Hexapot
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 519-540; 597-616 AND 857-874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 398-406; 520-540 AND 860-877
                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning and functional analysis of Drosophila TAF110 reveal properties expected of coactivators."; Cell 72:247-260(1993).
                                                                                                                                                                                                                                                                                                                                                                                                           Hoey T., Weinzierl R.O.J., Gill G., Chen J.-L., Dynlacht B.D.,
                                                                                                                        subunit (P110)
T2D3_DROME STANDARD; PRT; 921 AA. P47825; p49845; O9VUY7; O1-FEB-1996 (Rel. 33, Created) O1-FEB-1996 (Rel. 33, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Transcription initiation factor TFIID 110 kDa FAFII-110) (110 kDa TBP-assoclated factor) TAFIII OR CG5444.
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MEDLINE=20196006; Pubmed=10731132;
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MEDLINE-93317591; PubMed-8327460;
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MEDLINE=93145326; Pubmed=7678780;
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P51610;
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                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@libe.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                   FUNCTION: TFIID IS A MÚLTIMERIC PROTEIN COMPLEX THAT PLAYS A CHETRALL FOCHFALL WEDLAYLING PROMOTER RESPONSES TO VARIOUS ACTIVATORS AND REPRESSORS. MAY FUNCTION AS A COACTIVATOR BY SERVING AS A SITE OF PROTEIN-PROTEIN CONTACT BETWEEN ACTIVATORS LIKE SPI (OR BID)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 NITSRPAVPANPQTVKICTVPNSSSQ------LIKKVAVTPVKKLAQIGTTVVTTVP 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----QCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVS---VQT
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                                                                                                                                   SUBUNT: TFIID IS COMPOSED OF TATA BINDING PROFEIN (TBP) AND NUMBER OF TBP-ASSOCIATED FACTORS (TAFS).
SUBCELLULAR LOCATION: Nuclear.
SIMILARITY: BELONGS TO THE TAF2C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQPAGIPTGSSSK---QLFSLFHVVQQPSGGNEKQVTTISHSS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 18.2%; Score 775; DB 1; Length 921; Best Local Similarity 29.6%; Pred. No. 7.2e-33; Matches 258; Conservative 128; Mismatches 308; Indels 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-GLN.
27E6852859872767 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRANSFAC;
FlyBase; FBgn0010280; is...
FlyBase; FBgn003894; TAF_hom.
SMART; SM00549; TAFH; I.
Transcription regulation; Nuclear protein.
66 82 POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L06861; -; NOT_ANNOTATED_CDS.
EMBL; S63550; AAB27433.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE003528; AAF49536.1; -. TRANSFAC; T02121; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99338 MW;
                                                                                                               AND TFIID COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       921 AA;
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SEQUENCE
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Wilson A.C., Peterson M.G., Herr W.;

"The HCF repeat is an unusual proteolytic cleavage signal.";

"The HCF repeat is an unusual proteolytic cleavage signal.";

"Genes Dev. 9:2445-248(1995).

"Genes Dev. 9:2445-248(1995).

"I FRANSACIVATION INTO INFECTION OF PERMISSIVE CELLS, THE HSV
TRANSACIVATION PROTEIN VPI6 ASSOCIATES WITH HCF. BINDING TO HCF
ACTIVATES VPI6 FOR ASSOCIATION WITH THE OCFAMER MOTE-BINDING
ROTIVATING TRANSCRIPTION OF THE HSV IMMEDIATE EARLY GENES.

"IO TO 150 KDA AND A MINOR 300 KDA POLYPEPTIDES RANGING FROM
ILO TO 150 KDA AND A MINOR 300 KDA POLYPEPTIDE. THE MAJORITY OF N-
AND C-TERMINAL CLEAVAGE PRODUCTS REMAIN TIGHTLY, ALBEIT
NONCOVALENTLY, ASSOCIATED.

"IO TO CACATION: Nuclear:
"SHORT FORM: MAY BE PRODUCED BY ALTERNATIVE SPLICING. IN THE
SHORT FORM: MAY BE PRODUCED BY ALTERNATIVE FAIL TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   715 LELAQIQHRDANLTATAAIGPRKKRPLE----SGIEGLKDNLLASGTSSLTATKQLHRP 769
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                                654
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SAANSFFQQSSMSSMYGDDDINDVAAMGGVNLAEESQRILGC-TENIGTQIRSCKDEVFL
                                                                                                                                                                                                                                                                                  595 FIGALOKRILDIGKKHDITELNSDAVNLISQATQERLRGLLEKLTAIAQHRMTTYKASEN
                                                                                                                                                                                                                                                                                                                                                                             655 YILCSDTRSQLKFLEKLDQLEKQRKDLEEREMLLKAAKSRSNKEDPEQLRLKQKAKELQQ
                                                                                              PTQKNRIKENVTSCFRDEDDINDVTSMAGVNLNEENACILATNSELVGTLIQSCKDEPFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Host cell factor Cl (HCF) (VP16 accessory protein) (HFC1) (VCAF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ø
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                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                  PTM: EXISTS AS A FAMILY OF POLYPEPTIDES THAT ARISE THROUGH CLEAVAGE AT ONE OR MORE CENTRALLY LOCATED SITES. CLEAVAGE OCCURS AT A DEFINED SITE, PPCE/THET, WITHIN THE HCF REPEAT.
PTM: GLYCOSYLATED; CONTAINS O-LINKED N-ACETYLGLUCOSAMINE RESIDUES. SIMILARITY: CONTAINS 5 KELCH REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RP---AVPAN-------PQTVKICTVP----NSSSQLIKKVAVTPVKKLAQ 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      676 LISNLGKVMSVVQTKPVQTSAVTGQASTGPVTQIIQTKGPLPAGTILKLVTSADGKPTTI 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                    DOMAIN: THE HCF REPEAT IS A HIGHLY SPECIFIC PROTEOLYTIC CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 TLVTKVAPVSAPPKVSSGPRLP-----IQ 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 FPAN-----VTRAETTSNI---TS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     617 VGTSVSSATNTSTRPIITVHKSGTV-TVAQQAQVVTTVVGGVTKTITLVKSPISVPGGSA
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                         TISSUE SPECIFICITY: HIGHLY EXPRESSED IN FETAL TISSUES AND THE ADULT KIDNEY. PRESENT IN ALL TISSUES TESTED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89; Mismatches 245; Indels 229;
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InterPro; IPR001798; Kelch.
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
Nuclear protein; Repect; Alternative splicing; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPROXIMATE REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99207FBE875204C0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R -> A (IN REF. 1).
S -> SVS (IN REF. 2).
P -> S (IN REF. 1).
A -> G (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HCF REPEAT 2.
HCF REPEAT 4 (
HCF REPEAT 4 (
HCF REPEAT 5.
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HCF REPEAT 8.
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HCF REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208841 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HGNC:4839; HCFC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A);
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564
603
1164
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MIM; 300019;
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REPEAT
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CONFLICT
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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SUBCELLULAR LOCATION: NUCLOAR.
DOMAIN: THE HCF REPEAT IS A HIGHLY SPECIFIC PROTEOLYTIC CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       984 SP-----TTEOPTATVTIADSGGGDVQPGTVTLVCSNPPCETHETGTTNTATTTVVA 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: UPON LYTIC INFECTION OF PERMISSIVE CELLS, THE HSV TRANSACTIVATOR PROTEIN VP16 ASSOCIATES WITH HCF. BINDING TO HCF ACTIVATES VP16 FOR ASSOCIATION WITH THE OCTAMER MOTIF-BINDING PROTEIN OCT-1. TO FORM A MULTIPROTEIN-DNA COMPLEX RESPONSIBLE FOR ACTIVATING TRANSCRIPTION OF THE HSV IMMEDIATE EARLY GENES (BY
                                                                                                                                                                                                                 LPSVKPVVSFCWDHICKPVIGTPVQIKL-AQPGPVLSQPA-GIPTGSSSKQLFSLFHVVQ 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        473 QPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASI------LKQITLPG 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NKILSLQASPIQKNRIKENVTSCFRDEDDINDVTSMAGVNLNEENACILAINSELVGTLI 585
                                                                                                                                                                                                                                                                               357 GITAGIGLLQISKPLVTSVA--NIVITVSLQPEKPVVSGTAVILSLPAVTFGETSGAAIC 414
                                                                                                                                                                                                                                                                                                                                                                                                                         948 TITMOPV------SQPTQVTLITAPSGVEAQPVHDLPVS------ILA 983
                                            736 ITTTQASGAGTKPTILGI-----SOSOSPSTT---KPGTTTIKTIP 773
                                                                                                                                                                                                                                                                                                             NSQSFIQQCVQQTSSDMVIATCTTTVTT----SPVVT----TTVSSSQSEKSI
                                                                                                                                     774 MSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAPAKIITAVPKIATGHGQQGVTQV
                                                                                                                                                                                      315 IVSGA----TAPRT----VSVQTLNPLAGPVGAK--AGVVTLHSVGPTAATG
----EMGONVKKLVEOLLDAKIEAEEFTRKLYVELKSSPOPHLVPFLKKSVVALROLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Host cell factor Cl (HCF) (VPL6 accessory protein) (HFC1) (VCAF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL (BY SIMILARITY).
PTM: EXISTS AS A FAMILY OF POLYPEPTIDES THAT ARISE THROUGH
CLEAVAGE AT ONE OR MORE CENTRALLY LOCATED SITES. CLEAVAGE (
AT A DEFINED SITE, PPCE/THET, WITHIN THE HCF REPEAT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Gmene K.I., Nakabepu Y., Nishimoto T.; Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2090 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 5 KELCH REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mesocricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    586 QSCKDEP 592
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HFC1_MESAU
                                                                                                                                                                                                                                                                                                                                                                          415
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518 -LKQITLPGNKILSLQASPTQKNRIKENVTSCFRDEDDINDVTSMAGVNLNEENACILAT 576

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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilentials.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 AQICTTVV------TTVPKP------140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          537 IGSNPOMSGMAALAAAAAATQKIPPSSA---PTVLSVPAGTTIVKT-----VAVTPGTTT 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 TRAETTSNITSRPAVPANPQT------VKICTVPNSSSQ---LIKKVAVTPVKKL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         707 TQIIQTKGPLPAGTILKLVTSADGKPTTIITTTOASGAGSKPTILGISSVSPSTTKPGTT 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 PNLKAENSAAVQINLSPTMLENVKKCKNFLAML-IKLACSGSQSPEMGQNVKKLVEQLLD 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 AKIEAEEFTRKL-YVELKSSP-QPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            819 PKIATGHGQQGVTQVVLKGAPGQPG-----AILRTVP-------MSGVR 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVGPTAATGGTTAGTGLLQTSKPLVTSVA--NTVTTVSLQPEKPVVSGTAVTLSLPAVTF 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   464 LFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASI----- 517
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 IATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLH 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406 GETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKL-AQPGPVLSQPA-GIPTGSSSKQ 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 VSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLVSPQQTV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          939 TAAGGLTTPIIIMQPV-----SQPIQVTLIIAPSGVEAQPVHDLPVS----
                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 238; DB 1; Length 2090;
; Pred. No. 0.00012;
84; Mismatches 219; Indels 226;
                                                                                                                                                                                                                                          KELCH 5.

8 X 26 AA APPROXIMATE REPEATS
HCF REPEAT 1.
HCF REPEAT 2.
HCF REPEAT 3.
HCF REPEAT 4 (DEGENERATE).
HCF REPEAT 5.
HCF REPEAT 6.
HCF REPEAT 6.
HCF REPEAT 6.
HCF REPEAT 7 (DEGENERATE).
HCF REPEAT 9.
HCF REPEAT 9.
                                                                                                                                                                                                                                                             APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                                                                                                   1423 1448 HCF
2090 AA; 214942 MW;
                                                                                         EMBL; D45419; BAA08258.1; -.
InterPro; IPR0013961; FN_III.
InterPro; IPR001798; Kelch.
Pfam; PF00041; fn3; 2.
Pfam; PF01344; Kelch; S.
SMART; SM00060; FN3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                       5.68; 21.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 147; Conservative
                                                                                                                                                                           Nuclear protein; Repeat
REPEAT 44 89
                                                                                                                                                                                                                                 265
313
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1182
1320
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1010
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from Saccharomyces cerevisiae.";
FEBS Lett. 239:179-184(1988).
-1- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-
glucose residues successively from non-reducing ends of the chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=SPX101-1C;
MEDLINE=89031230; PubMed=3141213;
Pardo J.W., Ianez E., Zalacain M., Claros M.G., Jimenez A.;
"Similar short elements in the 5' regions of the STA2 and SGA genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M16164; AAA35014.1; -.
EMBL; M16165; AAA35015.1; -.
EMBL; X13857; CAA32069.1; -.
PIR; N26877; N26877.
PIR; A26877; A26877.
SGD; S0001458; MUC1.
Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-S288C AB972;
Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D., Churcher C.M., Connor R., Copsey T., Dear S., Deviln K., Fraser J Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones P. Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V., Walsh S.V., Whitehead S.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-87194600; Pubmed-3106330;
Yamashita I., Nakamura M., Fukui S.;
Gene fusion is a possible mechanism underlying the evolution of
STAI."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                              AWYH_YEAST STANDARD; PRT; 1367 AA.
P08640; P080689;
01-806-1988 (Rel. 08, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
610-0CM-2001 (Rel. 40, Last annotation update)
910-0CM-2001 (Rel. 40, Last annotation update)
510-0CM-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with release of beta-D-glucose.
SIMILARITY: TO S.POMBE SPBC215.13.
SIMILARITY: SOME, TO S.POMBE SPCC285.13C.
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                                                             ----GNVVRVCSNPP 1079
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577 NSELVGTLIQSCKDEP
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                   "The human MUC2 intestinal mucin has cysteine-rich subdomains located both upstream and downstream of its central repetitive region."; J. Biol. Chem. 267:21375-21383(1992).
                                                                                                                                                                 Gum J.R. Jr., Hicks J.W., Toribara N.W., Rothe E.-M., Lagace R.E., Kim Y.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUCIN 2.
APPROXIMATE REPEATS.
                                                                                                                                [3]
SEQUENCE OF 1343-1895 AND 4176-4195 FROM N.A.
                           SEQUENCE OF 626-1895 AND 4196-5179 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSO0022; EGF_1; UNKNOWN_1.
PROSITE; PS01185; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS01208; VWFC; 2.
  Biol. Chem. 269:2440-2446(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002400; GF_cysknot.
InterPro; IPR002919; TIL_Cysrich.
InterPro; IPR001007; WWF_C.
InterPro; IPR001046; WWF_D.
Pfam; PF00007; Cys_knot; 1.
Pfam; PF000093; wwc; 1.
Pfam; PF00094; wwd; 4.
                                         TISSUE=Colon;
MEDLINE=93016075; PubMed=1400449;
                                                                                                                                                           MEDLINE-91358717; PubMed=1885763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000359; Cys_knot.
InterPro; IPR000561; EGF-11ke.
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SMART; SM00214; VWC; 2.
SMART; SM00216; VWD; 4.
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InterPro;
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REPEAT
    22;
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                                                                                                                                                           110 -TPVKKLAQIGTTVVTT-----VPKPSSVQS-----VAVPTSVVTVTPGKPLNT- 152
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                                                                                                                                                                                                                        SSSAPVTSSTTESSSAPVTSSTTESSSAPVPTPSSSTTESSSAPV 737
                                                                                                                                                                                                                                                                                                      ------VTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSPTMLENVKKCKNFLA 201
                                                                                                                                                                                                                                                                                                                                                                                                            PFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSP----VVTTTVSSSQSE 311
                                                                                                                      Gaps
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                                                                                                                                              2 TLVTKVAPVSAPPKVSSGPRLPAP-----QIVAVKAPNTTTIQFPANLQLPPGTVLIK 54
                                                                                                                                                                                                                                                                  MLIKLACSGSQS-----PEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLV
                                                                                                                                                                                                                                                                                                                                                                                  ---APVSSSTTESSVAPVPTPSSSSNITSSAPSSIPFSSTTESFSTGTTVTPSSSK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 368 SKPLVTSVANT----VTTVSLQPEKPVVSGTAVTLSLPAVT--FGETSGAAIC----
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                      817 817 N-LINKED (GLCNAC. . .) (POTENTIAL)
874 874 N-LINKED (GLCNAC. . .) (POTENTIAL)
1367 Aa; 136110 MW; 91C00E2DBD61AA9D CRC64;
                                                                                                                  77; Mismatches 240; Indels 134;
                                                                                          Score 220; DB 1; Length 1367;
Pred. No. 0.00057;
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            GLUCOAMYLASE S1/S2.
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Last annotation update
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01.02817; 014878;
01.5078-1994 (Rel. 29, Created)
01-NOV-1997 (Rel. 35, Last sequence upda
15.5078-2002 (Rel. 41, Last annotation up
Mucin 2 precursor (Intestinal mucin 2);
MUC2 OR SMUC.
 POTENTIAL.
                                                                                          5.2%;
                                                                                                     Similarity 22.5%;
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4203 TAPIAEL--TISNPPPESSTPQTSRSTSSPLT----ESTILLSTLPPAIEMISTAPPST 4255
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   198 NFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFL 257
                                                                                                                                     258 KKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTT-----TVTTSPVVTTTVS 306
                      ----VPNSSSQLIKKVAVTPVKKLAQIGTTVVTTVPKPSSVQS-VAVP-TSVVTVTP--- 146
                                                                                                                                                                                                                ----TAGTGLLQTSKPL-----VTSVANTVTTVSLQP------EKPVVSGTAVTLSL 400
                                                           -----GKPLNTVTTLKPS-SLGASSTPSNEPNLKAENSAAVQINLSPTMLENVKKCK 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Testis;
MEDLINE-97271566; PubMed-9126492;
Gao Z., Harumi T., Garbers D.L.;
"Chromosome localization of the mouse zonadhesin gene and the human
                                                                     307 SSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAK----AGVVTLHSVGPTAATGGT----
                                                                                                                                                                                                                                                                                         SKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIP----TSQFPPAS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zonadhesin gene (ZAN).";
Genomics 41:119-122(1997).
-!- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA
OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
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Last annotation update)
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J. Biol. Chem. 273:3415-3421(1998)
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TISSUE-Testis;
MEDLINE-98123114; Pubmed-9452463;
                                                                                                                                                                                                                                                                                                                                                                                               ZAN_MOUSE STANDARD; PR 08879; 008647; 16-OCT-2001 (Rel. 40, Last seque 16-OCT-2001 (Rel. 40, Last seque 20nadhesin precursor.
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85CD7571FB9A5663 CRC64;
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SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.

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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE APICAL REGION OF THE SPERM HEAD.
TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00022; EGP_1; 1.
PROSITE; PS01186; EGF_2; 18.
PROSITE; PS00740; MAM_1; FALSE_NEG.
PROSITE; PS50066; MAM_2; FALSE_NEG.
Signal; Glycoprotein; Transmembrane; EGF-like domain; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 X HEPTAPEPTIDE REPEATS (APPROXIMATE) (MUCIN-LIKE DOMAIN).
                                TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS. DOMAIN: THE MAM DOMAINS PROBABLY MEDIATES SPERM ADHESION TO THE
                                                                             DOMAIN: DURING SPERM MIGRATION THROUGH THE REPRODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS. DOMAIN: THE VWFD DOMAIN 2 MAY MEDIATE COVALENT OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2). SIMILARITY: CONTAINS 25 WMFD DOMAINS. SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
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WWED 9 (PARTIAL).
WWED 10 (PARTIAL).
WWED 11 (PARTIAL).
WWED 13 (PARTIAL).
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InterPro; IPR0003645; FolN.
InterPro; IPR000998; MAM domain.
InterPro; IPR00338; TILa_Cysrich.
InterPro; IPR001308; TILa_Cysrich.
InterPro; IPR001846; VWF_C.
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Pfam; PF00629; wwd; 3.
Pfam; PF01826; TIL; 25.
Pfam; PF01345; TIL2; 25.
SWART; SW00181; EGF; 2.
SWART; SW00274; FOLN; 11.
SWART; SW00137; MAM; 2.
SWART; SW00216; VWC; 17.
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MEDLINE-3165730, PubMed-8434015;

MA Ballinger D.G., Xue N., Harshman K.D.;

Ballinger D.G., Xue N., Harshman K.D.;

"A Drosophila photoreceptor cell-specific protein, calphotin, binds calcium and contains a leucine alpear.";

Proc. Natl. Acad. Sci. U.S.A. 90:1536-1540(1993).

"I FUNCTION: MIGHT FUNCTION AS A CALCIUM-SEQUESTERING "SPONGE" TO REGULATE THE AMOUNT OF FREE CYTOPLASMIC CALCIUM. IT BINDS 0.3 MOLOF OF CONTAIN: HOMODIMER (PROBABLE).

"I SUBCELLULAR LOCATION: CYTOPLASMIC; HYPODENSE COMPARTMENT.

"I DEVELOPMENTAL STAGE: EXPRESSED EARLY IN PHOTORECEPTOR CELL DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Canton-S;
MEDLINE=93165729; PubMed=8094559;
Martin J.H., Benzer S., Rudnicka M., Miller C.A.;
"Calphotin: a Drosophila photoreceptor cell calcium-binding protein.";
Proc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).
                                                                                                                                               ---LQASPTQKNRIKENVT----SCFRDEDDI-NDVTSMAG--VNLNEENACILATNSE 579
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Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                        PTEETISTEVTTVSPEETTLPTEVPTVSTEVTNVS-----PEETSVPPEETI----
                         339 AKAGVVTLHSVGPTAATGGTTAGTGLL----QTSKPLVTSVANTVTTVS-----LQPEK
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(Rel. 28, Last annotation update)
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01-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 ASSTPSNEPNLKAENSAAVQINLSPTMLE-------NVKKCKNFLAMLIKLACS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GTLVTKV-APVSAP-----PKVSSGPRLPAP----QIVAVKAPNTTIQFPANLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 LPPGTVLIKSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNS-SSQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 KKVAVTPVKKL-AQIGTTVVTTVPKPSSVQSVAVPTSVVT-VTPGKPLNTVTTLKPSSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 GSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270 NSQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279 VSAS-----TEPPVAAATLTTAPET-PALAPVVAESQVAANTVVATPPTP-APEPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 VVATTPVPATL-AVTDPDVTASAV--PELPPVIAPSPVPSAVAETPVDLAPPVLPPVAAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330 LNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         390 VVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVS------FCWDHICKPVIGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 0.0015;
82; Mismatches 242; Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 865;
                                                                                                                                                                                                        A -> AVAPAVVA (IN REF. 2).
I -> Y (IN REF. 2).
I -> V (IN REF. 2).
T -> A (IN REF. 2).
VO -> PP (IN REF. 2).
VO -> PP (IN REF. 2).
I -> V (IN REF. 2).
S -> T (IN REF. 2).
S -> T (IN REF. 2).
S -> T (IN REF. 2).
C -> T (IN REF.
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                                                                                                                                                                                                    36
43 43
64 64
76 76
100
6 127
6 154
160
534
693
703
721
84781 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                497 GOKTMPVNTIIPTSQFPPASI 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -VSTPPTTASVPETTAPPAAV 493
EMBL; LO2111; AAA28405.1; -.
EMBL; LO5080; AAA28420.1; -.
PIR; A47282; A47282.
                                                                                  PIR; A47282; A47282.
FlyBase; FBgn0010218; Cpn.
Calclum-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 21.77
Matches 122; Conservative
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721 7
865 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., Fortin N., 7., Davies C.K.,
                                                                                                                                                                                                                                                                     898 TS-EATTTA-----TISCEDNEEDITSTETELLTLETTITSCSGGICTTLMSPVTTIN
  EISSSPESSTAITSTSTISFIAERTSSLYLSSSNMSSFTLSTFT----VSQSIVSSFSMEP
                                                                               410 GAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVLSQPAGIPTGSSSKQLFSLFH
                                                                                                                                                                                                                                        470 VVQQPSGGNEKQVTTI-SHSSTLTIQKCGQKTMPVNTIIPTSQFPPASILKQITLPGNKI
                                                                                                                                                                                                                                                                                                                               529 LSLQASPTQKNRIKENVTSCFRDEDDIND------VTSMAG-----VNLN
                                                352 TAATGGTTAGTGLLQTSKPLVTSV--ANTVTTVSLQPEKPVVSGTAVTLSLPAVTFGETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Hypothetical 138.1 kDa protein in FLO9-GDH3 intergenic precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-S288C / AB972;
MEDLINE-95249563; PubMed=7731988;
BUSSEY H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortil Hall J., Obellette B.F.F., Keng T., Barton A.B., Su Y., Davistorms R.K.;
"The nucleotide sequence of chromosome I from Saccharomyces
                                                                                                                                                                           Glycoprotein; Transmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL. HYPOTHETICAL PROTEIN YAL063C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ??
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
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InterPro; IPR001389; Flocculin.
Prfam: PF00624; Flocculin; 13.
Hypothetical protein; Glycoprote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    950 AKANTLTTTTTTTTTT 970
                                                                                                                                                                                                                                                                                                                                                                                                                        568 EENACILAINSELVGILIQSC 588
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388
775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAGGERAR RANK OCCOSTILLE FETTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      651 FTRSTVSAKSDVSGNSS-----TOSTTFFATPSTPLAVSSTVVTSSTDSVSPNIPFS 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || | : :|:| | : |::| | | | | 369 VTSSAEPTTVSEFTSSVE-PTRSSQVTSSAEPTTVS 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 -------MLVSPQQTVTRAETTSNI----TSRPAVPANPQTVKICT---VPNSSS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           428 EFTSSVEPTRSSQVTSSAEPTTVSEFTSSVEPTRSSQVTSSAEPTTVSEFTSSVEPTRSS 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 LKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPVVTTT------- 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 VTKVAPVSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPL--- 60
                                                                                                                                                                                                                                                                       543 VSSFGSTFSEITSSAEPLSFSKATTSAESISSNQITISSELIVSSVITSSSEIPSSIEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 IKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEE-----FTRKLYVELKSSPOPHLVPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     603 TSSGISSSVEP----TSLVGPSSDESISSTESLSATSTFTSAVVSSSKAA----DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 -SSLGAS---STPSNEP-----NLKAENSAAVQINLS-----PTMLENVKKCKNFLAML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -VSSSQSEKSIIVSGAT---APRTVSVQ-----TLNPLAGPVGAKAGVVTLHSVGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
CELL WALL PROTEIN DAN4.
REMOVED IN MATURE FORM (POTENTIAL).
                                             Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
4.8%; Score 205.5; DB 1; Length 1161;
Best Local Similarity 22.5%; Pred. No. 0.0026;
Matches 153; Conservative 102; Mismatches 251; Indels 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1161 AA; 118358 MW; 7954C15D69F0CA58 CRC64;
                                                                                                                                                                                     Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases
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Pfam; PF00660; SRP1_TIP1; 1.
PROSTIE; PS00724; SRP1_TIP1; 1.
Cell wall; Glycoprotein; Membrane; GPI-anchor; Signal.
                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacchasomycetales; Saccharomycetaceae; Saccharomyces.
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/ TIP1 FAMILY.
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                                                                                                                                                                                                                                                         MEDLINE=21113168; PubMed=11160904;
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DAN4 OR YJR151C OR J2223
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                                                                                                                                     SEQUENCE FROM N.A.
                                                                                       NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Potential)
                                                                                                                                                               Scarcez T.;
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                                                                                                                                                                                                                   VTRAETT------SNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVK 113
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                                    (GLCNAC. . .)
                                                                        (GLCNAC. . .)
                         (GLCNAC. . .)
                                                                                                                                Best Local Similarity 19.0%; Pred. No. 0.0038;
Matches 142; Conservative 114; Mismatches 276;
                                                             (GLCNAC.
                                                                                                                    Score 203.5; DB
Pred. No. 0.0038;
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                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: MEDIATES THE CELL SURFACE ATTACHMENT OF THE A-AGGLUTININ SUBUNIT. S.CEREVISIAE A AND ALPHA CELLS EXPRESS THE COMPLEMENTARY CELL SURFACE GLYCORROTEINS A-AGGLUTININ AND ALPHA-AGGLUTININ, RESPECTIVELY, WHICH INTERACT WITH ONE ANOTHER TO PROMOTE CELLULAR AGGREGATION DURING MATING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A-AGGLUTININ ATTACHMENT SUBUNIT.
2 X APPROXIMATE REPEATS.
1-1.
1-2.
18 X APPROXIMATE TANDEM REPEATS, SER/THR-RICH.
                                                                                                                                                                                                                                                                                                          JQ
                                                                                           [1]
SEQUENCE FROM N.A.
MEDLINE-91304412; PubMed=2072914;
ROY A., Lu C.F., Marykwas D.L., Lipke P.N., Kurjan J.;
ROY A., Lu C.F., Marykwas D.E., Lipke P.N., Kurjan J.;
"The AGA1 product is involved in cell surface attachment of the
"The AGA1 product is involved in cell surface attachment of the
Saccharomyces cerevisiae cell adhesion glycoprotein a agglutinin.";
MOL. Cell. Biol. 11:4196-4206(1991).
                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR AND/OR BY CARBOHYDRATE-MEDIATED COVALENT CROSS-LINKS (POSSIBLE).
                                                                                                                                                                                                                                                                                                    SUBUNIT: CONTAINS AT LEAST A BINDING SUBUNIT DISULFIDE-LINKED A CORE SUBUNIT.
01-ocr-1996 (Rel. 34, Last annotation update)
A-agglutinin attachment subunit precursor.
AGA1 Or YNRO44W OR N3431.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fung1; Ascomycota; Saccharomycotins; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M60590; AAA34382.1; -.
EMBL; Z71659; CAA96325.1; -.
PIR; S17031; S17031.
PIR; A41258; A41258.
SGD; S0005327; AGA1.
Glycoprotehi, Cell adhesion; Signal; GPI-anchor; Repeat; Pheromone response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.
70420C853B0B01F8 CRC64;
                                                                 Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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Pred. No. 0.0023;
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Best Local Similarity

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                                                                                                                                                                                                                            -i- FUNCTION: BINDS IN A SPECIES-SPECIFIC MANNER TO THE ZONA PELLUCIDA OF THE EGG. MAY BE INVOLVED IN GAMETE RECOGNITION AND/OR
                                                                                                                                                                                                                                                                                                        - SUBUNIT: PROBABLY FORMS COVALENT OLIGOMERS.
- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, EXCLUSIVELY ON THE APICAL REGION OF THE SPERM HEAD (BY SIMILARITY).
- TISSUE SPECIFICITY: IN TESTIS; PRIMARILY IN HAPLOID SPERMATIDS.
- DOMAIN: THE MAM DOMAINS PROBABLY MEDIATE SPERM ADHESION TO THE ZONA PELLUCIDA.
- DOMAIN: DURING SPERM MIGRATION TRROUGH THE REPRODUCTIVE TRACTS, THE MUCIN-LIKE DOMAIN MIGHT INHIBIT INAPPROPRIATE TRAPPING OF SPERMATOZOA OR PROMOTING ADHESION TO THE OVIDUCTAL ISTHMUS.
- DOMAIN: THE VWED DOMAINS 2 AND 3 MAY MEDIATE COVALENT OLIGOMERIZATION (BY SIMILARITY TO HUMAN INTESTINAL MUCIN MUC2).
- SIMILARITY: CONTAINS 4.5 WAFD DOMAINS.
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                                                                                                                     Gao Z., Harumi T., Garbers D.L.; "Chromosome localization of the mouse zonadhesin gene and the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell adhesion; Repeat.
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MIW, 602372.
MIW, 602727.
InterPro; IPR000561; EGF-11ke.
InterPro; IPR002998; MAM_domain.
InterPro; IPR002919; TIL_Cyarich.
InterPro; IPR003138; TILa_Cyarich.
InterPro; IPR001846; VWF_D.
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                                                                                     MEDLINE-97271566; PubMed-9126492;
                                OF 2338-2700 FROM N.A.
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Pfam; PF00629; MAM; 4.
Pfam; PF00629; TIL; 5.
Pfam; PF021345; TILa; 4.
SMART; SM00116; VWD; 1.
PROSITE; PS01186; BGF_2; 3.
PROSITE; PS00740; MAM_1; 1.
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                                                                                                                                                                          zonadhesin gene (ZAN).";
Genomics 41:119-122(1997).
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Tsui L.C., Rosenthal A.;

"Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTLI loci reveals 17 genes.";

Genome Res. 8:1060-1073(1998).
                                                                                                                                                                       97
                                                       VTKVAPVSAPPKVSSGPRLPAPQIVAVKAPN-----TTTIQFPANLQ----LPPGTVLI 53
                                                                                          : | : | | : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                    KSNSGPLML-----VSPQ----QTVTRAET---TSNITSRPAVPANP--QTVKICTVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399 FTTVSGVTTMYTTWCPYSSESETSTLTSMHETVTTDATVCTHESCMP------
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
Matches 144; Conservative 120; Mismatches 309; Indels 134;
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Zonadhesin (Fragment).
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SGD; SO003614; YUL078C.
InterPro; IPR001283; Allrgn_V5/Tpx1.
Pfam; PF00188; SCP; 1.
ProDom; PD000542; ALLrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 249353; CAA89370.1; -. EMBL; X83502; CAA88492.1; -. EMBL; X88851; CAA61314.1; -. HSSP; P04284; 1CFE.
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DOMAIN 166 37
                                                                                              Zimmermann F.K.;
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                                                                                                                                                        34;
                                                                                                                                                                                                                                  372 GTMLELLLGSPAGSPPIPLWKRVGSQRPYWQNTSVTVPSGHQQPWQLIFKGIQGSNTASV 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        611
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                                                                                                                                                                                                                                                                              39 QFPANLQLPPGTVLIKSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPN 98
                                                                                                                                                                                              1 GTLVTKV--APVSAPP------KVSSGPRLPAPQIV-AVKAPNTTTI 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSLGASSTPSNEPNLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGSQSPEMGQ
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                                                                                                                                                                                                                                                                                                                                                                                                 523 ----- NMPSEKPTIPSE-----KPTILTEKPTIPS-----EKPTIPSEKPTI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFI--Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384 LQPEKPVVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGT----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EK-----QVTTISHSSTLTIQKCGQKTMPVNTIIPT-----SQFPPASILKQITLPGNKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 779 EKLTIPTEKLTIPTEKPTIPIEETTISTEKLTIPTEKPTISPEKPTIS----TEKPTIPT
  (POTENTIAL).
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Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                   91; Mismatches 268; Indels 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical 89.2 kDa protein in SCP160-SMC3 intergenic region.
                                                                                                           ; DB 1; Length 2700; 0.017;
  N-LINKED (GLCNAC. . .) (POTENT NNQKMA -> RAGPGP (IN REF. 1).
2505 2505 N-LINKED (GLCNAC. . .) (POT: 2374 NNQKWA -> RAGPGP (IN REF. 1 2700 2700 2700 AA; 293013 MW; 80E60CC0B12277B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       881 AA
                                                                                                           4.7%; Score 199; 22.1%; Pred. No. 0
                                                                                                                                                     Conservative
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SEQUENCE FROM N.A.
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                                                                                                                               Best Local Sımı
Matches 147;
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P47033;
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SEQUENCE
CARBOHYD
                                                                                                         Query Match
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ID YJH8_X
ID YJH8_X
ID 01-FEB
DT 01-FEB
DT 16-OCT
DE HYDOTE
GN YJLO7F
OC SUCCHE
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                                                                                                                               "Sequence analysis of a 33.1 kb fragment from the left arm of Saccharomyces cerevisiae chromosome X, including putative proteins with leucine 12ppers, a fungal 2n(II)2-Cys6 binuclear cluster domain and a putative alpha 2-SCB-alpha 2 binding site."; Yeast 11:681-689(1995).
-i- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1; INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 KICTVPNSSSQLIKKVAVTPVK--KLAQIGTTVVTTVPKP-----SSVQSVAVPTSVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 ---VTPGKPLNTVTTLKPSSLGASSTPSNEPNLK-----AENSAAVQINLSPTMLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 881;
                                                  Baur
MEDLINE-96093911; PubMed-7483841;
Miosga T., Schaaff-Gerstenschlaeger I., Chalwatzis N., Bau
Boles E., Fournier C., Schmitt S., Velten C., Wilhelm N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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SEQUENCE 881 AA; 89152 MW; 37DBAC660CA9D12A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 4.6%; Score 197.5; DB 1; Best Local Similarity 21.0%; Pred. No. 0.0046; Matches 145; Conservative 87; Mismatches 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01009; SCP_AG5_PR1_SC7_1; 1. PROSITE; PS01010; SCP_AG5_PR1_SC7_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SATSATATASESSTTSQVSTASETISTLGTQNFTTTGSLLFPALSTEMINTTVVS--RKT 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQIGTIVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENSAAVQINLS--PTMLENVKKCKNFL---AMLIKLACSGSQSPEM-----GQNVKKLVE 225
                                                                                                                                                      713 TNTVVPASSFPSTT----TTCLENDDTAFSSIYTEVNAATIINPGETSSLASDFATSEKP 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            916 LIISTEVCS------HSKCVPTVITEVVTSK-------GTPSNGHSSQT 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TLVTKVAPVSAP-PKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPL 60
                                                                                660 NTITASCSTDSNFPTSAASSTDETAFTRTISTS-----CSTLNGASTQT-SELTTSPMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMP
                                                                                                                       VNTIIPTSQFPPASILKQITLPGNKILSLQASPTQKNRI-----KENVTSCFRDEDDI
                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.6%; Score 197.5; DB 1; Length: 21.1%; Pred. No. 0.01;
Live 106; Mismatches 327; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1609 AA; 166049 MW; 7D66AD7F85A7B852 CRC64;
TFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVL----
                                                                                                                                                                                                                                                                                                                                             01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Factor induced gene 2.
FIG2 OR YCR089W OR YCR1002.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi, Ascomycota; Saccharomycottina; Saccharomycetanes; Saccharomycetases
                                                                                                                                                                                                                                                                                                 PRT; 1609 AA
                                                                                                                                                                                                         NDVTSMAGVNLNEENACILATNSELVGTL 584
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                                                                                                                                                                                                                                                                                                                                01-MAY-1992 (Rel. 22, Created)
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                                                                                                                                                                                                                                                                                                 STANDARD;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                             FIG2_YEAST
P25653;
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Matches
                                                                                                                                                                                                                                                                  RESULT 15
FIG2_YEAST
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226 QLLDAKIEAEEFTRKLYVELKSSPQPHLVPFL---KKSVVALRQLLPNSQSFIQQCVQQT 282
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61 MLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGT 120
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Patent No. 5710025
GENERAL INFORMATION:
APPLICANT: Dikstein, Rivka
APPLICANT: Tjian, Robert
TITLE OF INVENTION: B-Cell Specific Transcription Factor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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99.9%; Pred. No. 9.6e-319;
11ve 0; Mismatches 1;
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US-07-757-022B-42
US-07-757-022B-142
US-07-757-022B-50
US-07-757-022B-60
US-07-757-022B-60
US-07-757-022B-48
US-07-757-022B-40
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US-07-757-022B-40
US-07-757-022B-40
US-07-757-022B-40
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US-07-741-940-2
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US-08-452-654-2
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APPLICATION NUMBER: US/08/725,012
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B97-005
TELECOMONICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 801 amino acids
TYPE: amino acid
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MOLECULE TYPE: protein

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                                                                                                                                      February 16, 2003, 21:59:29 ; Search time 21.8929 Seconds
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                 GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                   COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NORTH:
APPLICATION NOTHER:

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MLVSPQQTVTRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGT 120
                                                    TVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAA 180
                                                                             LYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMVIATCTTTVTTSPV 300
                                                                                                                                                                                                                                                                                             VTTTVSSSQSEKSI: IVSGATAPRTVSVQTLNPLAGPVGAKAGVVTLHSVGPTAATGGTTA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAVTFGETSGAAICLPSVKP 420
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APPLICANT: Comai, Lucio
APPLICANT: Comai, Lucio
APPLICANT: Horiact, Brian D.
APPLICANT: Horiact, Brian D.
APPLICANT: Horiact, Siegfried
APPLICANT: Tanese, Nacko
APPLICANT: Weinzieri, Robert O.J.
APPLICANT: Weinzieri, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS, TITLE OF INVENTION: UGLEIC ACIDS ENCODING TAFS AND METHODS OF NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
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STREET: 4 Embarcadero Center, Suite 3400
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Sequence 16, Application US/08188582
Patent No. 5534410
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CITY: San Francisco
STATE: California
COUNTRY: USA
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284 SDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGV 343
62 LVSPQQTVTR-----AETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKL 115
                                                                                                                                                                                                                                 228 IDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ----TS 283
                                                                                                                                                                                                                                                                                                                                                                                           344 VTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVVSGTAVTLSLPAV 403
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                                                                         116 AQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVT--TLKPSSLGASS----TPS
                                                                                                                                                     169 NE-PNLKAENSAAVQINLSPIMLENVKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQL
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APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Naoko
APPLICANT: Tanese, Naoko
APPLICANT: Wang, Edith
APPLICANT: Wang, Edith
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS (NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  756 GISSLTATKQLHRPRITRICLRDLIFCMEQEREMKYSRALYLALLK 801
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APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
APPLICANT: Dynlact, Brian D.
APPLICANT: Hoey, Timothy
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US-08-188-582-2
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                                  | :|| PTATTSGIRATLTPTVLAPRLPQP-----PQNPTNIQ---NFQLPPGMVLVRSENGQLL 118
                641 IAQHRMTTYKASENYILCSDTRSQLKFLEKLDQLEKQRKDLEEREMLLKAAKSRSNKEDP 700
                                                                                            EQLRLKQKAKELQQLELAQ1QHRDANLTATAAIGPRKKRPLE----SGIEGLKDNLLAS 755
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APPLICANT: Hoey, Timothy
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Naoko
APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
NUMBER OF SEUUROGES: 36
                                                                                                                Query Match 30.7%; Score 1307.5; DB 1; Length 737; Best Local Similarity 40.0%; Pred. No. 1.3e-98; Matches 330; Conservative 103; Mismatches 200; Indels 193;
                                                                                                                                                                                          E: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT 4 Embarcadero Center, Suite 3400
                                                                                                                                                                        GTSSLTATKQLHRPRITRICLRDLIFCMEQEREMKYSRALYLALLK 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 09-MAY-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/188,582
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/A
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/08646715
Patent No. 5637686
GENERAL INFORMATION:
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TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 16:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        California
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STREET: 4 E
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APPLICANT: C
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                                                                                                                                                                                                                                                                                           US-08-646-715-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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APPLICANT: Under Comal, Lucio
APPLICANT: Opnlact, Brian D.
APPLICANT: Dynlact, Brian D.
APPLICANT: Hopert, Siegfried
APPLICANT: Hopert, Siegfried
APPLICANT: Tanese, Nacko
APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
         655 YILCSDTRSQLKFLEKLDQLEKQRKDLEEREMLLKAAKSRSNKEDPEQLRLKQKAKELQQ 714
                                                                                                                                                                                                                                                             715 LELAQIQHRDANLTATAAIGPRKKRPLE----SGIEGLKDNLLASGTSSLTATKQLHRP 769
                                                                                                                                                                                                                                                                                                                                                                                       595 FIGALOKRILDIGKKHDITELNSDAVNLISQATQERLRGLLEKLTAIAQHRMTTYKASEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,715
FILING DATE: 09-MAY-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 775; DB 1;
Pred. No. 8.8e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Osman, Richard A
RECISTATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || |: |||::|||||| | |: ||
890 RIKRVNLRDMLFYMEQEREFCRSSMLFKTYLK 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       770 RITRICLRDLIFCMEQEREMKYSRALYLALLK 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US 08/188,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08646715
Patent No. 5637686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.2%;
29.6%;
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APPLICATION NUMBER: US 01
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 921 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Tjian, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-08-646-715-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RY: USA
94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-646-715-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 APQLPQITQIIPAQQSQQQVNNVSSAGGTATAVSSTTA------ATT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 TMLENVK-KCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELK 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----- LPNSQSFIQ--- 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 ----QCVQQTSSDMVIATCTTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVS---VQT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330 LNPLAGPVGAKAGVVTLHSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKP 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390 VVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIGTPVQIKLAQPGPVL 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                507 ------KLTAVKVGQTQTKAI-TPSLHP-----PSLAAISGGP-----PPTPTL 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : : : | :: | :: | :: | :: | : : :: | : :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                604 PHMERINASLTPIGAKTM------ARPPPAINKAIGKKKRDAMEMDAKLNTSSGGAA 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 POSPSITLSTLNTGQTPA-----LLVKTDNGFQLLRVGTTTGPPTVTQTITNTSNNS 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          535 PTQKNRIKENVTSCFRDEDDINDVTSMAGVNLNEENACILATNSELVGTLIQSCKDEPFL 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 PQIVAVKAPNTTIQFPANLQLPPGTVLIKSNSGPLML-----VSPQQTVTRAETTS 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 921;
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                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,582
FILING DATE: 28-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.2%; Score 775; DB 1; I Similarity 29.6%; Pred. No. 8.8e-55; BB; Conservative 128; Mismatches 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A-57650-2/AJT/RAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 SSPQPHLVPFLKKSVVALRQL------
                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/POCKET NUMBER: A 557
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-188-582-2
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                         94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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Best Local Simi
Matches 258;
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322 PRT-----VSVQTLNPLAGPVGAK--AGVVTLHSVGPTAATGGTTAGTGLLQTS 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        688 QTKPVQTSAVTGQASTGPVTQIIQTKGPLPAGTILKLVTSADGKPTTIITTTQASGAGTK 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 KLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSGSFIQGCVQQ 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DHICKPVIGTPVQIKL-AQPGPVLSQPA-GIPTGSSSKQLFSLFHVVQQPSGGNEKQVTT 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLVSPQQTV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             004 ASLATPITTLGTIATLSSQ-----VINPTAITVSAAQTTLTAAGGLTTPTITMQPV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---VTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLK-PSSL-GASSTPSNEPNL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTILGI ------SSVSPSTT---KPGTTTIIKTIPMSALITQAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 TSSDMVIATCTTTVTT-----SPVVT----TTVSSSQSEKSIIVSGA----TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 TRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --KAENSAAVQINLSPTMLENVKKCKNFL--AMLIKLACSGSQSP-----EMGQNVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2035;
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                                                     ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/046,585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 237; DB 1; L; Pred. No. 4.2e-10; 84; Mismatches 239;
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                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
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Similarity 22.6%;
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LENGTH: 2035 amino acids
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US-08-046-585-5
                                 CORRESPONDENCE ADDRESS:
                                                                                                          CITY: San Francisco
STATE: CA
     NUMBER OF SEQUENCES:
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94111-4187
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TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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Matches 148;
                                                                                                                                                                  COUNTRY:
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Best Local S
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                                                                                    128 KPSSVQSVAVPTSVVTVTPGKPLNTVTTLKPSSLGASSTPSNEPNLKAENSAAVQINLSP 187
                                                                                                                                                                                                                                                                                                                          244 APQLPQITQIQTIPAQQSQQQVNNVSSAGGTATAVSSTTA------ATT 287
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                                                  PQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLML-----VSPQQTVTRAETTS 76
  Gaps
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128; Mismatches 308; Indels 178;
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Sequence 5, Application US/08046585
Sequence 5, Application US/08046585
Patent No. 5453362
Patent No. 5453362
Patent No. 5453362
Patent Invention:
APPLICANT: Lamarco, Kelly
APPLICANT: Winship
Patent OF INVENTION: A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN:
TITLE OF INVENTION: HOST CELL FACTOR
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258; Conservative
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988 EQPTATVIADSGQGDVQPGTVTLVCSNPPCETHETGTTNTATTTVVAN--LGGHPQPTO 1045
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  222 KLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ 281
                                              ----SSVSPSTT---KPGTTTIIKTIPMSAIITQAGATG 785
                                                                                                                                                                                                                                                         369 KPLVTSVA--NTVTTVSLQPEKPVVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCW 426
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TITLE OF INVENTION: HOST CELL FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC_DOS/AG-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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FILING DATE: 03-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application PC/TUS9311721 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: FP
TELECOMMUNICATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 5:
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APPLICANT: Wilson, Angus
APPLICANT: Herr, Winship
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
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CORRESPONDENCE ADDRESS:
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                                            748 PTILGI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                       988 EQPIATVIIADSGQGDVQPGTVTLVCSNPPCETHETGTTNTATTTVVAN -- LGGHPQPTQ 1045
---LKQITLPGNKILSLQASPTQ 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 TRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTV----- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 --KAENSAAVQINLSPTMLENVKKCKNFL--AMLIKLACSGSQSP------EMGQNVK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1046 VQFV-----CDRQEAAASLVTSTVG----QQN-------GSVVRVCSNPP 1079
                                                                                 538 KNRIKENVTSCFRUEDDINDVTSMAGVNLNEENACILATNSELVGTLIQSCKDEP 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84; Mismatches 239; Indels 184;
                                                                                                                                                                                                                                                                                        APPLICANT: Lamarco, Kelly
APPLICANT: Wilson, Angus
APPLICANT: Herr, Winship
TITLE OF INVENTION: A NOVEL EKARYOTIC TRANSCRIPTION PROTEIN:
TITLE OF INVENTION: HOST CELL FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DB 1; Length 2035; 4.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT: 4 Embarcadero Center, Sulte 3400
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,703
FILING DATE: 24-FEB-1995
CLASSIFICATION: 435
485 ISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.6%; Score 237;
22.6%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                 Sequence 5, Application US/08393703
Patent No. 5585239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111-4187
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS: ADDRESSE: FLEHR, HC
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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528 ILSLQASP----TQKNRIKENVT-----SCFRDEDDINDVTSMAGVNLNEENACILAT 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 QSPEMGQNVKKLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNS 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 QSFIQQCVQQTSSDMVIATCTTTV-TTSPVVTTTVSS------SQSEKSIIV---- 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 VANTVITVSLQPEKPVVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCWDHIC---- 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             536 ATTSQETAS------SLPPATTTKTSEQTTLV-----TVTSCESHVCTESI 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSQLIKKVAVTPVKKLAQIGTTVVTTVPKPSSVQSVAVPTSVVTVTPGKPLN-TVTTLK- 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --SGATAPRIVSVQTLNPLAGPVGAKAGVVILHSVGPTAATGGTTAGTGLLQTSKPLVTS 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSGQITSSI-------GSRPIITPFYPS-----NG
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VTISSCESDVCSKTASPAIVSTSTATINGVTTEYTTWCPISTTESRQQTTLVTVTSCESG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 PSSLGASSTPSNEP----NLKAENSAAVQINLSPTMLENVKKCKNFLAMLIKLACSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        431 KPVIGTPVQIKLAQPGPVLSQPAGIPTGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 862;
                        PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.6%; Score 198; DB 1; I
llarity 19.1%; Pred. No. 1.7e-07;
Conservative 110; Mismatches 278;
                                                      APPLICATION DATA

PELLING DATE: 18-NOV-1994
CLASSIFICATION: 435
PCLASSIFICATION: 435
PCLASSIFICATION DATA:
APPLICATION NUMBER: JP PCT/JP94/00290
FILING DATE: 24-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 38871/1993
FILING DATE: 26-FEB-1993
ATTONEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                          24,618
ER: 2589-023-0XPCT
                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
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Best Local Similarity 19.1%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 862 amino acids
                                          CURRENT APPLICATION DATA:
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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                                                                                                                                                        70 TRAETTSNITSRPAVPANPQTVKICTVPNSSSQLIKKVAVTPVKKLAQIGTTV----- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---VTTVPKPSSVQSVAVPTSVVTVTPGKPLNTVTTLK-PSSL-GASSTPSNEPNL---- 173
                                                                                                                                                                                                                                                          748 PTILGI-----SSVSPSTT---KPGTTTIIKTIPMSAIITQAGATG 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 PRT-----VSVQTLNPLAGPVGAK--AGVVTLHSVGPTAATGGTTAGTGLLQTS 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --KAENSAAVQINLSPTMLENVKKCKNFL--AMLIKLACSGSQSP------EMGQNVK 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282 TSSDMVIATCTTTVTT-----TPVVT----TTVSSSQSEKSIIVSGA----TA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 KPLVTSVA--NTVTTVSLQPEKPVVSGTAVTLSLPAVTFGETSGAAICLPSVKPVVSFCW 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    904 ASLATPITTLGTIATLSSQ----VINPTAITVSAAQTTLTAAGGLTTPTITMQPV---- 954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          485 ISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASI-----LKQITLPGNKILSLQASPTQ 537
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                            KLVEQLLDAKIEAEEFTRKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQ 281
                                                                           10 VSAPPKVSSGPRLPAPQIVAVKAPNTTTIQFPANLQLPPGTVLIKSNSGPLMLVSPQQTV 69
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5.6%; Score 237; DB 5; Length 2035; 22.6%; Pred. No. 4.2e-10; tive 84; Mismatches 239; Indels 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WATATA, JUNJI
APPLICANT: WATATA, YOSHIHIRO
APPLICANT: OCAWA, MASAHIRO
APPLICANT: ONNELA, MELJA
APPLICANT: ONNELA, MALJA-LEENA
APPLICANT: ONNERATION: CONTAINING THEM
NUMBER OF SEQUENCES: 7
CONTAINING THEM
NUMBER OF SEQUENCES: 7
CONTAINING THEM
STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08325267A Patent No. 5585271 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
Query Match
Best Local Similarity 22.69
Matches 148; Conservative
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STATE:
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RESULT 12
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                                                                            746 NIVAAETIINIGAAETKIVVISSLSRSNHAETQIASAIDVIGHSSSVVSVSETGNIKSLI 805
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                                               577 NSELVGTLIQSCKDEPFLFIGALQKR--------ILDIGKKHDITELN 616
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23.7%; Pred. No. 1.5e-06;
Live 75; Mismatches 240; Indels 136;
                                                                                                                                                                                                                                                                   APPLICANT: Christa, John
APPLICANT: Christa, John
APPLICANT: Yacluk, Peter
TITLE OF INVENTION: SNF2 Related CBP Activator Protein (SRCAP)
FILE REPERENCE: 16153-4247
CURRENT APPLICATION NUMBER: US/09/579,181
CURRENT FILING DATE: 2000-05-25
PRIOR FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Vor: 2.0
                                                                                                                                    806 SSGLSTMSQQPRSTPASSMVGYST-ASLEISTYAGSANSLL 845
                                                                                                              617 SDAVNLISQATQERLRGLLEKLTAIAQHRMTTYKASENYIL 657
                                                                                                                                                                                                                          Sequence 2, Application US/09579181
Patent No. 6365372
GENERAL INFORMATION:
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Matches 140; Conservative
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; ORGANISM: Human
US-09-579-181-2
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LENGTH: 2972
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                                                                                                                                                                                                                                  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chrivia, John
APPLICANT: Yaciuk, Peter
TITLE OF INVENTION: SNR2 Related CBP Activator Protein (SRCAP)
FILE REFERENCE: 16153-4247
CURRENT PAPLICATION NUMBER: US/09/579,181
CURRENT FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 66/136,620
PRIOR PILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
                                                  1552 ASTQSPA-----SQASSLVVSASGAAPLPVIMVSRLPVSKDEPDTL 1592
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470 V-VQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTI--IPTSQFPPASI 517
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                                                                                                                                RESULT 11
US-09-579-181-1
: Sequence 1, Application US/09579181
: Patent No. 6365372
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Best Local Similarity 23.7%;
Matches 140; Conservative
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US-09-579-181-1
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Immobilized proteins with specific binding capacities and their use in processes and products.
    559 FISSESSKSPTYSS------SELPLYTSATTSQETAS------SLP 592
                                                                                                                                                                                                                                                                                                                                            158 GSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPASI 517
                                                                                                                                                                                                                                                                                                                                                                                 EYITWCPISTIETTKOTKGTTEQTIETTKQTTVVTISSC-ESDVCSKTASPAIVSTSTAT 696
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                                                                   SPVVTTTVSS------SQSEKSIIV-----SGATAPRTVSVQTLNPLAGPVGAKA 341
                                                                                                                                                                                                                                                   102 AVTFGETSGAAICLPSVKPVVSFCWDHIC----KPVIGTPVQIKLAQPGPVLSQPAGIPT 457
                                                                                                                                                                                                                                                                                             593 PATTIKISEQITLV----TVTSCESHVCTESISPAIVSTATVTV-----SGVTT 637
                                                                                                                                                                                                                                                                                                                                                                                                                                  518 LKQITLPGNKILSLQASPTQKNRIKENVTSCFRDEDDINDVTSMAGVNLNEENACILATN 577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SORTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/971,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          431 TVTGTNGLPTD-ETVIVVKT-PTTAISSSLSSSSGQITSSI---
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Patent No. 6114147
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity
Matches 123; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-971-692-15
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                                                                                                                              TITLE OF INVENTION: PROCESS FOR IMMOBILIZING ENZYMES TO THE TITLE OF INVENTION: CELL WALL OF A MICROBIAL CELL BY PRODUCING A FUSION NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATORS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 6.1e-07;
87; Mismatches 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 04-JAN-1995

PRIOR APPLICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92202080.5

FILING DATE: 08-JUL-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92203899.7

FILING DATE: 14-DEC-1992

PRIOR APPLICATION NUMBER: EP 92203899.7

FILING DATE: 14-DEC-1993

APPLICATION NUMBER: PCT/EP93/01763

FILING DATE: 07-JUL-1993

ATORNEY AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773

RECENENCE/DOCKET NUMBER: 213289/T7020(V)

TELEPHONE: (202) 861-3000

TELEFAX: (202) 822-0944

TELEFAX: (202) 822-0944

TELEFAX: (202) 822-0944
                                                                                                                                                                                                                                                                     S: CUSHMAN DARBY & CUSHMAN, L.L.P.
1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUFTWARE, ASSETTION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,525
FILING DATE: 04-JAN-1995
ARRETFICATION: 435
  Sequency; Sequency; Sequency; Patent No. 602/yılv; GENERAL INFORMATION: APPLICANT: SCHREUDER, MARTEN P. APPLICANT: TOSCHRA, HOLSER Y. APPLICANT: VERRIPS, CORNELIS T. APPLICANT: VERRIPS, CORNELIS T. APPLICANT: PROCESS FOR I
Sequence 22, Application US/08362525
Patent No. 6027910
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COMPUTER READABLE FORM:
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us-09-763-909-2.rai

RESULT 15 US-08-700-651-5 ; Sequence 5, Application US/0 ; Patent No. 6015882 ; GENERAL INFORMATION: ; APPLICANT: PETERSEN, CAROLY ; APPLICANT: LEECH, JAMES ; APPLICANT: GUT, JIRI ; TITLE OF INVENTION: VACCINE ; TITLE OF INVENTION: FOR PRO	HION APPLICATION DATA: HION APPLICATION DATA: PRICA APPLICATION NUMBER: HION APPLICATION DATA: APPLICATION NUMBER: APPLICATION NUMBER: HION APPLICATION: HAPLICATION NUMBER: HEGISTRATION NUMBER: TELECOMMUNICATION INFORMATION:
QY 622 LISQATQERLEGLLEKLTAI : : : Db 1486 TMSQQPRSTPASSMVGXST-	APPLICATIO FILING DAT CLASSIFICA
QY 582 GTLIQSCKDEPFLFIGALQK	COMPUTER: IBS OPERATING SYST SOFTWARE: Pat CURRENT APPLICAT
1366	COMPUTER
Qy 533 ASPTQKNRIKENVI	
	STREET: 1755 S. JEFFERSON DAVIS HWY, SUITE 40C CITY ARLINGTON
1256 STATVTV	NOMBER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS: A
QY 436 TPVQIKLAQPGPVLSQPAGI	; TITLE OF INVENTION: YEAST AGGLUTINATION GENES AND YEAST; TITLE OF INVENTION: CONTAINING THEM
Db 1216 ETASs	; APPLICANT: PENTILA, MERJA ; APPLICANT: ONNELA, MAJJA-LEENA . ADDITANT: FEDAND, CIDERA
380 ITVSLOPEKPVVS	; APPLICANT: TAKATA, YOSHIHIRO ; APPLICANT: OGAWA, WASAHIRO
Qy 320 TAPRIVSVQTLNPLAGPVGA :	; Patent No. 35822/1); ; GENERAL INFORMATION: ; APPLICANT: WATARI. JINII
П	US-08-325-267A-2 Sequence 2, Application US/08325267A
QY 277 QCVQQTSSDMVIATCTTTV-	RESULT 14
	: : 738 PAIVSTATATVND
217	SELVGTLIOSCKD 590
Oy 163 ASSTPSNEPNLKAE	OY 518 LKQITLPGNKILSI,QASPTQKNRIKENVTSCFRDEDDINDVTSMAGVNLNEENACILATN 577 : :
Oy 105 KKVAVTPVKKLAQIGTIVVJ	dy 430 GSSSAQLESSLEHVVQPSGGGREAQVITISHSSELFIQKCGQKIMPVNTIIPTSGEPPASI 517 :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 50 TVLIKSNSGPLMLVSPQ : : : : : :	OY 40Z AVIEGEISGAALCLESVKEVVSECWDHICKPVIGIPVQIKLAQPGFVLSQPAGIPT 457
Ouery Match 4.3 Best Local Similarity 19.3 Matches 134; Conservative	
interior int	Qy 298 SPVVTTTVSSSQSEKSIIVSGATAPRIVSVQTLNPLAGPVGAKA 341
2488: ON FOR S E CHARAC	QY 239 RKLYVELKSSPQPHLVPFLKKSVVALRQLLPNSQSFIQQCVQQTSSDMYIATCTTTV-TT 297 : : : :: :: : : Db 471TSSRPLITPFYPSNGTSVISSSVISSSVTSSLFTS 505

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NES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS ROPHYLAXIS AND TREATMENT OF CRYPTOSPORIGHUM parvum
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AAINGVTEYTTWCPISTTESRQOTTLVTVTSCESGVCSET 1365
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                                                                                                                                                                    .3%; Score 184.5; DB 1; Length 1537;
.3%; Pred. No. 5.4e-06;
e 104; Mismatches 257; Indels 201; Gaps
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TTATTITISETESVIKPDEWCWLEKNGECEAKGATYVGVIGKDGRIENGMAFTMIPNDD 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 HSVGPTAATGGTTAGTGLLQTSKPLVTSVANTVTTVSLQPEKPVV-----SGTAVTLSL 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----VKKCKNFLAMLIKLACSGSQSPEMGQNVKKLVEQLLDAKIE--AEEFTRKLY 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             459 THVRFRFKVKDVGNTISVRCRKGAGKLEFP-----DRSLDFTIPPVAGHNSCSII 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VELKSSPQPHLVPFLKKSVVALRQLLPNSQSF---IQQCV-----QQTSSDMVIA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TC---TTTVTTSPVVTTTVSSSQSEKSIIVSGATAPRTVSVQTLNPLAGPVGAKAGVVTL 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 PAVTFGETSGAAICLPSVKPVVSFCWDHICKPVIG----TPVQIKLAQPGPVLSQPAGIP 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGSSSKQLFSLFHVVQQPSGGNEKQVTTISHSSTLTIQKCGQKTMPVNTIIPTSQFPPAS 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----KMLDKYTRMIYDYNSG----LLLDSNDEPIPGSQAGQ-----IADTSNLFPVQ 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           517 ILKQITLPGNKILSLQASPTQKNRI-------KENVTSCFRDEDDIN--D 557
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                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                          35 TTTIQFPANLQLPPGTVLIKSNSGPLMLVSPQQTVTRAETTSNITSRPAVPANPQTVKIC 94
                                                                                                                                                                                                                                                                           Query Match
4.2%; Score 178; DB 3; Length 1721;
Best Local Similarity 20.0%; Pred. No. 2.2e-05;
Matches 137; Conservative 82; Mismatches 293; Indels 172;
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              FILE REFERENCE: 480.19-4(HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                           TYPE: PRT : ORGANISM: Cryptosporidium parvum US-08-700-651-5
TITLE OF INVENTION: INFECTIONS
                                                                                                                                                                             LENGTH: 1721
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Search completed: February 16, 2003, 22:02:26 Job time : 40.8929 secs

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February 16, 2003, 22:29:40; Search time 6475 Seconds (without alignments) 11497.294 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                    OM nucleic - nucleic search, using sw model
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em_htg_inv:*
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em_htg_vrt:*
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Maximum DB seq length: 2000000000
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Submitted (07-NOV-1996) R. Dikstein, Weizmann Institute of
Dept. Blochemistry, Rehovot, 76100, ISRAEL
                                              ATTTGGAAGAAAGAGAAATGTTACTTAAGGCAGCCAAGAGTCGTTCTAATAAAGAGATC
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/product="TBP associated factor"
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/db_xref="GI:1669689"
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/db xref="taxon:9606"
/clone_lib="HeLa"
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AC017007 182805 bp DNA linear PRI 10-AUG-2002 HOMO Sapiens BAC clone RP11-119H12 from 4, complete sequence. AC017007 GI:22138721
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Sulston, J.E. and Waterston, R. Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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Harris,A. and Meyer,R.
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'rpt_family="(CAATT)n"
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                                                                                                                                                                                                                    Direct Submission
Submitted (08-AUG-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MnO 63108, USA
6 (bases 1 to 182805)
                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (10-AUG-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Aug 8, 2002 this sequence version replaced gi:21240754.
                                                                                                      Submitted (29-MAY-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as Compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTICE: This sequence may not represent the entire insert of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       donor, as described by Osoegawa.K., Woon, P.Y., Zhao, B., Frengen, B. Attaeno, M., Catanese, J. J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at http://www.resgen.com) or Pleter de Jong VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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The RPCI-11 human BAC library was made from the blood of one male
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                         4 (bases 1 to 182805)
Waterston, R.H.
Direct Submission
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                                                                                                                                                                                            Bitten, B., Lintcon, L. Bastlen, V. Bloom, T. Bogusiadarkiy, L. Allen, N. Anderson, S. Barna, N. Bastlen, V. Bloom, T. Bogusiadarkiy, L. Anderson, S. Barna, N. Camardia, J. Campopiano, A. Chang, J. Chases I. Brown, A. Camardia, J. Campopiano, A. Chang, J. Chastro, B. Errelra, P. Colangelo, M. Collins, S. Collymore, A. Chang, J. Chastro, B. Chocepel, Y. Colangelo, M. Collins, S. Collymore, A. Gonder, P. Charlen, M. Chang, J. Stato, S. Ferrelra, P. Barna, L. Canadan, J. Gardd Pierre, N. Garda, A. Kartaes, R. Landers, T. Lehoczky, Hulme, W. Illev, I. Johnson, R., Jones, C. Kamat, A. Kartaes, A. Kalls, C. Landerge, D. Johnson, R., Landers, T. Lehoczky, J. Levine, R. Lindblad-Toh, Matthews, C. Macdonald, P. Major, J. Marquis, N. Matthews, C. Mardonald, R. Murphy, T. Naylon, J. Peterson, R. Pollara, V. Rymond, C. Retta, R. Raback, M. Santos, S. Schauer, S. Scha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (18-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA OA MAU 18, 2002 this sequence version replaced 91:20806496. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 119081)
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is not known and their order in this sequence record as arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                   Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 18, clone RP11-25D3
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Center clone name: 25_D_3
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     Homo sapiens
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ORGANISM
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TITLE
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52785 TITCCAGAAAAGCGTGGTTGCCTTACGACAACTTCTGCCTAACTCCCAGAGCTTCATCCA 52726 52546 52486 52425 AAACACAGGGCCACGGTCTCACTGCAACCTGAAAAGCCAGTTGTCTCTGGAACAGCAGT 52366 52306 AGTGGGAGCAAAAGCTGGAGTTGTACACTTCATTCTGTGGGCCCAACTGCTGCAACAGG 1068 TTCTGGAGCAACAGCACCCAGAACTGTGTCAGTGCAAACTTTGAACCCACTTGCTGGTCC 1008 AAACACAGTGACCACGGTCTCACTGCAACCTGAAAAGCCAGTTGTCTCTGGAACAGCAGT 1188 1249 ATCTGTGAAACCTGTTGTTTCCTTCTGCTGGGACCACATCTG-CAAGCCTGTTATTGGGA 1307 1308 CTCCAGTTCAAATCAAAACTTGCCCAGCCGGGCCCTGTCCTTTCACAACCAGCTGGGATTC 1367 829 GCAATGTGTTCAGCAGACTTCTAGTGACATGGTCATTGCTACCTGTACTACAACAGTAAC 888 889 AACTICICCIGIGGIGACAACTACAGIGICCICAAGCCAGICIGAAAAGICAATIATIGI 948 769 TCTTAAGAAAAGCGTGGTTGCCTTACGACAACTTCTGCCTAACTCCCAGAGCTTCATCCA 828 Gaps 52545 AGTGGGAGCAAAAGCTGGAGTTGTGACACTTCATTCTGTGGGCCCAACTGCTGCAACAAG AACACTGTCCCTTCCAGCAGTAACTTTGGAGAAACTTCAGGTGCAGCTATTTGTCTTCC runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. AGGAACAACAGCTGGAACTGGTTTGCTTCAGACTTCAAAACCACTTGTGACATCTGTGGC 5 Length 119081; 1 46756: contig of 46756 bp in length
46757 46856: gap of 100 bp
69257 69356: gap of 100 bp
69357 90157: contig of 22400 bp in length
90158 90257: app of 100 bp
90158 119081: contig of 28824 bp in length.
Location/Qualifiers 492 others 15; Indels bp in length /clone_lib="RPCI-11 Human Male BAC" a 23957 c 23213 g 31632 t 492 Query Match 22.7%; Score 580; DB 2; I Best Local Similarity 97.3%; Pred. No. 3.6e-141; Matches 611; Conservative 0; Mismatches 15;

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Direct Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 120 Charles Street, Cambridge, MA 02141, USA

E (bases I to 16924)

Burren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Baguslavkiy, L., Changal, E., Brown, A., Camparata, J., Campoplano, A., Chang, J., Changal, V., Campoplano, A., Chang, J., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferrelia, P., FittGerald, M., FittHugh, W., Gage, D., Galagan, J., Gardyna, S., Gilnde, S., Goyette, M., Ilev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kalls, C., Lander, K., Lamazares, R., Landers, T., Macchan, C., Macthean, C., Macchan, C., Macchan, C., Macchan, P., Marchin, P., Marchin, J., Marchin, M., McEwan, P., Marchin, T., Mupoh, T., Naylor, J., Nathews, C., McCarthy, M., McEwan, P., McKernan, K., Maldrim, J., Macchan, C., Macchan, P., Morkernan, P., Marchin, J., Naylor, J., Oliver, J., Peterson, R., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, R., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Voung, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

All repeats were identified using Repeathmasker:

Bull repeats were identified using Repeathmasker:

Center, Marker, Conne, Conne, Center, For Genome Research, 320 Charles Street, Cambridge, MA 0214, USA

On Jun 16, 2002 this sequence version replaced 91:21263339.

All repeats were identified using Repeathmasker:

Center, Mitched Conne, Conne, Center for Genome Research, 320 Charles Street, Cambridge, MA 0214, USA

Center, Marker, Marker
                                           Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nebu, C., Norbu, C., Netera, P., Phunkhang, P., Plerrer, N., Peterason, K., Phunkhang, P., Plerrer, N., Petera, R., Ribe, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbeck, R., Seamen, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, M., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vasallac, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
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/rpt_family="L2"
complement(3529. .4480)
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/rpt_family="(TTCA)n"
complement(324. .389)
/rpt_family="L3"
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/rpt_fam11y="Alusx"
/rpt_fam11y="MIR"
/rpt_fam11y="MIR"
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Direct Submission

Submitted (15-3AN-200) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

1 (bases 1 to 169240)

Sa barren, B., Linton, L., Nusbaum, C., Lander, B., All, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boquslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J., Chargelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Golde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Landers, S., Landers, R., Lindplad-Toh, K., Liu, G., MacLean, C., Mardonald, P., Major, J. J., Marquis, N., Matchews, C., McCarthy, M., McEwan, P., Major, J., Johnson, R., Landers, L., Mhova, T., Manga, V., Maylor, J., Nuphor, T., Nuylor, J., Norman, C., Norman, C. H., O'Connor, T., O'Donnell, P., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Schupback, R., Starauss, M., Strauss, R., Subramenian, Tanders, S., Severy, P., Spencer, B., Schupback, R., Starauss, M., Travers, M., Travis, N., Travillio, J., Vossillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Piref, Submission, R., Wassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Piref, Submission
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Burren, B. Lintcon, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Campollano, T., Campollano, M., Chang, J., Chararo, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farco, S., Ferreita, P., FitzGerald, M., FitzHugh, W., Gage, D., Gand Plerre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Liu, G., MacLean, C., Macdenald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J.,
                                                   PRI 16-JUN-2002
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 169240)
169240 bp DNA linear AC022069.6 GI:21429684
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Unpublished
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 190782)

1 Hattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

1 Homo sapiens 190,782 genomic DNA of 18q11.2

2 (bases 1 to 190782)

2 (bases 1 to 190782)

3 Hattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Brilyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

L Submitted (10-JUL-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mall:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 bp DNA linear HTG 13-JUL-2000 clone RP11-802C10 map 18q11.2, WORKING
                                                                                                                                                                                                                                                                                 DD 153484 CTCCAGTTCAAATCAAACTTGCCCAGCCGGCCCTGTCCTTTCACAACCAGCTGGGATTC 153425
    Db 153843 TTCTGGAGCAACAGCACCCAGAACTGTGAGTGCAAACTTTGAACCCACTTGCTGGTCC 153784
                                                                                                                                        153723 AGGAACAGCTGGAACTGGTTTGCTTCAGACTTCAAAACCACTTGTGACATCTGTGGC 153664
                                                                                                                                                                                                AGGAACAACAACTGGAACTGGTTTGCTTCAGACTTCAAAACCACTTGTGACATCTGTGGC 1128
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCCAGTTCAAATCAAACTTGCCCAGCCGGGCCCTGTCCTTTCACAACCAGCTGGGATTC 1367
                                           AGTGGGAGCAAAAGCTGGAGTTGTGACACTTCATTCTGTGGGCCCAACTGCTGCAACAGG
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Contact: hattori@gsc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DRAFT SEQUENCE, 38 unordered pieces. AP002752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASEI; HTGS_DRAFT.
Homo sapiens DNA, clone:RP11-802C10.
Homo sapiens
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Center project name: Humbraft18
Center clone name: RP11-802C10
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5300.5608
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5600.5979
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[0856, 11150
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complement(6900..7100)
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complement(7253..7425)
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8908. .9205
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9206. .9737
/rpt_family="AluJb"
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/rpt_family="AluJb"
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13500, .13529
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5990. .6469
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                             NOTE: This is a 'working draft' sequence. It currently consists of 38 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the configs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Quality coverage: 4.15x in Q20 bases; sum-of-contigs
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                                 Ruppert, S.,
                                                                                                                                                                         Length 3603;
 Unclassified.

1 (bases 1 to 3603)

1 Tjian,R., Comai,L., Dynlacht,B.D., Hoey,T., Ruppert,S.Wang,E. and Weinzlerl,R.O.J.

TATA binding protein associated factors drug screens Patent: US 5534410-A 15 09-JUL-1996;

1 Cocation/Qualifiers
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Pred. No. 1.4e-77;
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US 5534410.
/note="assembly_fragment"
57845. .68839
/note="assembly_fragment"
68940. .77568
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Best Local Similarity 97.3%;
Matches 611; Conservative
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Tjian,R., Comai,L., Dynlact,B.D., Hoey,T., Ruppert,S., Tanese,N.,
Wang,E. and Weinzlerl,R.O.J.
Tata-binding protein associated factor, nucleic acids
Patent: US 5637686-A 15 10-JUN-1997;
Location/Qualifiers
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                       DNA
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961 c 830 g
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13.2%;
Best Local Similarity 63.9%;
Matches 536; Conservative
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                                                                                               Unclassified.
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                               DEFINITION
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Submitted (17-0cr-1996) Microbiology, NVU Medical Center, 550 First Ave., New York, NY 10016, USA
See GenBank Accession Number 105309 for hTAFII100; the 5' end is missing from the cDNA as this region is rich in GC residues; a few ambiguities remain in the CDNA sequence that may affect the reading frame near the 5' end; repeated efforts to obtain the full cDNA have been unsuccessful; numerous sequence runs have been performed to clarify the GC sequence ambiguities; the process is still
                                                                                                                                                                                                                                         HSU75308 4233 bp mRNA linear PRI 14-DEC-1996
Human TBP-associated factor (hTAFII130) mRNA, partial cds.
U75308
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dTAPIII10, Swiss-Prot Accession Number P47825; 130 kDa TAF
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4233)
2291 CAAACAGTTGCATGGTCCAAGAATCACGAGAATCTGCCTCAGGGACTTGATATTTTGTAT 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tanese, N., Saluja, D., Vassallo, M.F., Chen, J.L. and Admon, A. Molecular cloning and analysis of two subunits of the human complex: hTAFII130 and hTAFII100
Proc. Natl. Acad. Sci. U.S.A. 93 (24), 13611-13616 (1996)
                         2097 CAGACAGTICACGCGACAAGAAGAATCACGCGGGTCAACCTCAGGGACCTCATATTIGITI
                                                                                                                GGAACAGGAACGGGAGATGAAGTATTCTCGAGCTCTATACCTGGCCCTTCTGAAGTGAC
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    4233
    organism="Homo sapiens"
    /db_xref="taxon:9606"

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1. .4233
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/gene="hTAFII130"
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Tanese, N.
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/protein_if="Cah72189".1"
//bcotein_if="Cah72189".1"
//db_xref="G1:2058326"
//db_xref="G1:205826"
/
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Submitted (18-FEB-1997) I. Davidson, IGBMC, 1 Rue Laurent Fries.,
BP163, F- 67404 Illkirch, FRANCE
Related sequences Y09321, U75308.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="TAFII135"
/function="potentiates ligand dependent transcriptional
activation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'product="subunit of RNA polymerase II transcription
                                     Mengus, G., May, M., Carre, L., Chambon, P. and Davidson, I. Human TAF(II)135 potentiates transcriptional activation by tAF-2s of the retinoic acid, vitamin D3, and thyroid hormone receptors in mammalian cells Genes Dev. 11 (11), 1381-1395 (1997)
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Pred. No. 2.6e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hela"
1. 3252
/gene="TAFII135"
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/gene="TAFII135"
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ilarity 63.8%;
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Davidson, I.
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                                                                                                            TCTGTCACTTCAAGCATCTCCTACTCAGAAAATAGAATAAAAGAGAATGTAACATCATG 1645
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RNA polymerase II; TAFIII35 gene; transcription factor TFIID.
Homo sapiens
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                                     DB 9;
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                                   Score 338.2; DB Pred. No. 1.4e-77 0; Mismatches 28
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Mus musculus TATA-binding protein associated factor TAFII135 mRNA,
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
TAAAGATGAACCAFTTCTTTTTTTTTTGGAGCTCTACAAAAGAGAATCTTAGACATTGGTAA 1825
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Metsis,M., Brunkhorst,A. and Neuman,T.
Cell Type Specific Expression of the TFIID Component TAFII135
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Exp. Cell Res. (2001) In press
2 (bases 1 to 2196)
2 (bases 1 to 2196)
Direct Submission
Submitted (06-JUN-2001) Medical Chemistry and Blochemistry,
Rarolinska Institute, Retzius vag 1, Stockholm 1717, Sweden
                                                    AAAGCATGACATTACAGAACTTAACTCTGATGCTGTGAACTTGATCTCCCAAGCAACACA
                                                                     2655 AAAACATGGTATAACGGAATTACATCCAGATGTAGTAAGTTATGTATCACATGCCACGCA
                                                                                                                         2715 ACAAAGGCTACAGAATCTTGTAGAGAAAATATCAGAAACAGCTCAGCAGAAGAACTTTTC
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/strain="BALB/c"
/db_xref="taxon:10090"
/tissue_type="PO brain"
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/codon_start=3
product="TATA-1anding protein associated factor TAFII135"
/protein_id="AAK94779.1"
/db_xref="G1:15375062"
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Pred. No. 2.6e-74;
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Sequence updated (26-May-2000).

* NOTE: This is a "working draft' sequence. It currently * Consists of 30 contigs. The true order of the places * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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16829 31270: contig of 14442 bp in length
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45656 59177: contig of 13522 bp in length
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126254 131007: contig of
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59278 70338:
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                                                                                                                                                                                                                      HTG 30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (18-FEB-2000) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

Hobses; 1 to 17422)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Published Only in DataBase (2000)

2 (bases 1 to 17422)
2 (bases 1 to 17422)
2 (bases 1 to 17422)
Fujiyama,A., Yada,T., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                    Homo sapiens chromosome 18 clone RPI1-775B10 map 18q11.2, WORKING DRAFT SEQUENCE, 30 unordered pieces.
and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@sc.riken.go.jp, Tel:81-42-778-9923, Fax:81-42-778-9924)
ONL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
ON May 30, 2000 this sequence version replaced gi:7023969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available and the accession number will be
                                                                                        Quality coverage: 4.35x in Q20 bases; sum-of-contigs
                                                               2349 ATGGAACAGGAACGGGAGATGAAGTATTCTCGAGCTCTATACCTGGCCCTTCT 2401
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13522 bp
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9772 bp
9772 bp
6806 bp
6806 bp
6861 bp
5870 bp
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Contact: hattori@gsc.riken.go.jp
------ Project Information
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                                                                                                                                                                                                                      DNA
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HTG; HTGS_PHASE1; HTGS_DRAFT.
HOMO sapiens DNA, clone:RP11-775B10.
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70338 contig
80210 contig
89495 contig
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AP001197/C
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2475

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AP001096 175553 bp DNA linear HTG 13-JUL-2000 Homo sapiens chromosome 18 clone RP11-813H9 map 18q11.2, WORKING DRAFT SEQUENCE, 12 unordered pleces.
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On Jul 14, 2000 this sequence version replaced gi:8117851.
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Hobses; 1 to 17553)

Hattori,M., Ishi,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Published Only in Database (2000)

Chases 1 to 17553;

Chases 1 to 17553;

Lattori,M., Ishil,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                            173966 AGTTGCATCGTCCAAGAATCACGAGAATCTGCCTCAGGGACTTGATATTTGTATGGAAC 173907
                                                                                                                                                 Db 173906 AGGAACGGGAGATGAAGTATTCTCGAGCTCTATACCTGGCCCTTCTGAAGTGACCACTCC 173847
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Center clone name: RP11-813H9
Center clone name: RP11-813H9
Center clone name: RP11-813H9
Center clone name: RP11-813H9
Center clone name: RP1-813H9
Sequencing vector: PCR products; 100% of reads
Sequencing vector: PCR products; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 173065 bases at least Q30
Consensus quality: 173065 bases at least Q30
Consensus quality: 174451 bases at least Q30
Consensus quality: 174017 bases at least Q30
Consensus quality: 174051 bases at least Q30
                                                                                                                                                                                                                                                      Db 173846 ACTCTTCCATCCAGATCCTTGCTATTACTGCCAAAGAAGACACAAAGCATTGTTGCACT
           2296 AGTTGCATCGTCCAAGAATCACGAGAATCTGCCTCAGGGACTTGATATTTTGTATGGAAC
                                                                                                                                                                                                                                                                                                                                    2476 GICCIGAAAITICAATITCIGGAAAATAA-CACCAACAIGAAAGAGCATIGITIACGAIT
                                                                                                                     2356 AGGAACGGGAGATGAAGTATTCTCGAGCTCTATACCTGGCCCTTCTGAAGTGACCACTCC
                                                                                                                                                                                                                               ACTUTTCCATCCACATCCTTGCTATTTACTGCCAAAGAAGACACAAAGCATTGTTGCACT
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Web site: http://hpp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
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AP001096.4 GI:9188475
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:RP11-813H9.
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VERSION
KEYWORDS
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AP001096
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1. 16728
//note="assembly_fragment"
16829. 31370
//note="assembly_fragment"
31371. 45555
//note="assembly_fragment"
45656. 59178
//note="assembly_fragment"
70439. 38020
//note="assembly_fragment"
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80311. 89495
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//note="assembly_fragment"
80502. 1102565
//note="assembly_fragment"
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//note="assembly_fragment"
102666. 109526
//note="assembly_fragment"
115597. 115102
//note="assembly_fragment"
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//note="assembly_fragment"
115597. 115103
//note="assembly_fragment"
115597. 113108
113108. 113531
//note="assembly_fragment"
113108. 113531
//note="assembly_fragment"
113108. 113531
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162095 163533: contig of 1439 bp in length 163534 163633: gap of 100 bp 163634 165427: contig of 1794 bp in length 165428 165527: gap of 100 bp 165718 167111: contig of 1584 bp in length 167112 16213: contig of 2002 bp in length 169213 169213: contig of 2002 bp in length 169214 169313: gap of 100 bp 165714 169313: gap of 100 bp 165714 169313: gap of 100 bp 165714 1707070: contig of 1657 bp in length 1707070: contig of 1657 bp in length
                                                                                                                                                                                                                                        170971 171070; gap of 100 bp 171071 173121: contig of 2051 bp in length 173122 173222: contig of 100 bp 173222 174222: contig of 1001 bp in length. Location/Qualifiers
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/note="assembly_fragment"
153092. .157112
/note="assembly_fragment"
157213. .159965
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/db_xref="taxon:9606"
/chromosome="18"
/map="18q11.2"
/clone="RP11-775B10"
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138945 .142268 /note="assembly_fragment"
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/note="assembly_fragment"
146177. .149651
/note="assembly_fragment"
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Best Local Similarity 98.29
Matches 319; Conservative
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Submitted (08-JUL-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 1 bases 1 to 182884) Nusbaum,C., Lander,E., All,A., Allen,N., Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkly,L., Boukhgalter,B., Brown,A., Campoplano,A., Chang,J., Changaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
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//note="assembly_fragment"
66095. .80769
//note="assembly_fragment"
80870. .95586
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95687. .108410
//note="assembly_fragment"
122178. .132077
//note="assembly_fragment clone_end:T7 vector_side:left"
//note="assembly_fragment"
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/note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is
  65994 bp in length 14675 bp in length 14717 bp in length 13724 bp in length 13723 bp in length 13731 bp in length 9539 bp in length 6541 bp in length 1982 bp in length 1982 bp in length 1599 bp in length 1599 bp in length
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66095 80769: contig of 14675 bp in length
80770 80869: gap of 100 bp
80870 95586: contig of 14717 bp in length
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108411 108510: gap of 100 bp
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14932. 158870
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95687 108410: cont
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Dipublished

Dibases I to 182884)

Baker, J., Baldwin, J., Barna, M., Beckerly, R., Benn, J., Brown, M.,

Baker, J., Baldwin, J., Barna, M., Beckerly, R., Benn, J., Brown, A.,

Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K.,

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Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C.,

Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P.,

Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J.,

Maldrim, J., Molla, M., O'Connor, T., O'Donnell, P., Pavlin, B.,

Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A.,

Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A.,

Wheeler, J., Wux, X., Wyman, D., Ye, W.J. and Zody, M.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 182884)
                                                                                                                                                                                                                                                                                                                 DD 104707 TTTAGGGCTTAAAAGACAACCTTCTTGCTTCTGGGACATCCAGCCTGACAGCCACCAAAC 104766
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Homo sapiens chromosome 18, clone RP11-9E17, complete sequence.
ACO07996
                                                                                                                                                                                                                Gaps
                                                                                                                                            Length 175553;
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                                   1100 others
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                                                                                                                                        DB 2;
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Best Local Similarity 98.2%;
Matches 319; Conservative
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complement(7157. .720
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18092. .18335
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complement(18939. .
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Hagos, D., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, P., Horton, L., Hulme, W., Iliev, I., Grand-Pierre, N., Karatas, A., Kalls, C., Lancoque, K., Lamazares, R., Landers, T., Lehoczky, J., Leyne, R., Lindblad, Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., MacCarth, W., McEvan, P., McKernan, K., Medidim, J., Matthews, C., Minova, T., Mlenga, V., Murphy, T., Naylor, J., Mengas, D., Murphy, T., Naylor, J., Mouyen, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Riback, M., Riles, K., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramantan, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Submission
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Direct Submission

Submitted (10-ARR-2022) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

(Dasas 1 to 182884)

Burron, B., Lanton, L., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Chagalter, B., Erowh, A., Camerata, J., Campoplano, A., Changy, J., Chaegel, Y., Clangoplano, A., Canpoplano, A., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (122-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 10, 2002 this sequence version replaced g1:16041571. All repeats were identifiating RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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NOTE: This is a 'working draft' sequence. It currently consists of 38 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
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                                                                                                            Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329 consensus quality: 162369 bases at least Q40 consensus quality: 175182 bases at least Q30 Consensus quality: 182192 bases at least Q20
                                                                                                                                                                                                           Quality coverage: 4.15x in Q20 bases; sum-of-contigs
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  Center: RIKEN Genomic Sciences Center(GSC)
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Contact: hattori@gsc.riken.go.jp
                                                                                                                                                                                              Insert size: 187082; sum-of-contigs
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Center clone name: RP11-802C10
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 190782)
1. Shii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Homo sapiens 190,782 genomic DNA of 18q11.2
1. Dases 1 to 190782
1. (bases 1 to 190782)
1. Attori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P.,
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
1. Submitted (10-JUL-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan
(E-mall:hattoriegsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
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Homo sapiens chromosome 18 clone RP11-802C10 map 18q11.2, WORKING
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Pred. No. 3.2e-66;
           complement(19418. .19730)
/rpt_family="Alu3x"
complement(19731. .19875)
/rpt_family="Alu3b"
19876. .19954
/rpt_family="MER5A"
complement(19973. .20322)
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Homo sapiens DNA, clone:RP11-802C10.
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                                                                                                                                                                           complement(21241. .21337)
                                                                                                                                                                                                           complement(21690. .21817)
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20465. .20888
/rpt_family="MLT1B"
20986. .21136
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/rpt_family="AluJb"
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VERSION
KEYWORDS
SOURCE
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REFERENCE
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12 49011; gap of 100 bp 112 57744; contig of 8733 bp in length 45 57844; gap of 100 bp                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107298 107397; cont.14 of 6551 bp in length 107398 107397; gap of 100 bp 113949 113949 113949 113949 113949 113949 113949 113949 113949 113949 113949 113949 113949 113949 113949 114049 120684 120684 120684 120684 120684 120683; cont.15 of 6142 bp in length 120625 127026 120525; cont.15 of 6142 bp in length 120952 130951; cont.15 of 100 bp 130952 130951; cont.15 of 100 bp 134721 134721; gap of 100 bp 138721 gap of 100 bp 138722 143486; cont.15 of 5215 bp in length 138172 138271; gap of 100 bp 14586 143867; gap of 100 bp 14586 143867; gap of 100 bp 155998 155994; cont.15 of 100 bp 155998 155994; cont.15 of 3352 bp in length 152298 155994; cont.15 of 3352 bp in length 152398 155994; cont.15 of 3352 bp in length 155995 156094; gap of 100 bp 155995 156095 156094; gap of 100 bp 155995 156094; gap of 100 bp 155995 156094; gap of 100 bp 155995 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 156095 1560
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100 bp in length
1336 bp in length
    100 bp
10689 bp in length
                                                                                                          rap of 100 bp
:: contig of 11882 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101064: gap of 100 bp
107297: contig of 6233 bp in length
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504 bp in length
00 bp
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78785 180676: contig of 1892 bp in length
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84673 186271: contig of 1599 bp in length
86272 186371: gap of 100 bp
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100 bp
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100 bp
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82367 184572: contig of 2206 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1717 bp in length
100 bp
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190686 190782: contig of 97 bp in length.
Location/Qualiflers
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188088: contig of 17
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177259: contig of 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80677 180776: gap of 10
80777 182266: contig of 14
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39414 190585; contig of 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165656: gap of 168139: contig of 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7260 177359: gap of 10.360 178684: contig of 13
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38189 189313: contig of 11
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053 165556: contig of 2
40: gap of
36929: contig of
                                                                                                          gap of
                                                                                                                                                 48911
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~ D 153393 TTTAGGGCTTAAAAGACAACCTTCTTGCTTCTGGGACATCCAGCCTGACAGCCACAAAC 153334 153273 AGGAACGGGAGATGAAGTATTCTCGAGCTCTATACCTGGCCCTTCTGAAGTGACCACCTCC 153214 DD 153153 GTCTGAAATTTCAATTTCTGGAAAATAATCACCAACATGAAAGAGCATTGTTACAGTT 153094 87758. .93985 /note="assembly_fragment clone_end:T7 vector_side:left" 94086. .100964 2355 2415 2416 ACTCTTCCATCCACATCCTTGCTATTTACTGCCAAAGAAGACACAAAGCATTGTTGCACT 2475 2476 GTCCTGAAATTTCAATTTCTGGAAAATAA-CACCAACATGAAAGAGCATTGTTTACGATT 2534 2236 TTGAGGGCTTAAAAGACAACCTTCTTGCTTCTGGGACATCCAGCCTGACAGCCACCAAAC 2295 2356 AGGAACGGGAGATGAAGTATTCTCGAGCTCTATACCTGGCCCTTCTGAAGTGACCACTCC 2296 AGTTGCATCGTCCAAGAATCACGAGAATCTGCCTCAGGGACTTGATATTTTGTATGGAAC Length 190782; Indels Score 294.6; DB 2; Pred. No. 3.1e-66; 0; Mismatches 4; 37030. .48911 /note-"assembly_fragment" 49012. .57744 /note-"assembly_fragment" 57845. .68839 68940. .77568 /note="assembly_fragment" 77669. .8765714910 'note="assembly_fragment" 15011. .26140 /note="assembly_fragment" 26241. .36929 /note="assembly_fragment" 37030. .48911 note-"assembly_fragment" 77669. .87657 /note="assembly_fragment" 87758. .93985 /note="assembly_fragment" 101065, .107297 /note="assembly_fragment" 107398, .113948 Search completed: February 17, 2003, 02:40:41 Job time : 9051 secs 190782
 /organism="Homo sapiens" /db_xref="taxon:9606" Db 153093 AGAAACTTTATTAACTCTTACCTAT 153069 /clone="RP11-802C10" 2535 AG-AACTTTATTAACTCTTACCTAT 2558 11.5%; 98.2%; Query Match
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Description	227	21 H.sapie	AC017007 Homo sapi	OHOH 6	2752 Homo	Sequenc	59 Sequenc	Ja Human I	Mus	Homo sapi	AP001096 Homo sapi	AC007996 Homo sapi	AC125091 Mis miscii	AC016839 Homo sapi	AC118057 Homo sapi	AC125105 Mus muscu	ACIZ//67 Rattus no	AY069807 Drosophil	L06861 Drosophila	I23459 Sequence 1	duence	Kattus Homo ga	AC125105 Mus muscu	Rattu		Kattu	Human D	Mus mu	Mus	ALSS3067 Mus muscu		Drose		Drosophi	528 Dro	34 Sequence	37077 Human D	364
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181227 2556 bp Sequence 1 from patent US 5710025. 181227 181227.1 GI:3209517 Unknown. LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 1 181227

PAT 10-JUN-1998

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ALIGNMENTS

W.W. M.Wown.
Unclassified.
E 1 (bases 1 to 2556)
& Dikstein,R. and Tjian,R.
Cell-type specific transcription factor
(AL Patent: US 5710025-A 1 20-JAN-1998;
Location/Qualifiers

REFERENCE AUTHORS TITLE JOURNAL FEATURES

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